

PATENT
ATTORNEY DOCKET NO. 06132/047002

Certificate of Mailing	
Date of Deposit: <u>June 15, 2001</u>	Label Number: <u>EL509219211US</u>
I hereby certify under 37 C.F.R. § 1.8(a) that this correspondence is being deposited with the United States Postal Service as Express Mail Post Office to Addressee with sufficient postage on the date indicated above and is addressed to: BOX PATENT APPLICATION, Assistant Commissioner for Patents, Washington, D.C. 20231.	
<u>Guy Beardsley</u>	<u>Guy Beardsley</u>
Printed name of person mailing correspondence	Signature of person mailing correspondence

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant:	Harold Kleanthous et al.	Art Unit:	Not Yet Assigned
Serial No.:	Not Yet Assigned	Examiner:	Not Yet Assigned
Filed:	June 15, 2001	Customer No.:	21559
Title:	Identification of Polynucleotides Encoding Novel Helicobacter Polypeptides in the Helicobacter Genome		

Assistant Commissioner For Patents
Washington, D.C. 20231

STATEMENT UNDER 37 C.F.R. § 1.821

As part of the patent application filed herewith, enclosed is a sequence listing in accordance with the requirements of 37 C.F.R. §§ 1.821 through 1.825 and consisting of 883 pages.

As required by 37 C.F.R. § 1.821(c), the sequence listing appears as a separate part of the application and is found after the Combined Declaration and Power of Attorney. Each sequence in the application appears separately in the sequence listing. And each sequence in the sequence listing is assigned a separate sequence identifier.

06132/047002

As required by 37 C.F.R. § 1.821(d), the sequence identifiers are used throughout the application description and claims to refer to their respective sequences.

As required by 37 C.F.R. § 1.821(e), enclosed is a diskette containing a copy of the sequence listing in computer readable form.

As required by 37 C.F.R. § 1.821(f), I hereby state that the contents of the computer readable form are the same as the contents of the paper copy.

As required by 37 C.F.R. § 1.821(g), I hereby state that this submission contains no new matter.

If there are any charges, or any credits, please apply them to Deposit Account No. 03-2095.

Respectfully submitted,

Date: June 15, 2001

Susan M. Michaud
Susan M. Michaud, Ph.D.
Reg. No. 42,885

Clark & Elbing LLP
176 Federal Street
Boston, MA 02110
Telephone: 617-428-0200
Facsimile: 617-428-7045
F:\06132\06132.047002 Sequence Statement.wpd



21559

PATENT TRADEMARK OFFICE

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Kleanthous, Harold
Al-Garawi, Amal
Miller, Charles
Tomb, Jean Francois
Oomen, Raymond P.
- (ii) TITLE OF THE INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES ENCODING
NOVEL HELICOBACTER POLYPEPTIDES IN THE HELICOBACTER GENOME
- (iii) NUMBER OF SEQUENCES: 638
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Clark & Elbing LLP
(B) STREET: 176 Federal Street
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02110
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Clark, Paul T.
(B) REGISTRATION NUMBER: 30,162
(C) REFERENCE/DOCKET NUMBER: 06132/047001
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 617-428-0200
(B) TELEFAX: 617-428-7045
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1613 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 64...1551

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TAAGAAAAAC	CGCTAGAGTG	CAATACAATT	CTTGAAAGAT	ATGAAATTAA	AAAAGGAGAC	60
TTT	ATG	TTA	AAA	ATC	AAA	108
Met	Leu	Lys	Ile	Lys	Leu	
1			5		10	15
GCT	GAA	TGC	AGT	TTA	GTT	156
Ala	Glu	Cys	Ser	Leu	Val	
			20		25	30
TGG	GTC	AAA	AAT	AAA	GAG	204
Trp	Val	Lys	Asn	Lys	Glu	
		35			40	45
GGC	GTA	TTT	TTA	GAC	CAA	252
Gly	Val	Phe	Leu	Asp	Gln	
		50			55	60
GAA	GAT	GAT	GTG	CAT	TTA	300
Glu	Asp	Asp	Val	His	Leu	
		65			70	75
ACC	CTT	AAA	AAA	CTC	GCT	348
Thr	Leu	Lys	Lys	Leu	Ala	
				85		90
TGT	GGT	GCA	CAT	TCT	AAA	396
Cys	Gly	Ala	His	Ser	Lys	
			100		105	110
CTG	TTT	TTG	GGC	TTG	AAA	444
Leu	Phe	Leu	Gly	Leu	Lys	
		115			120	125
TCC	AAC	AAA	AAA	GAA	AGC	492
Ser	Asn	Lys	Lys	Glu	Ser	
		130			135	140
TTG	CAC	AAA	CCT	TGC	GAA	540
Leu	His	Lys	Pro	Cys	Glu	
		145			150	155
GCT	AAA	GAA	GCG	TTA	AAA	588
Ala	Lys	Glu	Ala	Leu	Lys	
				165		170
ATC	GTT	AAA	GAT	CTA	GTC	636
Ile	Val	Lys	Asp	Leu	Val	
				180		185

TAT Tyr	ATG Met	GCT Ala	GAA Glu 195	GTG Val	GCG Ala	CAA Gln	AAA Lys	GTG Val 200	GCT Ala	AAA Lys	GAA Glu	AAC Asn 205	CAT His	TTA Leu	GAA Glu	684
ATC Ile	CAT His	GTT Val 210	CAT His	GAT Asp	GAA Glu	AAA Lys	TTT Phe 215	TTA Leu	GAA Glu	GAA Glu	AAG Lys 220	AAA Lys	ATG Met	AAC Asn	GCC Ala	732
TTT Phe	TTA Leu 225	GCG Ala	GTC Val	AAT Asn	AAA Lys	GCC Ala 230	TCT Ser	CTT Leu	AGC Ser	GTC Val	AAT Asn 235	CCT Pro	CCT Pro	CGC Arg	TTG Leu	780
ATC Ile 240	CAT His	TTA Leu	GTC Val	TAT Tyr 245	AAG Lys	CCT Pro	AAA Lys	AAA Lys	GCG Ala	AAG Lys 250	AAA Lys	AAA Lys	ATC Ile	GCT Ala	TTA Leu 255	828
GTG Val	GGT Gly	AAG Lys	GGC Gly	TTG Leu 260	ACT Thr	TAT Tyr	GAT Asp	TGT Cys 265	GGG Gly	GGT Gly	TTG Leu	AGC Ser	TTG Leu	AAA Lys 270	CCG Pro	876
GCC Ala	GAT Asp	TAC Tyr 275	ATG Met	GTT Val	ACT Thr	ATG Met	AAA Lys	GCG Ala 280	GAT Asp	AAA Lys	GGC Gly	GGT Gly 285	GGC Gly	TCT Ser	GCG Ala	924
GTG Val	ATT Ile 290	GGG Gly	CTT Leu	TTA Leu	AAC Asn	GCA Ala	TTA Leu 295	GCC Ala	AAA Lys	CTA Leu	GGC Gly 300	GTG Val	GAG Glu	GCT Ala	GAA Glu	972
GTG Val	CAT His 305	GGC Gly	ATT Ile	ATT Ile	GGG Gly	GCT Ala 310	ACA Thr	GAA Glu	AAC Asn	ATG Met 315	ATA Ile	GGC Gly	CCA Pro	GCC Ala	GCT Ala	1020
TAT Tyr 320	AAA Lys	CCA Pro	GAT Asp	GAT Asp	ATT Ile 325	TTG Leu	ATC Ile	TCC Ser	AAA Lys	GAA Glu 330	GGC Gly	AAG Lys	AGC Ser	ATA Ile	GAG Glu 335	1068
GTC Val	CGT Arg	AAT Asn	ACC Thr 340	GAC Asp	GCT Ala	GAG Glu	GGG Gly	CGT Arg 345	TTG Leu	GTT Val	TTA Leu	GCG Ala	GAT Asp	TGT Cys 350	TTG Leu	1116
AGC Ser	TAC Tyr	GCT Ala	CAA Gln 355	GAT Asp	TTA Leu	AAC Asn	CCT Pro	GAT Asp 360	GTG Val	ATC Ile	GTG Val	GAT Asp	TTT Phe 365	GCG Ala	ACC Thr	1164
CTT Leu	ACT Thr 370	GGG Gly	GCA Ala	TGC Cys	GTT Val	GTA Val	GGC Gly 375	TTA Leu	GGC Gly	GAA Glu	TTC Phe	ACT Thr 380	TCA Ser	GCG Ala	ATC Ile	1212
ATG Met	GGG Gly 385	CAT His	AAT Asn	GAA Glu	GAG Glu	TTA Leu 390	AAA Lys	AAC Asn	CTC Leu	TTT Phe 395	GAA Glu	ACT Thr 395	TCA Ser	GGG Gly	TTA Leu	1260
GAA Glu 400	TCC Ser	GGC Gly	GAA Glu	TTA Leu	TTA Leu 405	GCC Ala	AAA Lys	CTC Leu	CCC Pro	TTT Phe 410	AAC Asn	CGC Arg	CAT His	TTA Leu	AAG Lys 415	1308
AAA Lys	TTG Leu	ATT Ile	GAA Glu	TCT Ser	AAA Lys	ATC Ile	GCT Ala	GAT Asp	GTG Val	TGC Cys	AAT Asn	ATT Ile	TCT Ser	TCT Ser	TCA Ser	1356

	420		425		430	
CGC TAT GGC GGT GCG ATC ACA GCG GGC TTG TTT TTA AAT GAA TTT ATT						1404
Arg Tyr Gly Gly Ala Ile Thr Ala Gly Leu Phe Leu Asn Glu Phe Ile						
	435		440		445	
AGA GAT GAG TTT AAG GAT AAG TGG CTA CAC ATT GAC ATT GCA GGC CCT						1452
Arg Asp Glu Phe Lys Asp Lys Trp Leu His Ile Asp Ile Ala Gly Pro						
	450		455		460	
GCT TAT GTG GAA AAA GAA TGG GAT GTG AAT AGC TTT GGA GCG AGT GGG						1500
Ala Tyr Val Glu Lys Glu Trp Asp Val Asn Ser Phe Gly Ala Ser Gly						
	465		470		475	
GCT GGC GTG AGA GCT TGC ACA GCT TTT GTG GAA GAG CTT TTG AAA AAG						1548
Ala Gly Val Arg Ala Cys Thr Ala Phe Val Glu Glu Leu Leu Lys Lys						
	480		485		490	495
GCT TGAAATGGGC TTGTCTGTAG GCATTGTGGG TTTGCCTAAT GTGGGCAAAT CCAGCA						1607
Ala						
CCTTTA						1613

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Leu	Lys	Ile	Lys	Leu	Glu	Lys	Thr	Thr	Phe	Glu	Asn	Ala	Lys	Ala
1				5					10					15	
Glu	Cys	Ser	Leu	Val	Phe	Ile	Ile	Asn	Lys	Asp	Phe	Ser	His	Ala	Trp
			20					25					30		
Val	Lys	Asn	Lys	Glu	Leu	Leu	Glu	Thr	Phe	Lys	Tyr	Glu	Gly	Glu	Gly
			35				40					45			
Val	Phe	Leu	Asp	Gln	Glu	Asn	Lys	Ile	Leu	Tyr	Ala	Gly	Val	Lys	Glu
	50					55					60				
Asp	Asp	Val	His	Leu	Leu	Arg	Glu	Ser	Ala	Cys	Leu	Ala	Val	Arg	Thr
	65				70					75				80	
Leu	Lys	Lys	Leu	Ala	Phe	Lys	Ser	Val	Lys	Val	Gly	Val	Tyr	Thr	Cys
			85					90					95		
Gly	Ala	His	Ser	Lys	Asp	Asn	Ala	Leu	Leu	Glu	Asn	Leu	Lys	Ala	Leu
			100					105					110		
Phe	Leu	Gly	Leu	Lys	Leu	Gly	Leu	Tyr	Glu	Tyr	Asp	Thr	Phe	Lys	Ser
		115				120						125			
Asn	Lys	Lys	Glu	Ser	Val	Leu	Lys	Glu	Ala	Ile	Val	Ala	Leu	Glu	Leu
	130					135					140				
His	Lys	Pro	Cys	Glu	Lys	Thr	Cys	Ala	Asn	Ser	Leu	Glu	Lys	Ser	Ala
	145				150					155				160	
Lys	Glu	Ala	Leu	Lys	Tyr	Ala	Glu	Ile	Met	Thr	Glu	Ser	Leu	Asn	Ile
			165					170						175	

GGCGAAATCG GGTTAATTTT AGCAGGGATT GCCAGCTATA CCGGTCAT ATG CAT TTA	57
Met His Leu	
1	
GGG TTA GCC ATT TTA GTC GCA GGG ATT GGG GGC TTT GTG GGG GAT CAG	105
Gly Leu Ala Ile Leu Val Ala Gly Ile Gly Gly Phe Val Gly Asp Gln	
5 10 15	
ATC TAT TTT TAC ATC GGC CGC ACC AAT AAA GCT TAC ATC CAA AAA AAG	153
Ile Tyr Phe Tyr Ile Gly Arg Thr Asn Lys Ala Tyr Ile Gln Lys Lys	
20 25 30 35	
CTA GAA AAA CAA CGC CGA AAA CTA GCC CTA GCC CAT TTA TTG TTG CAA	201
Leu Glu Lys Gln Arg Arg Lys Leu Ala Leu Ala His Leu Leu Leu Gln	
40 45 50	
AAA CAC GGC TGG TTT ATC ATT TTT ATC CAA CGC TAT ATG TAT GGC ATG	249
Lys His Gly Trp Phe Ile Ile Phe Ile Gln Arg Tyr Met Tyr Gly Met	
55 60 65	
CGC ACC ATC ATT CCC ATT AGC ATA GGT CTC ACG CGT TAT AGC GCT TTA	297
Arg Thr Ile Ile Pro Ile Ser Ile Gly Leu Thr Arg Tyr Ser Ala Leu	
70 75 80	
AAA TTC GCT ATC ATC AAT CTC ATT AGC GCG ATG GTG TGG GCG AGC ATT	345
Lys Phe Ala Ile Ile Asn Leu Ile Ser Ala Met Val Trp Ala Ser Ile	
85 90 95	
ACC ATT ATT CTA GCG TGG TAT TTA GGA GAA GAG TTA TTG CAT GCG TTA	393
Thr Ile Ile Leu Ala Trp Tyr Leu Gly Glu Glu Leu Leu His Ala Leu	
100 105 110 115	
GGG TGG CTT AAA AAA CAC CCT TAT GCG CTA ATA TTA CTA TTA GTA TCT	441
Gly Trp Leu Lys Lys His Pro Tyr Ala Leu Ile Leu Leu Leu Val Ser	
120 125 130	
TTC TTG GCG TTA GTG CTG TGG TAT TTC CAA TAC TAT AGT AAG AAA AAC	489
Phe Leu Ala Leu Val Leu Trp Tyr Phe Gln Tyr Tyr Ser Lys Lys Asn	
135 140 145	
CGC TAGAGTGCAA TACAATTCTT GAAAGATATG AAATTAAAAA AGGAGACTTT ATGTTA	548
Arg	
AAAATCAAAT TA	560

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met His Leu Gly Leu Ala Ile Leu Val Ala Gly Ile Gly Gly Phe Val
 1 5 10 15
 Gly Asp Gln Ile Tyr Phe Tyr Ile Gly Arg Thr Asn Lys Ala Tyr Ile
 20 25 30
 Gln Lys Lys Leu Glu Lys Gln Arg Arg Lys Leu Ala Leu Ala His Leu
 35 40 45
 Leu Leu Gln Lys His Gly Trp Phe Ile Ile Phe Ile Gln Arg Tyr Met
 50 55 60
 Tyr Gly Met Arg Thr Ile Ile Pro Ile Ser Ile Gly Leu Thr Arg Tyr
 65 70 75 80
 Ser Ala Leu Lys Phe Ala Ile Ile Asn Leu Ile Ser Ala Met Val Trp
 85 90 95
 Ala Ser Ile Thr Ile Ile Leu Ala Trp Tyr Leu Gly Glu Glu Leu Leu
 100 105 110
 His Ala Leu Gly Trp Leu Lys Lys His Pro Tyr Ala Leu Ile Leu Leu
 115 120 125
 Leu Val Ser Phe Leu Ala Leu Val Leu Trp Tyr Phe Gln Tyr Tyr Ser
 130 135 140
 Lys Lys Asn Arg
 145

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 609 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 61...600
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TAAAAACGCT ATAATAAATC AAAATTCTAC AACCAATCCG TTATATTAAA GGAAATCAAA 60
 ATG AAT GAA ACG CTC AAA GAA GAA CTT TTA CAA AGC ATC AGA GAA GTG 108
 Met Asn Glu Thr Leu Lys Glu Glu Leu Leu Gln Ser Ile Arg Glu Val
 1 5 10 15
 AAA GAC TAC CCT AAA AAA GGG ATT TTA TTC AAA GAC ATT ACC ACG CTA 156
 Lys Asp Tyr Pro Lys Lys Gly Ile Leu Phe Lys Asp Ile Thr Thr Leu
 20 25 30
 CTC AAC TAC CCT AAA CTC TTT AAC AAA CTC ATT GAC ACG CTC AAA AAA 204
 Leu Asn Tyr Pro Lys Leu Phe Asn Lys Leu Ile Asp Thr Leu Lys Lys
 35 40 45
 CGC TAT CTC GCT CTC AAT ATA GAC TTT ATC GTG GGC ATT GAA GCG AGA 252
 Arg Tyr Leu Ala Leu Asn Ile Asp Phe Ile Val Gly Ile Glu Ala Arg
 50 55 60
 GGG TTT ATT TTA GGC TCT GCT CTC GCT TAT GCG CTT GGG GTG GGT TTT 300
 Gly Phe Ile Leu Gly Ser Ala Leu Ala Tyr Ala Leu Gly Val Gly Phe

65	70	75	80	
GTG CCT GTG AGG AAA AAG GGC AAA CTC CCC GCA CAC ACC CTA TCT CAA				348
Val Pro Val Arg Lys Lys Gly Lys Leu Pro Ala His Thr Leu Ser Gln				
	85	90	95	
AGC TAC AGC CTA GAA TAC GGG AGC GAC AGC ATA GAA ATC CAC TCC GAC				396
Ser Tyr Ser Leu Glu Tyr Gly Ser Asp Ser Ile Glu Ile His Ser Asp				
	100	105	110	
GCT TTT AGG GGA ATT AAG GGG GTA AGG GTG GTG TTG ATT GAT GAT TTA				444
Ala Phe Arg Gly Ile Lys Gly Val Arg Val Val Leu Ile Asp Asp Leu				
	115	120	125	
TTA GCC ACT GGA GGC ACA GCT TTA GCG AGC CTT GAG CTT ATC AAA GCC				492
Leu Ala Thr Gly Gly Thr Ala Leu Ala Ser Leu Glu Leu Ile Lys Ala				
	130	135	140	
CTA CAA GCC GAA TGC ATA GAA GCA TGC TTT TTG ATA GGG TTA AAA GAA				540
Leu Gln Ala Glu Cys Ile Glu Ala Cys Phe Leu Ile Gly Leu Lys Glu				
	145	150	155	160
TTA CCG GGT ATC CAA CTT TTA GAA GAA CGC GTG AAA ACC TTT TGT TTG				588
Leu Pro Gly Ile Gln Leu Leu Glu Glu Arg Val Lys Thr Phe Cys Leu				
	165	170	175	
TTA GAG TTA GAA TAAGGGTGA				609
Leu Glu Leu Glu				
	180			

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asn	Glu	Thr	Leu	Lys	Glu	Glu	Leu	Leu	Gln	Ser	Ile	Arg	Glu	Val
1				5					10					15	
Lys	Asp	Tyr	Pro	Lys	Lys	Gly	Ile	Leu	Phe	Lys	Asp	Ile	Thr	Thr	Leu
			20					25					30		
Leu	Asn	Tyr	Pro	Lys	Leu	Phe	Asn	Lys	Leu	Ile	Asp	Thr	Leu	Lys	Lys
			35				40					45			
Arg	Tyr	Leu	Ala	Leu	Asn	Ile	Asp	Phe	Ile	Val	Gly	Ile	Glu	Ala	Arg
			50			55				60					
Gly	Phe	Ile	Leu	Gly	Ser	Ala	Leu	Ala	Tyr	Ala	Leu	Gly	Val	Gly	Phe
65					70				75					80	
Val	Pro	Val	Arg	Lys	Lys	Gly	Lys	Leu	Pro	Ala	His	Thr	Leu	Ser	Gln
			85					90					95		
Ser	Tyr	Ser	Leu	Glu	Tyr	Gly	Ser	Asp	Ser	Ile	Glu	Ile	His	Ser	Asp
			100					105					110		

Ala Phe Arg Gly Ile Lys Gly Val Arg Val Val Leu Ile Asp Asp Leu
115 120 125
Leu Ala Thr Gly Gly Thr Ala Leu Ala Ser Leu Glu Leu Ile Lys Ala
130 135 140
Leu Gln Ala Glu Cys Ile Glu Ala Cys Phe Leu Ile Gly Leu Lys Glu
145 150 155 160
Leu Pro Gly Ile Gln Leu Leu Glu Glu Arg Val Lys Thr Phe Cys Leu
165 170 175
Leu Glu Leu Glu
180

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 28...357
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTTCGCTAAA AAGGATATTT TAACAGA ATG TTT ACC CAA TGG TTT ATT CTC ACT	54
Met Phe Thr Gln Trp Phe Ile Leu Thr	
1 5	
ATC GCT ATT GTT TTT ATC CTT TAT ATG GGT GTG CGC ACT TTC TTT TTT	102
Ile Ala Ile Val Phe Ile Leu Tyr Met Gly Val Arg Thr Phe Phe Phe	
10 15 20 25	
AAA ACC GTG GCT AAA CGG CAA GAA CGC ACC AAC GCA TCC ATG AAG CTC	150
Lys Thr Val Ala Lys Arg Gln Glu Arg Thr Asn Ala Ser Met Lys Leu	
30 35 40	
ACC TTA CAA GAA GCT GAA ATT TTG ATC CAA AAA CAC CAG TTG CAA CTC	198
Thr Leu Gln Glu Ala Glu Ile Leu Ile Gln Lys His Gln Leu Gln Leu	
45 50 55	
CAA AGG GCT TTG GGC AAT ATT GAT ATT CTC ACC CAA GAA ATG AGC TCG	246
Gln Arg Ala Leu Gly Asn Ile Asp Ile Leu Thr Gln Glu Met Ser Ser	
60 65 70	
TTA AAA ACA GAA CTA AAA GCC CTT AAA CAG CGC AAC TCT GAA TAC AAA	294
Leu Lys Thr Glu Leu Lys Ala Leu Lys Gln Arg Asn Ser Glu Tyr Lys	
75 80 85	
GGC GAA TCG GAT AAA TAT AAA AAT CGT ATT AAA GAA TTG GAG CAA AAA	342
Gly Glu Ser Asp Lys Tyr Lys Asn Arg Ile Lys Glu Leu Glu Gln Lys	
90 95 100 105	
ATA GAA GCT CTC CTT TAAAAACGCT ATAATAA	374

Ile Glu Ala Leu Leu
110

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Phe	Thr	Gln	Trp	Phe	Ile	Leu	Thr	Ile	Ala	Ile	Val	Phe	Ile	Leu	
1				5				10						15		
Tyr	Met	Gly	Val	Arg	Thr	Phe	Phe	Phe	Lys	Thr	Val	Ala	Lys	Arg	Gln	
			20					25					30			
Glu	Arg	Thr	Asn	Ala	Ser	Met	Lys	Leu	Thr	Leu	Gln	Glu	Ala	Glu	Ile	
		35					40					45				
Leu	Ile	Gln	Lys	His	Gln	Leu	Gln	Leu	Gln	Arg	Ala	Leu	Gly	Asn	Ile	
	50				55					60						
Asp	Ile	Leu	Thr	Gln	Glu	Met	Ser	Ser	Leu	Lys	Thr	Glu	Leu	Lys	Ala	
65				70				75						80		
Leu	Lys	Gln	Arg	Asn	Ser	Glu	Tyr	Lys	Gly	Glu	Ser	Asp	Lys	Tyr	Lys	
			85					90					95			
Asn	Arg	Ile	Lys	Glu	Leu	Glu	Gln	Lys	Ile	Glu	Ala	Leu	Leu			
			100				105						110			

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 78...728
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAAAAAGAAA	ACGCAACGCA	TTAAGGTTTT	TTGTGCAATT	TTTTGATTTC	TCTTTAGAAA	60						
GTTTTATTAC	CACCTTA	ATG AAA	ATC CTA	GCC CTT	TTA ATC	GCT ATC	ATA	110				
		Met	Lys	Ile	Leu	Ala	Leu	Ile	Ala	Ile	Ile	
		1			5				10			
GGG CAT	GAG ATC	ATG CAT	GGC TTG	AGC GCG	TTT TTA	TTT GGG	GAT AGG	158				
Gly His	Glu Ile	Met His	Gly Leu	Ser Ala	Phe Leu	Phe Gly	Asp Arg					
	15		20			25						

AGC Ser	ACT Thr	AAA Lys	GAC Asp	GCT Ala	AGG Arg	CGT Arg	TTG Leu	AGT Ser	TTA Leu	AAC Asn	Pro	CCT Ile	ATC Arg	AGG His	CAT Leu	TTA	206
303540																	
GAC Asp	ATG Met	ATG Met	GGT Gly	TCG Ser	GTG Val	CTT Leu	TTA Leu	CCG Pro	GCT Ala	TTA Leu	TTA Leu	CTC Leu	ATT Ile	TTT Phe	CAA Gln		254
455055																	
GCC Ala	CCT Pro	TTT Phe	TTG Leu	TTT Phe	GGG Gly	TGG Trp	GCC Ala	AAA Lys	CCC Pro	GTG Val	CCT Pro	GTT Val	GAT Asp	ATG Met	CGC Arg		302
60657075																	
TAC Tyr	ATT Ile	GTC Val	TCT Ser	CAA Gln	AAA Lys	GGC Gly	TCT Ser	CTA Leu	GCA Ala	TGC Cys	GTA Val	GTG Val	GTG Val	AGT Ser	TTA Leu		350
808590																	
GCC Ala	GGG Gly	GTG Val	GCT Ala	TAT Tyr	AAT Asn	TTC Phe	ACT Thr	CTG Leu	GCC Ala	GTT Val	CTG Leu	CTC Leu	GCT Ala	TTC Phe	ATC Ile		398
95100105																	
ACG Thr	CAT His	TGG Trp	AGC Ser	TTC Phe	CAA Gln	CAA Gln	CTA Leu	GGG Gly	ATC Ile	AAC Asn	GCT Ala	TTA Leu	AGC Ser	ATT Ile	GAT Asp		446
110115120																	
GAA Glu	TTG Leu	AAT Asn	CTT Leu	TAT Tyr	CAG Gln	CTC Leu	GCT Ala	TTA Leu	GTA Val	ACC Thr	TTT Phe	CTC Leu	ATT Ile	CAA Gln	GGC Gly		494
125130135																	
ATT Ile	CTT Leu	TAT Tyr	AAT Asn	CTT Leu	GTC Val	TTA Leu	GGC Gly	GTT Val	TTC Phe	AAT Asn	AGC Ser	CTC Leu	CCT Pro	ATC Ile	CCG Pro		542
140145150155																	
CCC Pro	TTA Leu	GAC Asp	GGC Gly	TCC Ser	AAA Lys	GCG Ala	TTA Leu	GGC Gly	TTT Phe	TTA Leu	GCG Ala	TTG Leu	CAT His	TTT Phe	AAA Lys		590
160165170																	
AGT Ser	GCG Ala	TTT Phe	TTA Leu	TTG Leu	GAA Glu	TGG Trp	TTT Phe	TCT Ser	AAA Lys	ATG Met	GAA Glu	CGC Arg	TAC Tyr	GGC Gly	TTG Leu		638
175180185																	
TTG Leu	GTA Val	GTG Val	TTT Phe	ATT Ile	TTT Phe	TTG Leu	TTT Phe	ATC Ile	CCC Pro	CCT Pro	TTA Leu	TCG Ser	GAG Glu	TTT Phe	TTT Phe		686
190195200																	
ATC Ile	CAT His	GCG Ala	CCC Pro	ACA Thr	AGA Arg	TTT Phe	TTA Leu	TTT Phe	TCT Ser	TTA Leu	CTC Leu	CTC Leu	TCT Ser	TAATCTTTT			737
205210215																	
ATCAAGGAGA GTTTATGAAT AAGCTCTTAA AGTTTTCTCA A																	
778																	

(2) INFORMATION FOR SEQ ID NO:10:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Lys Ile Leu Ala Leu Leu Ile Ala Ile Ile Gly His Glu Ile Met
1 5 10 15
His Gly Leu Ser Ala Phe Leu Phe Gly Asp Arg Ser Thr Lys Asp Ala
20 25 30
Arg Arg Leu Ser Leu Asn Pro Ile Arg His Leu Asp Met Met Gly Ser
35 40 45
Val Leu Leu Pro Ala Leu Leu Ile Phe Gln Ala Pro Phe Leu Phe
50 55 60
Gly Trp Ala Lys Pro Val Pro Val Asp Met Arg Tyr Ile Val Ser Gln
65 70 75 80
Lys Gly Ser Leu Ala Cys Val Val Val Ser Leu Ala Gly Val Ala Tyr
85 90 95
Asn Phe Thr Leu Ala Val Leu Leu Ala Phe Ile Thr His Trp Ser Phe
100 105 110
Gln Gln Leu Gly Ile Asn Ala Leu Ser Ile Asp Glu Leu Asn Leu Tyr
115 120 125
Gln Leu Ala Leu Val Thr Phe Leu Ile Gln Gly Ile Leu Tyr Asn Leu
130 135 140
Val Leu Gly Val Phe Asn Ser Leu Pro Ile Pro Pro Leu Asp Gly Ser
145 150 155 160
Lys Ala Leu Gly Phe Leu Ala Leu His Phe Lys Ser Ala Phe Leu Leu
165 170 175
Glu Trp Phe Ser Lys Met Glu Arg Tyr Gly Leu Leu Val Val Phe Ile
180 185 190
Phe Leu Phe Ile Pro Pro Leu Ser Glu Phe Phe Ile His Ala Pro Thr
195 200 205
Arg Phe Leu Phe Ser Leu Leu Ser
210 215

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 70...336
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CATCAGATAT TATCCAAGCG CCTTTTAAAA TCTTGCGCCG TATTTTCACA CCTATTGACA 60
TCATCGTGG ATG AAG TCA AAA AAA ACA TTG ATT CAA AAA GGA AGT AAA ATG 111
Met Lys Ser Lys Lys Thr Leu Ile Gln Lys Gly Ser Lys Met
1 5 10
ACG CTC AAT GAA GCC ATT AAA GAC AAA GTT TAT GAA ATC GTA GAA ATC 159
Thr Leu Asn Glu Ala Ile Lys Asp Lys Val Tyr Glu Ile Val Glu Ile

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCCAGTTA ATTCCATGGT TTCATAAGTG ATTTTTTGGG GCTGT ATG AGG AGC TGT	57
Met Arg Ser Cys	
1	
TTG TTT TTG AAA ACT AAT TCG GTT TTA TCC ATT TTA ATG GGC GAT AAG	105
Leu Phe Leu Lys Thr Asn Ser Val Leu Ser Ile Leu Met Gly Asp Lys	
5 10 15 20	
CCA TCA TTA AAA ACG ACT GAA GGC TTC ATC AAA GTG GCT TTA ATT ACA	153
Pro Ser Leu Lys Thr Thr Glu Gly Phe Ile Lys Val Ala Leu Ile Thr	
25 30 35	
GAA TTT TTT AAA AGC GAT GGG ACA AAC TCG CTA GGA GTG AAA TTG GCT	201
Glu Phe Phe Lys Ser Asp Gly Thr Asn Ser Leu Gly Val Lys Leu Ala	
40 45 50	
TTG ATT GAA GCG TTA TCA ATC TTA AAG CTA GCG AAT TGG ATC TTA TCA	249
Leu Ile Glu Ala Leu Ser Ile Leu Lys Leu Ala Asn Trp Ile Leu Ser	
55 60 65	
AAA ATC CAT GTT TTT AAA TTT TTT TGC GAT TGG CGT TGG AAA AGA GGC	297
Lys Ile His Val Phe Lys Phe Phe Cys Asp Trp Arg Trp Lys Arg Gly	
70 75 80	
TTT AAA AAC GCC AGG CTT TTC ATT ACA GAA GTG TTA ATT TTT AAT TCT	345
Phe Lys Asn Ala Arg Leu Phe Ile Thr Glu Val Leu Ile Phe Asn Ser	
85 90 95 100	
ATG GTT TTT AAA TCG GTT AGC CCT TGC AAA TAAATTGCAG CGCTGGGTTC GAT	398
Met Val Phe Lys Ser Val Ser Pro Cys Lys	
105 110	
TAAGGGCTTG ACAATCAAAT TAAACGCCAT TTCCTAGCT TTGGGTGAAT AG	450

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Arg Ser Cys Leu Phe Leu Lys Thr Asn Ser Val Leu Ser Ile Leu	
1 5 10 15	
Met Gly Asp Lys Pro Ser Leu Lys Thr Thr Glu Gly Phe Ile Lys Val	
20 25 30	
Ala Leu Ile Thr Glu Phe Phe Lys Ser Asp Gly Thr Asn Ser Leu Gly	
35 40 45	
Val Lys Leu Ala Leu Ile Glu Ala Leu Ser Ile Leu Lys Leu Ala Asn	

AATGCGTGAG ATTATTTCTG ATGGGAATGA ATTAGTCGCT AAAGCGGCGA TTGAA

450

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Met Ala Lys Met Ser Ala Pro Asp Gly Val Ala Val Trp Val Asn Glu
 1           5           10           15
Asp Arg Cys Lys Gly Cys Asp Ile Cys Val Ser Val Cys Pro Ala Gly
          20           25           30
Val Leu Gly Met Gly Ile Glu Lys Glu Arg Val Leu Gly Lys Val Ala
          35           40           45
Lys Val Ala Tyr Pro Glu Ser Cys Ile Gly Cys Val Gln Cys Glu Leu
          50           55           60
His Cys Pro Asp Phe Ala Ile Tyr Val Ala Asp Arg Lys Asp Phe Lys
65           70           75           80
Phe Ala Lys Val Ser Lys Glu Ala Gln Glu Arg Ser Glu Lys Val Lys
          85           90           95
Ala Asn Lys Tyr Met Leu Leu Glu Glu Thr Ile Leu Glu Gly Arg Asp
          100          105          110
Lys

```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 127...1251
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

TGTGGCTGAC AGGAAGGATT TCAAATTCGC TAAAGTTTCT AAAGAAGCCC AAGAAAGAAG      60
CGAAAAGGTT AAGGCCAATA AATACATGCT CTTAGAAGAG ACTATTTTAG AAGGGAGAGA      120
CAAATA ATG CGT GAG ATT ATT TCT GAT GGG AAT GAA TTA GTC GCT AAA      168
      Met Arg Glu Ile Ile Ser Asp Gly Asn Glu Leu Val Ala Lys
          1           5           10

GCG GCG ATT GAA GTG GGG TGT CGG TTT TTT GGG GGC TAT CCT ATC ACG      216
Ala Ala Ile Glu Val Gly Cys Arg Phe Phe Gly Gly Tyr Pro Ile Thr
15           20           25           30

```


CCA Pro	AGT Ser	TCG Ser	GAT Asp	ATT Ile 35	ATG Met	CAT His	GCG Ala	ATG Met	AGC Ser 40	GTG Val	GCT Ala	TTA Leu	CCC Pro	AAA Lys 45	TGC Cys	264
GGC Gly	GGT Gly	CAT His	TTT Phe 50	ATC Ile	CAA Gln	ATG Met	GAA Glu	GAT Asp 55	GAA Glu	ATC Ile	AGC Ser	GGG Gly	ATT Ile 60	AGC Ser	GTG Val	312
TCT Ser	TTA Leu	GGA Gly 65	GCG Ala	AGC Ser	ATG Met	AGC Ser	GGG Gly 70	ACG Thr	AAG Lys	TCT Ser	ATG Met	ACA Thr 75	GCA Ala	AGC Ser	TCT Ser	360
GGG Gly	CCT Pro 80	GGT Gly	ATT Ile	TCA Ser	TTG Leu	AAA Lys 85	GTG Val	GAG Glu	CAA Gln	ATC Ile	GGT Gly 90	TAT Tyr	TCT Ser	TTC Phe	ATG Met	408
GCG Ala 95	GAA Glu	ATC Ile	CCT Pro	TTA Leu	GTG Val 100	ATC Ile	GCT Ala	GAT Asp	GTG Val	ATG Met 105	CGT Arg	TCA Ser	GGC Gly	CCA Pro	TCA Ser 110	456
ACC Thr	GGA Gly	ATG Met	CCC Pro	ACT Thr 115	CGT Arg	GTG Val	GCT Ala	CAA Gln	GGC Gly 120	GAT Asp	GTG Val	AAT Asn	TTC Phe	TTA Leu 125	AGA Arg	504
CAC His	CCC Pro	ATA Ile	CAT His 130	GGG Gly	GAT Asp	TTT Phe	AAA Lys	GCC Ala 135	GTC Val	GCG Ala	CTC Leu	GCT Ala	CCT Pro 140	GCG Ala	AAT Asn	552
TTA Leu	GAA Glu 145	GAA Glu Ala	GCT Ala Tyr	TAC Tyr Thr	ACC Thr Glu	GAA Glu Thr	ACC Thr Val	GTT Val	CGC Arg	GCG Ala	TTC Phe	AAT Asn 155	TTG Leu	GCT Ala	GAA Glu	600
ATG Met 160	CTC Leu	ATG Met	ACT Thr	CCT Pro	GTA Val	TTC Phe	TTG Leu	CTC Leu	ATG Met	GAT Asp	GAA Glu 170	ACC Thr	GTG Val	GGG Gly	CAT His	648
ATG Met 175	TAT Tyr	GGC Gly	AAG Lys	GTG Val	CAA Gln	ATC Ile	CCA Pro	GAT Asp	TTA Leu	GAA Glu 185	GAA Glu	GTG Val	CAA Gln	AAG Lys	ATG Met 190	696
ACT Thr	ATT Ile	AAT Asn	CGT Arg	AAG Lys 195	GAA Glu	TTT Phe	CTG Leu	GGC Gly	GAT Asp 200	AAA Lys	AAA Lys	GAC Asp	TAC Tyr	AAG Lys 205	CCT Pro	744
TAT Tyr	GGG Gly	GTC Val	GCA Ala	CAA Gln	GAC Asp	GAG Glu	CCG Pro	GCT Ala 215	GTT Val	TTG Leu	AAC Asn	CCT Pro	TTC Phe 220	TTT Phe	AAA Lys	792
GGT Gly	TAT Tyr	CGC Arg	TAC Tyr	CAT His	GTT Val	TCA Ser	GGC Gly 230	TTG Leu	CAC His	CAT His	GGG Gly	CCT Pro 235	ATT Ile	GGC Gly	TTT Phe	840
CCT Pro 240	ACT Thr	GAA Glu	GAC Asp	GCT Ala	AAA Lys	ATT Ile 245	GGT Gly	GGG Gly	GAT Asp	TTG Leu	ATT Ile 250	GAC Asp	AGA Arg	TTA Leu	TTT Phe	888
AAT Asn	AAG Lys	ATT Ile	GAA Glu	TCC Ser	AAG Lys	CAA Gln	GAC Asp	ATT Ile	ATC Ile	AAC Asn	GAA Glu	AAT Asn	GAG Glu	GAA Glu	ATG Met	936

TAT	TTA	GGC	TTA	AAC	CCA	AAA	CGC	ACC	ACC	AAA	AGC	GCC	ACA	GCC	CCT	104
Tyr	Leu	Gly	Leu	Asn	Pro	Lys	Arg	Thr	Thr	Lys	Ser	Ala	Thr	Ala	Pro	
			5					10					15			
ATT	AAA	ATC	ATG	TTG	ATG	CGT	TGC	GCC	CAG	CAA	AAA	ATA	CAA	GGC	GAA	152
Ile	Lys	Ile	Met	Leu	Met	Arg	Cys	Ala	Gln	Gln	Lys	Ile	Gln	Gly	Glu	
			20				25						30			
TCT	TTC	AAA	ACA	TAGCCAAAAT			AACCTTAAAA			AACGCTTT						192
Ser	Phe	Lys	Thr													
			35													

GGG Gly 25	CGT Arg	TAC Tyr	CTT Leu	AGC Ser	GAA Glu 30	TAC Tyr	CAA Gln	GAG Glu	AGC Ser	CGT Arg 35	AAA Lys	AAA Lys	GCG Ala	GGG Gly	AGT Ser 40	149
TTC Phe	TTG Leu	GAA Glu	TTG Leu	TGT Cys 45	AAA Lys	AAT Asn	AGC Ser	GAT Asp	CTA Leu 50	GCC Ala	ACA Thr	GAA Glu	GTT Val	ACC Thr 55	TTA Leu	197
CAG Gln	CCG Pro	GTA Val	GAG Glu 60	ATT Ile	TTA Leu	GGC Gly	GTG Val	GAT Asp 65	GCG Ala	GCT Ala	ATT Ile	TTG Leu	TTT Phe 70	AGC Ser	GAT Asp	245
ATT Ile	TTA Leu	GTA Val 75	GTG Val	CCT Pro	TTG Leu	GAA Glu	ATG Met 80	GGC Gly	TTG Leu	AAT Asn	TTG Leu	GAG Glu 85	TTT Phe	ATC Ile	CCC Pro	293
AAA Lys	AAG Lys 90	GGG Gly	CCG Pro	CAT His	TTT Phe	TTA Leu 95	GAG Glu	ACG Thr	ATT Ile	ACG Thr	GAT Asp 100	TTA Leu	AAA Lys	AGC Ser	GTG Val	341
GAA Glu 105	AGC Ser	CTA Leu	AAA Lys	GTA Val	GGG Gly 110	GCT Ala	TAT Tyr	AAA Lys	CAA Gln	CTA Leu 115	AAC Asn	TAT Tyr	GTC Val	TAT Tyr	GAT Asp 120	389
ACG Thr	ATT Ile	TCT Ser	CAA Gln	ACG Thr 125	CGC Arg	CAA Gln	AAG Lys	CTT Leu	TCT Ser 130	AGA Arg	GAG Glu	AAA Lys	GCG Ala	TTA Leu 135	ATC Ile	437
GGT Gly	TTT Phe	TGC Cys	GGA Gly 140	TCG Ser	CCT Pro	TGG Trp	ACT Thr	TTA Leu 145	GCG Ala	ACT Thr	TAC Tyr	ATG Met 150	ATA Ile	GAA Glu	GGC Gly	485
GAG Glu	GGG Gly 155	AGC Ser	AAA Lys	TCG Ser	TAT Tyr	GCC Ala	AAA Lys 160	AGC Ser	AAG Lys	AAA Lys	ATG Met 165	CTT Leu 165	TAT Tyr	AGC Ser	GAG Glu	533
CCT Pro	GAA Glu 170	GTT Val	TTA Leu	AAA Lys	GCG Ala	CTT Leu 175	TTA Leu	GAA Glu	AAA Lys	TTA Leu 180	AGC Ser	CTT Leu	GAA Glu	TTG Leu	ATA Ile	581
GAG Glu 185	TAT Tyr	TTG Leu	AGC Ser	CTT Leu	CAA Gln 190	ATC Ile	CAA Gln	GCA Ala	GGG Gly 195	GTC Val	AAT Asn	GCA Ala	GTG Val	ATG Met	ATC Ile 200	629
TTT Phe	GAC Asp	TCA Ser	TGG Trp	GCT Ala 205	AGC Ser	GCT Ala	TTA Leu	GAA Glu	AAA Lys 210	GAA Glu	GCG Ala	TAT Tyr	TTG Leu	AAA Lys 215	TTC Phe	677
AGT Ser	TGG Trp	GAT Asp	TAT Tyr 220	TTG Leu	AAA Lys	AAA Lys	ATC Ile	TCT Ser 225	AAA Lys	GAG Glu	CTT Leu	AAA Lys	AAA Lys 230	CGC Arg	TAT Tyr	725
GCG Ala	CAT His	ATC Ile 235	CCA Pro	GTT Val	ATC Ile	CTT Leu	TTC Phe 240	CCT Pro	AAA Lys	GGG Gly	ATT Ile 245	GGC Gly	GCT Ala	TAT Tyr	TTG Leu	773
GAT Asp	AGC Ser	ATA Ile	GAT Asp	GGG Gly	GAA Glu	TTT Phe	GAT Asp	GTG Val	TTT Phe	GGC Gly	GTG Val	GAT Asp	TGG Trp	GGC Gly	ACG Thr	821

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met	Met	Ile	Phe	Ile	Asp	Ala	Cys	Phe	Arg	Lys	Glu	Thr	Pro	Tyr	Thr
1				5					10					15	
Pro	Ile	Trp	Met	Met	Arg	Gln	Ala	Gly	Arg	Tyr	Leu	Ser	Glu	Tyr	Gln
			20					25					30		
Glu	Ser	Arg	Lys	Lys	Ala	Gly	Ser	Phe	Leu	Glu	Leu	Cys	Lys	Asn	Ser
			35				40					45			
Asp	Leu	Ala	Thr	Glu	Val	Thr	Leu	Gln	Pro	Val	Glu	Ile	Leu	Gly	Val
			50			55				60					
Asp	Ala	Ala	Ile	Leu	Phe	Ser	Asp	Ile	Leu	Val	Val	Pro	Leu	Glu	Met
65					70				75					80	
Gly	Leu	Asn	Leu	Glu	Phe	Ile	Pro	Lys	Lys	Gly	Pro	His	Phe	Leu	Glu
				85				90					95		
Thr	Ile	Thr	Asp	Leu	Lys	Ser	Val	Glu	Ser	Leu	Lys	Val	Gly	Ala	Tyr
			100					105					110		
Lys	Gln	Leu	Asn	Tyr	Val	Tyr	Asp	Thr	Ile	Ser	Gln	Thr	Arg	Gln	Lys
			115				120					125			
Leu	Ser	Arg	Glu	Lys	Ala	Leu	Ile	Gly	Phe	Cys	Gly	Ser	Pro	Trp	Thr
			130			135					140				
Leu	Ala	Thr	Tyr	Met	Ile	Glu	Gly	Glu	Gly	Ser	Lys	Ser	Tyr	Ala	Lys
145					150					155					160
Ser	Lys	Lys	Met	Leu	Tyr	Ser	Glu	Pro	Glu	Val	Leu	Lys	Ala	Leu	Leu
				165					170					175	
Glu	Lys	Leu	Ser	Leu	Glu	Leu	Ile	Glu	Tyr	Leu	Ser	Leu	Gln	Ile	Gln
			180					185					190		
Ala	Gly	Val	Asn	Ala	Val	Met	Ile	Phe	Asp	Ser	Trp	Ala	Ser	Ala	Leu
			195			200						205			
Glu	Lys	Glu	Ala	Tyr	Leu	Lys	Phe	Ser	Trp	Asp	Tyr	Leu	Lys	Lys	Ile
			210			215					220				
Ser	Lys	Glu	Leu	Lys	Lys	Arg	Tyr	Ala	His	Ile	Pro	Val	Ile	Leu	Phe
225					230					235					240
Pro	Lys	Gly	Ile	Gly	Ala	Tyr	Leu	Asp	Ser	Ile	Asp	Gly	Glu	Phe	Asp
				245					250					255	
Val	Phe	Gly	Val	Asp	Trp	Gly	Thr	Pro	Leu	Thr	Ala	Ala	Lys	Lys	Ile
			260				265						270		
Leu	Gly	Gly	Lys	Tyr	Val	Leu	Gln	Gly	Asn	Leu	Glu	Pro	Thr	Arg	Leu
			275				280					285			
Tyr	Asp	Lys	Asn	Ala	Leu	Glu	Gly	Val	Glu	Thr	Ile	Leu	Lys	Val	
			290			295				300					
Met	Gly	Asn	Gln	Gly	His	Ile	Phe	Asn	Leu	Gly	His	Gly	Met	Leu	Pro
305					310					315					320
Asp	Leu	Pro	Arg	Glu	Asn	Ala	Lys	Tyr	Leu	Val	Gln	Leu	Val	His	Ala
				325					330					335	
Lys	Thr	Arg	Arg												
			340												

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...732
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TAGACGACTA TGTGCATTAA GGGAATGAAA ATG ATA CGA AAA ATT TTA ATA GGA	54
Met Ile Arg Lys Ile Leu Ile Gly	
1 5	
CTT TTT TTG AGT TTT TTG AGC ATG GAA GCT GGC GAA AAA GTG TAT GCG	102
Leu Phe Leu Ser Phe Leu Ser Met Glu Ala Gly Glu Lys Val Tyr Ala	
10 15 20	
ATT TTC AAT GTG AAA GCG ACA CAA GAT TCC AAA CTC ACC TTA GAC AGC	150
Ile Phe Asn Val Lys Ala Thr Gln Asp Ser Lys Leu Thr Leu Asp Ser	
25 30 35 40	
ACA GGA ATT GTG GAT AGC ATT AAG GTT ACT GAG GGG AGC GTG GTC AAA	198
Thr Gly Ile Val Asp Ser Ile Lys Val Thr Glu Gly Ser Val Val Lys	
45 50 55	
AAG GGC GAT GTT TTG TTG CTT TTA TAT AAT CAA GAC AAA CAG GCT CAA	246
Lys Gly Asp Val Leu Leu Leu Leu Tyr Asn Gln Asp Lys Gln Ala Gln	
60 65 70	
AGC GAT TCC ACC GAA CAA CAA CTC ATT TTC GCT AAA AAG CAA TAC CAA	294
Ser Asp Ser Thr Glu Gln Gln Leu Ile Phe Ala Lys Lys Gln Tyr Gln	
75 80 85	
CGA TAC AGC AAA ATT GGG GGC GCT GTG GAT AAA AAC ACT CTA GAG GGT	342
Arg Tyr Ser Lys Ile Gly Gly Ala Val Asp Lys Asn Thr Leu Glu Gly	
90 95 100	
TAT GAG TTC ACT TAC AGG CGC TTG GAG TCT GAT TAC GCT TAT TCT ATT	390
Tyr Glu Phe Thr Tyr Arg Arg Leu Glu Ser Asp Tyr Ala Tyr Ser Ile	
105 110 115 120	
GCG GTA TTG AAT AAA ACC ATT TTA AGA GCC CCT TTT GAT GGC GTG ATA	438
Ala Val Leu Asn Lys Thr Ile Leu Arg Ala Pro Phe Asp Gly Val Ile	
125 130 135	
GCG AGT AAA AAC ATT CAA GTG GGC GAA GGG GTG AGC GCG AAT AAC ACG	486
Ala Ser Lys Asn Ile Gln Val Gly Glu Gly Val Ser Ala Asn Asn Thr	
140 145 150	
GTG TTA TTG AGA TTA GTC AGC CAT GCT AGG AAA TTA GTT ATT GAA TTT	534

Val	Leu	Leu	Arg	Leu	Val	Ser	His	Ala	Arg	Lys	Leu	Val	Ile	Glu	Phe		
	155						160					165					
GAT	TCT	AAA	TAT	ATT	AAT	GCG	GTC	AAA	GTA	GGG	GAC	ACT	TAC	ACC	TAT	582	
Asp	Ser	Lys	Tyr	Ile	Asn	Ala	Val	Lys	Val	Gly	Asp	Thr	Tyr	Thr	Tyr		
	170					175				180							
TCT	ATA	GAC	GGG	GAT	TCT	AAT	CAG	CAT	GAA	GCT	AAA	ATC	ACT	AAG	ATT	630	
Ser	Ile	Asp	Gly	Asp	Ser	Asn	Gln	His	Glu	Ala	Lys	Ile	Thr	Lys	Ile		
	185				190				195						200		
TAC	CCC	ACG	GTT	GAT	GAA	AAC	ACC	AGG	AAA	GTG	AGC	GCT	GAA	GCC	CTT	678	
Tyr	Pro	Thr	Val	Asp	Glu	Asn	Thr	Arg	Lys	Val	Ser	Ala	Glu	Ala	Leu		
				205					210					215			
TTA	TCT	AAG	CCT	ATG	GCA	GTG	GGG	CTT	TTT	GGC	GAT	GGG	TTT	ATC	CAA	726	
Leu	Ser	Lys	Pro	Met	Ala	Val	Gly	Leu	Phe	Gly	Asp	Gly	Phe	Ile	Gln		
			220				225						230				
ACG	AAA	TAATAGGATA	TTTTGATGTA	TAAAACAGCG	ATTA											766	
Thr	Lys																

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Ile	Arg	Lys	Ile	Leu	Ile	Gly	Leu	Phe	Leu	Ser	Phe	Leu	Ser	Met		
1				5					10					15			
Glu	Ala	Gly	Glu	Lys	Val	Tyr	Ala	Ile	Phe	Asn	Val	Lys	Ala	Thr	Gln		
			20					25				30					
Asp	Ser	Lys	Leu	Thr	Leu	Asp	Ser	Thr	Gly	Ile	Val	Asp	Ser	Ile	Lys		
		35				40					45						
Val	Thr	Glu	Gly	Ser	Val	Val	Lys	Lys	Gly	Asp	Val	Leu	Leu	Leu	Leu		
	50				55					60							
Tyr	Asn	Gln	Asp	Lys	Gln	Ala	Gln	Ser	Asp	Ser	Thr	Glu	Gln	Gln	Leu		
65				70					75					80			
Ile	Phe	Ala	Lys	Lys	Gln	Tyr	Gln	Arg	Tyr	Ser	Lys	Ile	Gly	Gly	Ala		
			85					90					95				
Val	Asp	Lys	Asn	Thr	Leu	Glu	Gly	Tyr	Glu	Phe	Thr	Tyr	Arg	Arg	Leu		
			100				105					110					
Glu	Ser	Asp	Tyr	Ala	Tyr	Ser	Ile	Ala	Val	Leu	Asn	Lys	Thr	Ile	Leu		
		115				120						125					
Arg	Ala	Pro	Phe	Asp	Gly	Val	Ile	Ala	Ser	Lys	Asn	Ile	Gln	Val	Gly		
	130				135						140						
Glu	Gly	Val	Ser	Ala	Asn	Asn	Thr	Val	Leu	Leu	Arg	Leu	Val	Ser	His		
145					150					155					160		
Ala	Arg	Lys	Leu	Val	Ile	Glu	Phe	Asp	Ser	Lys	Tyr	Ile	Asn	Ala	Val		
			165					170						175			

Lys	Val	Gly	Asp	Thr	Tyr	Thr	Tyr	Ser	Ile	Asp	Gly	Asp	Ser	Asn	Gln
			180					185					190		
His	Glu	Ala	Lys	Ile	Thr	Lys	Ile	Tyr	Pro	Thr	Val	Asp	Glu	Asn	Thr
		195					200					205			
Arg	Lys	Val	Ser	Ala	Glu	Ala	Leu	Leu	Ser	Lys	Pro	Met	Ala	Val	Gly
	210					215					220				
Leu	Phe	Gly	Asp	Gly	Phe	Ile	Gln	Thr	Lys						
225					230										

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 62...544
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ACGCCAAAGA	GAGCAACGGG	GAGTTTTTAG	TCGCTTTAGC	GNAGCGNTTG	TGCTGATTTA	60
T ATG ATT TTA	GCG GCG TTG	TAT GAG TCC	ATT TTA GAG	CCT TTT ATC	ATC	109
Met Ile Leu	Ala Ala Leu	Tyr Glu Ser	Ile Leu Glu	Pro Phe Ile	Ile	
1	5	10	15			
ATG GTT ACC	ATG CCT TTA	AGT TTT TCA	GGG GCG TTT	TTT GCT CTA	GGT	157
Met Val Thr	Met Pro Leu	Ser Phe Ser	Gly Ala Phe	Phe Ala Leu	Gly	
	20	25	30			
TTA GTC CAT	CAG CCT TTG	AGC ATG TTC	TCT ATG ATA	GGC TTG ATT	TTG	205
Leu Val His	Gln Pro Leu	Ser Met Phe	Ser Met Ile	Gly Leu Ile	Leu	
	35	40	45			
CTC ATT GGT	ATG GTG GGT	AAA AAC GCC	ACG CTT TTA	ATT GAT GTG	GCG	253
Leu Ile Gly	Met Val Gly	Lys Asn Ala	Thr Leu Leu	Ile Asp Val	Ala	
	50	55	60			
AAT GAA GAG	CGT AAA AAA	GGT TTG AAT	ATC CAA GAG	GCC ATT TTA	TTT	301
Asn Glu Glu	Arg Lys Lys	Gly Leu Asn	Ile Gln Glu	Ala Ile Leu	Phe	
65	70	75	80			
GCC GGC AAA	ACC CGT CTA	AGA CCG ATT	TTA ATG ACG	ACC ATT GCG	ATG	349
Ala Gly Lys	Thr Arg Leu	Arg Pro Ile	Leu Met Thr	Thr Ile Ala	Met	
	85	90	95			
GTT TGC GGG	ATG CTG CCT	TTA GCG TTG	GCG AGT GGG	GAT GGA GCG	GCG	397
Val Cys Gly	Met Leu Pro	Leu Ala Leu	Ala Ser Gly	Asp Gly Ala	Ala	
	100	105	110			
ATG AAA TCC	CCT ATA GGG	ATT GCG ATG	AGT GGG GGC	TTG ATG ATT	TCT	445
Met Lys Ser	Pro Ile Gly	Ile Ala Met	Ser Gly Gly	Leu Met Ile	Ser	

115	120	125	
ATG GTG TTA AGC TTA CTC ATT GTG CCG GTG TTT TAT CGT TTG CTC GCT	493		
Met Val Leu Ser Leu Leu Ile Val Pro Val Phe Tyr Arg Leu Leu Ala			
130 135 140			
CCC ATA GAC GAC AAA ATC AAG CGG TTT TAT CAA AAC CAA AAA ACT TTA	541		
Pro Ile Asp Asp Lys Ile Lys Arg Phe Tyr Gln Asn Gln Lys Thr Leu			
145 150 155 160			
GAA TGAAAAAAT TGCTTTCATT TTGGCTTTAT GGGTGGGCTT GTTAGGGGCG TTTGAG	600		
Glu			
CCTAAAAAAA GTCATATTTA TTTTGGGGCT	630		

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met	Ile	Leu	Ala	Ala	Leu	Tyr	Glu	Ser	Ile	Leu	Glu	Pro	Phe	Ile	Ile
1				5					10					15	
Met	Val	Thr	Met	Pro	Leu	Ser	Phe	Ser	Gly	Ala	Phe	Phe	Ala	Leu	Gly
			20					25					30		
Leu	Val	His	Gln	Pro	Leu	Ser	Met	Phe	Ser	Met	Ile	Gly	Leu	Ile	Leu
		35					40					45			
Leu	Ile	Gly	Met	Val	Gly	Lys	Asn	Ala	Thr	Leu	Leu	Ile	Asp	Val	Ala
	50					55				60					
Asn	Glu	Glu	Arg	Lys	Lys	Gly	Leu	Asn	Ile	Gln	Glu	Ala	Ile	Leu	Phe
65				70					75					80	
Ala	Gly	Lys	Thr	Arg	Leu	Arg	Pro	Ile	Leu	Met	Thr	Thr	Ile	Ala	Met
			85						90					95	
Val	Cys	Gly	Met	Leu	Pro	Leu	Ala	Leu	Ala	Ser	Gly	Asp	Gly	Ala	Ala
			100					105					110		
Met	Lys	Ser	Pro	Ile	Gly	Ile	Ala	Met	Ser	Gly	Gly	Leu	Met	Ile	Ser
	115						120					125			
Met	Val	Leu	Ser	Leu	Leu	Ile	Val	Pro	Val	Phe	Tyr	Arg	Leu	Leu	Ala
	130					135					140				
Pro	Ile	Asp	Asp	Lys	Ile	Lys	Arg	Phe	Tyr	Gln	Asn	Gln	Lys	Thr	Leu
145					150					155					160
Glu															

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 19...945
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TAAAAGGTTT TTACAAAC	ATG ATA AAA AGC CAA AAA GAA TAT TTA GAA AGA	51
	Met Ile Lys Ser Gln Lys Glu Tyr Leu Glu Arg	
	1 5 10	
ATT GCA TAT TTA AAC ACC CTA TCG CAC CAT TAT TAC AAC CTT GAT GAA	99	
Ile Ala Tyr Leu Asn Thr Leu Ser His His Tyr Tyr Asn Leu Asp Glu		
	15 20 25	
CCC ATC GTA AGC GAT GCG ATC TAT GAT GAA CTT TAC CAA GAA TTG AAA	147	
Pro Ile Val Ser Asp Ala Ile Tyr Asp Glu Leu Tyr Gln Glu Leu Lys		
	30 35 40	
GCT TAT GAA GAA AAA AAC CCT AAT GGC ATT CAA GCT AAT TCC CCT ACC	195	
Ala Tyr Glu Glu Lys Asn Pro Asn Gly Ile Gln Ala Asn Ser Pro Thr		
	45 50 55	
CAA AAA GTG GGG GCT ACT ACC ACC AAT TCG TTC AAT AAA AAC CCC CAT	243	
Gln Lys Val Gly Ala Thr Thr Thr Asn Ser Phe Asn Lys Asn Pro His		
	60 65 70 75	
TTA ATG CGG ATG TGG AGC TTA GAT GAT GTG TTC AAT CAA AGC GAA TTG	291	
Leu Met Arg Met Trp Ser Leu Asp Asp Val Phe Asn Gln Ser Glu Leu		
	80 85 90	
CAA GCG TGG TTG CAA CGC ATT TTA AAA GCC TAT CCT AGT GCT TCG TTC	339	
Gln Ala Trp Leu Gln Arg Ile Leu Lys Ala Tyr Pro Ser Ala Ser Phe		
	95 100 105	
GTG TGT TCG CCC AAA CTT GAT GGG GTT TCG CTC AAT CTT TTG TAT CAA	387	
Val Cys Ser Pro Lys Leu Asp Gly Val Ser Leu Asn Leu Leu Tyr Gln		
	110 115 120	
CAT GGC AAG CTA GTG AAG GCG ACC ACT AGG GGC AAC GGC TTA GAA GGA	435	
His Gly Lys Leu Val Lys Ala Thr Thr Arg Gly Asn Gly Leu Glu Gly		
	125 130 135	
GAA TTA GTT AGC GCA AAC GCT AAA CAC ATC GCT AAT ATC CCC CAC GCT	483	
Glu Leu Val Ser Ala Asn Ala Lys His Ile Ala Asn Ile Pro His Ala		
	140 145 150 155	
ATC GCT TAT AAT GGA GAA ATA GAA ATC AGG GGC GAA GTG ATC ATT TCT	531	
Ile Ala Tyr Asn Gly Glu Ile Glu Ile Arg Gly Glu Val Ile Ile Ser		
	160 165 170	
AAA AAG GAT TTT GAC GCT TTG AAT CAA GAG CGC TTA AAC GCT AAT GAA	579	
Lys Lys Asp Phe Asp Ala Leu Asn Gln Glu Arg Leu Asn Ala Asn Glu		
	175 180 185	

CCC CTA TTC GCT AAC CCC AGA AAC GCC GCA TCA GGG AGT TTG AGG CAA	627
Pro Leu Phe Ala Asn Pro Arg Asn Ala Ala Ser Gly Ser Leu Arg Gln	
190 195 200	
CTT GAT AGC GAA ATC ACT AAA AAG CGT AAA TTG CAA TTC ATT CCT TGG	675
Leu Asp Ser Glu Ile Thr Lys Lys Arg Lys Leu Gln Phe Ile Pro Trp	
205 210 215	
GGC GTG GGC AAG CAT TCT TTA AAT TTT TTA AGC TTT AAG GAG TGT TTG	723
Gly Val Gly Lys His Ser Leu Asn Phe Leu Ser Phe Lys Glu Cys Leu	
220 225 230 235	
GAT TTT ATC GTC TCG TTA GGT TTT AGC GCC ATT CAA TAC TTA AGC CTA	771
Asp Phe Ile Val Ser Leu Gly Phe Ser Ala Ile Gln Tyr Leu Ser Leu	
240 245 250	
AAC AAA AAC CAC CAA GAA ATA GAA GAC AAT TAC CAC ACC CTA ATT AGA	819
Asn Lys Asn His Gln Glu Ile Glu Asp Asn Tyr His Thr Leu Ile Arg	
255 260 265	
GAA AGG GAG GGC TTT TTT GCC CTT TTA GAC GGC ATG GTG ATC GTT GTG	867
Glu Arg Glu Gly Phe Phe Ala Leu Leu Asp Gly Met Val Ile Val Val	
270 275 280	
AAT GAA TTA AAT ATT CAA AAG GAG CTA GGC TAC ACG CAA AAA TCC CCT	915
Asn Glu Leu Asn Ile Gln Lys Glu Leu Gly Tyr Thr Gln Lys Ser Pro	
285 290 295	
AAA TNG CTT GCG CTT ATA AAT TCC CGG CTT TAGAAAAACA CACCAAAATT GTA	968
Lys Xaa Leu Ala Leu Ile Asn Ser Arg Leu	
300 305	
GGAGTCATTA ACCAAGTGGG GCGCASSGGG CGATCACAC	1007

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Ile Lys Ser Gln Lys Glu Tyr Leu Glu Arg Ile Ala Tyr Leu Asn	
1 5 10 15	
Thr Leu Ser His His Tyr Tyr Asn Leu Asp Glu Pro Ile Val Ser Asp	
20 25 30	
Ala Ile Tyr Asp Glu Leu Tyr Gln Glu Leu Lys Ala Tyr Glu Glu Lys	
35 40 45	
Asn Pro Asn Gly Ile Gln Ala Asn Ser Pro Thr Gln Lys Val Gly Ala	
50 55 60	
Thr Thr Thr Asn Ser Phe Asn Lys Asn Pro His Leu Met Arg Met Trp	
65 70 75 80	
Ser Leu Asp Asp Val Phe Asn Gln Ser Glu Leu Gln Ala Trp Leu Gln	
85 90 95	

```

Arg Ile Leu Lys Ala Tyr Pro Ser Ala Ser Phe Val Cys Ser Pro Lys
      100      105      110
Leu Asp Gly Val Ser Leu Asn Leu Leu Tyr Gln His Gly Lys Leu Val
      115      120      125
Lys Ala Thr Thr Arg Gly Asn Gly Leu Glu Gly Glu Leu Val Ser Ala
      130      135      140
Asn Ala Lys His Ile Ala Asn Ile Pro His Ala Ile Ala Tyr Asn Gly
      145      150      155      160
Glu Ile Glu Ile Arg Gly Glu Val Ile Ile Ser Lys Lys Asp Phe Asp
      165      170      175
Ala Leu Asn Gln Glu Arg Leu Asn Ala Asn Glu Pro Leu Phe Ala Asn
      180      185      190
Pro Arg Asn Ala Ala Ser Gly Ser Leu Arg Gln Leu Asp Ser Glu Ile
      195      200      205
Thr Lys Lys Arg Lys Leu Gln Phe Ile Pro Trp Gly Val Gly Lys His
      210      215      220
Ser Leu Asn Phe Leu Ser Phe Lys Glu Cys Leu Asp Phe Ile Val Ser
      225      230      235      240
Leu Gly Phe Ser Ala Ile Gln Tyr Leu Ser Leu Asn Lys Asn His Gln
      245      250      255
Glu Ile Glu Asp Asn Tyr His Thr Leu Ile Arg Glu Arg Glu Gly Phe
      260      265      270
Phe Ala Leu Leu Asp Gly Met Val Ile Val Val Asn Glu Leu Asn Ile
      275      280      285
Gln Lys Glu Leu Gly Tyr Thr Gln Lys Ser Pro Lys Xaa Leu Ala Leu
      290      295      300
Ile Asn Ser Arg Leu
305

```

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 937 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 44...880
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

GTGCTTTAGA TTAGATGCAG AAAAAGACGC CCAACTTTAT GGC ATG AAT ATT TTT      55
                               Met Asn Ile Phe
                               1

AAG ATC CGA GAA ATT ATC CAT TAT GAC GGG GAG GTT ACA GAG ATT CTT      103
Lys Ile Arg Glu Ile Ile His Tyr Asp Gly Glu Val Thr Glu Ile Leu
  5              10              15              20

GGG GGG AGC GAT GGC GTG ATG CTC GGG TTT CTT AGC GTT AGG GGC GAG      151
Gly Gly Ser Asp Gly Val Met Leu Gly Phe Leu Ser Val Arg Gly Glu
      25              30              35

```

TCT Ser	ATC Ile	CCT Pro	TTA Leu 40	GTG Val	GAT Asp	GTG Val	AAA Lys	AGG Arg 45	TGG Trp	TTG Leu	CAT His	TAT Tyr	AAC Asn 50	GCT Ala	AAT Asn	199
GAT Asp	CCG Pro	AGC Ser 55	CGT Arg	GAT Asp	CTA Leu	AAA Lys	GAA Glu 60	TGC Cys	AGC Ser	GTT Val	AAA Lys	GAT Asp 65	GAC Asp	CAT His	AAT Asn	247
TTG Leu	GTG Val 70	ATT Ile	GTG Val	TGC Cys	CAT His	TTT Phe 75	TCT Ser	AAC Asn	CAT His	TCC Ser	ATC Ile 80	GCT Ala	CTA Leu	AAG Lys	GTT Val	295
TTA Leu 85	AAA Lys	ATT Ile	GAA Glu	AGG Arg	ATC Ile 90	ATC Ile	CAT His	AAA Lys	AAT Asn	TGG Trp 95	ACT Thr	GAG Glu	ATT Ile	AGC Ser	GCT Ala 100	343
GGG Gly	GAC Asp	AAA Lys	CAA Gln	GGC Gly 105	ATT Ile	AAT Asn	GAA Glu	GAG Glu 110	GGT Gly	AAG Lys	CTT Leu	AGC Ser	GCT Ala	ATC Ile 115	ACT Thr	391
CGT Arg	TTT Phe	GAT Asp	GAA Glu 120	GAA Glu	CGA Arg	GTG Val	GTG Val	CAG Gln 125	ATC Ile	TTA Leu	GAT Asp	GTG Val	GAA Glu 130	AAA Lys	ATG Met	439
ATT Ile	AGC Ser	GAT Asp 135	GTT Val	TTC Phe	CCT Pro	AGC Ser	TTG Leu 140	AAA Lys	GAT Asp	TTA Leu	GAC Asp	GAT Asp 145	TTG Leu	ACT Thr	TTG Leu	487
CGT Arg	TGC Cys 150	ATA Ile	GAA Glu	GCC Ala	ATT Ile	CAA Gln 155	AGC Ser	CAA Gln	AAA Lys	CTC Leu	ATT Ile 160	TTA Leu	ATC Ile	GCT Ala	GAA Glu	535
GAC Asp 165	TCC Ser	CTA Leu	AGC Ser	GCT Ala	CTT Leu 170	AAA Lys	ACC Thr	TTA Leu	GAA Glu	AAG Lys 175	ATC Ile	GTT Val	CAA Gln	ACT Thr	TTA Leu 180	583
GAA Glu	TTG Leu	CGT Arg	TAT Tyr	TTA Leu 185	GCT Ala	TTT Phe	CCA Pro	AAC Asn	GGG Gly 190	AGG Arg	GAA Glu	TTG Leu	TTG Leu	GAT Asp 195	TAT Tyr	631
TTG Leu	TAT Tyr	GAA Glu	AAA Lys 200	GAA Glu	CAT His	TAC Tyr	CAA Gln	CAA Gln 205	GTT Val	GGC Gly	GTG Val	GTC Val	ATT Ile 210	ACG Thr	GAT Asp	679
TTA Leu	GAA Glu	ATG Met 215	CCT Pro	AAC Asn	ATT Ile	TCA Ser	GGG Gly 220	TTT Phe	GAA Glu	GTG Val	TTA Leu	AAA Lys 225	ACC Thr	ATT Ile	AAA Lys	727
GCT Ala	GAT Asp 230	CAT His	AGA Arg	ACT Thr	GAG Glu	CAT His 235	CTT Leu	CCT Pro	GTG Val	ATT Ile 240	ATC Ile	AAT Asn	TCG Ser	TCC Ser	ATG Met	775
AGC Ser 245	AGC Ser	GAT Asp	TCT Ser	AAC Asn	CGC Arg 250	CAG Gln	TTA Leu	GCC Ala	CAA Gln	TCT Ser 255	TTA Leu	GAA Glu	GCG Ala	GAT Asp	GGT Gly 260	823
TTT Phe	GTG Val	GTA Val	AAA Lys	TCT Ser	AAC Asn	ATT Ile	CTT Leu	GAA Glu	ATC Ile	CAT His	GAA Glu	ATG Met	CTT Leu	AAA Lys	AAA Lys	871

265

270

275

ACG CTT TCA TAAATTTAAT TTTTGTTTTA ATTTAAAGGG ATAAAACATG CGAAGTCAT 929
 Thr Leu Ser

TTTTGCAC

937

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Asn Ile Phe Lys Ile Arg Glu Ile Ile His Tyr Asp Gly Glu Val
 1 5 10 15
 Thr Glu Ile Leu Gly Gly Ser Asp Gly Val Met Leu Gly Phe Leu Ser
 20 25 30
 Val Arg Gly Glu Ser Ile Pro Leu Val Asp Val Lys Arg Trp Leu His
 35 40 45
 Tyr Asn Ala Asn Asp Pro Ser Arg Asp Leu Lys Glu Cys Ser Val Lys
 50 55 60
 Asp Asp His Asn Leu Val Ile Val Cys His Phe Ser Asn His Ser Ile
 65 70 75 80
 Ala Leu Lys Val Leu Lys Ile Glu Arg Ile Ile His Lys Asn Trp Thr
 85 90 95
 Glu Ile Ser Ala Gly Asp Lys Gln Gly Ile Asn Glu Glu Gly Lys Leu
 100 105 110
 Ser Ala Ile Thr Arg Phe Asp Glu Glu Arg Val Val Gln Ile Leu Asp
 115 120 125
 Val Glu Lys Met Ile Ser Asp Val Phe Pro Ser Leu Lys Asp Leu Asp
 130 135 140
 Asp Leu Thr Leu Arg Cys Ile Glu Ala Ile Gln Ser Gln Lys Leu Ile
 145 150 155 160
 Leu Ile Ala Glu Asp Ser Leu Ser Ala Leu Lys Thr Leu Glu Lys Ile
 165 170 175
 Val Gln Thr Leu Glu Leu Arg Tyr Leu Ala Phe Pro Asn Gly Arg Glu
 180 185 190
 Leu Leu Asp Tyr Leu Tyr Glu Lys Glu His Tyr Gln Gln Val Gly Val
 195 200 205
 Val Ile Thr Asp Leu Glu Met Pro Asn Ile Ser Gly Phe Glu Val Leu
 210 215 220
 Lys Thr Ile Lys Ala Asp His Arg Thr Glu His Leu Pro Val Ile Ile
 225 230 235 240
 Asn Ser Ser Met Ser Ser Asp Ser Asn Arg Gln Leu Ala Gln Ser Leu
 245 250 255
 Glu Ala Asp Gly Phe Val Val Lys Ser Asn Ile Leu Glu Ile His Glu
 260 265 270
 Met Leu Lys Lys Thr Leu Ser
 275

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 21...593
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATAATTAA	AGGATACGAT	ATG AAA CAA CTA TTT TTG ATC ATT GGA GCC	50
		Met Lys Gln Leu Phe Leu Ile Ile Gly Ala	
		1 5 10	
CCA GGG AGT GGT AAA ACC ACT GAT GCA GAG CTT ATC GCT AAA AAT AAC	98		
Pro Gly Ser Gly Lys Thr Thr Asp Ala Glu Leu Ile Ala Lys Asn Asn		15 20 25	
AGC GAA ACA ATC GCT CAT TTT TCT ACC GGG GAT TTA CTC AGG GCT GAG	146		
Ser Glu Thr Ile Ala His Phe Ser Thr Gly Asp Leu Leu Arg Ala Glu		30 35 40	
AGC GCT AAA AAG ACC GAG CGA GGC TTA TTG ATT GAA AAA TTC ACT TCT	194		
Ser Ala Lys Lys Thr Glu Arg Gly Leu Leu Ile Glu Lys Phe Thr Ser		45 50 55	
CAA GGC GAA TTA GTG CCT TTA GAA ATT GTG GTA GAA ACG ATC CTT TCA	242		
Gln Gly Glu Leu Val Pro Leu Glu Ile Val Val Glu Thr Ile Leu Ser		60 65 70	
GCG ATT AAA AGC TCT GGT AAA GGG ATC ATT TTA ATT GAT GGT TAT CCT	290		
Ala Ile Lys Ser Ser Gly Lys Gly Ile Ile Leu Ile Asp Gly Tyr Pro		75 80 85 90	
AGG AGC GTG GAA CAA ATG CAG GCT TTG GAT AAG GAA TTG AAC GCT CAA	338		
Arg Ser Val Glu Gln Met Gln Ala Leu Asp Lys Glu Leu Asn Ala Gln		95 100 105	
AAC GAA GTG ATC TTA AAA AGC GTG ATT GAA GTA GAA GTG AGT GAA AAC	386		
Asn Glu Val Ile Leu Lys Ser Val Ile Glu Val Glu Val Ser Glu Asn		110 115 120	
ACT GCT AAA GAA AGG GTT TTA GGG CGC TCT AGG GGG GCT GAT GAT AAT	434		
Thr Ala Lys Glu Arg Val Leu Gly Arg Ser Arg Gly Ala Asp Asp Asn		125 130 135	
GAA AAG GTG TTT CAT AAC CGC ATG CGG GTG TTT TTG GAT CCG TTG GGC	482		
Glu Lys Val Phe His Asn Arg Met Arg Val Phe Leu Asp Pro Leu Gly		140 145 150	
GAG ATC CAA AAT TTT TAC AAG AAT AAG AAG GTG TAT AAA GCG ATC GAT	530		
Glu Ile Gln Asn Phe Tyr Lys Asn Lys Lys Val Tyr Lys Ala Ile Asp			

155		160		165		170	
GGG GAG AGG AGC ATT GAA GAG ATT GTG GGC GAA ATG CAA GAG TAT ATC							578
Gly Glu Arg Ser Ile Glu Glu Ile Val Gly Glu Met Gln Glu Tyr Ile							
		175		180		185	
TTG TCT TTC GGT AAT TAAAATGCAC TCTCAAGGAG AATAGCTGTG ATTTCTG							630
Leu Ser Phe Gly Asn							
		190					

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met	Lys	Gln	Leu	Phe	Leu	Ile	Ile	Gly	Ala	Pro	Gly	Ser	Gly	Lys	Thr
1				5					10					15	
Thr	Asp	Ala	Glu	Leu	Ile	Ala	Lys	Asn	Asn	Ser	Glu	Thr	Ile	Ala	His
			20					25					30		
Phe	Ser	Thr	Gly	Asp	Leu	Leu	Arg	Ala	Glu	Ser	Ala	Lys	Lys	Thr	Glu
		35					40					45			
Arg	Gly	Leu	Leu	Ile	Glu	Lys	Phe	Thr	Ser	Gln	Gly	Glu	Leu	Val	Pro
	50					55					60				
Leu	Glu	Ile	Val	Val	Glu	Thr	Ile	Leu	Ser	Ala	Ile	Lys	Ser	Ser	Gly
65					70					75				80	
Lys	Gly	Ile	Ile	Leu	Ile	Asp	Gly	Tyr	Pro	Arg	Ser	Val	Glu	Gln	Met
				85					90					95	
Gln	Ala	Leu	Asp	Lys	Glu	Leu	Asn	Ala	Gln	Asn	Glu	Val	Ile	Leu	Lys
			100					105					110		
Ser	Val	Ile	Glu	Val	Glu	Val	Ser	Glu	Asn	Thr	Ala	Lys	Glu	Arg	Val
		115					120					125			
Leu	Gly	Arg	Ser	Arg	Gly	Ala	Asp	Asp	Asn	Glu	Lys	Val	Phe	His	Asn
	130					135					140				
Arg	Met	Arg	Val	Phe	Leu	Asp	Pro	Leu	Gly	Glu	Ile	Gln	Asn	Phe	Tyr
145					150					155					160
Lys	Asn	Lys	Lys	Val	Tyr	Lys	Ala	Ile	Asp	Gly	Glu	Arg	Ser	Ile	Glu
				165					170					175	
Glu	Ile	Val	Gly	Glu	Met	Gln	Glu	Tyr	Ile	Leu	Ser	Phe	Gly	Asn	
			180					185					190		

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

Figure 1: Schematic representation of the experimental design. The diagram shows a flow from 'Study 1' to 'Study 2'. Study 1 involves 'Pretest' and 'Main Study'. Study 2 involves 'Pretest' and 'Main Study'. The 'Main Study' in Study 2 is divided into 'Control' and 'Intervention' groups. The 'Intervention' group is further divided into 'Intervention 1' and 'Intervention 2'. The 'Control' group is further divided into 'Control 1' and 'Control 2'. The 'Intervention 1' and 'Intervention 2' groups are further divided into 'Intervention 1a' and 'Intervention 1b' and 'Intervention 2a' and 'Intervention 2b'. The 'Control 1' and 'Control 2' groups are further divided into 'Control 1a' and 'Control 1b' and 'Control 2a' and 'Control 2b'. The 'Intervention 1a' and 'Intervention 1b' groups are further divided into 'Intervention 1a1' and 'Intervention 1a2' and 'Intervention 1b1' and 'Intervention 1b2'. The 'Intervention 2a' and 'Intervention 2b' groups are further divided into 'Intervention 2a1' and 'Intervention 2a2' and 'Intervention 2b1' and 'Intervention 2b2'. The 'Control 1a' and 'Control 1b' groups are further divided into 'Control 1a1' and 'Control 1a2' and 'Control 1b1' and 'Control 1b2'. The 'Control 2a' and 'Control 2b' groups are further divided into 'Control 2a1' and 'Control 2a2' and 'Control 2b1' and 'Control 2b2'. The 'Intervention 1a1' and 'Intervention 1a2' groups are further divided into 'Intervention 1a1a' and 'Intervention 1a1b' and 'Intervention 1a2a' and 'Intervention 1a2b'. The 'Intervention 1b1' and 'Intervention 1b2' groups are further divided into 'Intervention 1b1a' and 'Intervention 1b1b' and 'Intervention 1b2a' and 'Intervention 1b2b'. The 'Intervention 2a1' and 'Intervention 2a2' groups are further divided into 'Intervention 2a1a' and 'Intervention 2a1b' and 'Intervention 2a2a' and 'Intervention 2a2b'. The 'Intervention 2b1' and 'Intervention 2b2' groups are further divided into 'Intervention 2b1a' and 'Intervention 2b1b' and 'Intervention 2b2a' and 'Intervention 2b2b'. The 'Control 1a1' and 'Control 1a2' groups are further divided into 'Control 1a1a' and 'Control 1a1b' and 'Control 1a2a' and 'Control 1a2b'. The 'Control 1b1' and 'Control 1b2' groups are further divided into 'Control 1b1a' and 'Control 1b1b' and 'Control 1b2a' and 'Control 1b2b'. The 'Control 2a1' and 'Control 2a2' groups are further divided into 'Control 2a1a' and 'Control 2a1b' and 'Control 2a2a' and 'Control 2a2b'. The 'Control 2b1' and 'Control 2b2' groups are further divided into 'Control 2b1a' and 'Control 2b1b' and 'Control 2b2a' and 'Control 2b2b'. The 'Intervention 1a1a' and 'Intervention 1a1b' groups are further divided into 'Intervention 1a1a1' and 'Intervention 1a1a2' and 'Intervention 1a1b1' and 'Intervention 1a1b2'. The 'Intervention 1a2a' and 'Intervention 1a2b' groups are further divided into 'Intervention 1a2a1' and 'Intervention 1a2a2' and 'Intervention 1a2b1' and 'Intervention 1a2b2'. The 'Intervention 1b1a' and 'Intervention 1b1b' groups are further divided into 'Intervention 1b1a1' and 'Intervention 1b1a2' and 'Intervention 1b1b1' and 'Intervention 1b1b2'. The 'Intervention 1b2a' and 'Intervention 1b2b' groups are further divided into 'Intervention 1b2a1' and 'Intervention 1b2a2' and 'Intervention 1b2b1' and 'Intervention 1b2b2'. The 'Intervention 2a1a' and 'Intervention 2a1b' groups are further divided into 'Intervention 2a1a1' and 'Intervention 2a1a2' and 'Intervention 2a1b1' and 'Intervention 2a1b2'. The 'Intervention 2a2a' and 'Intervention 2a2b' groups are further divided into 'Intervention 2a2a1' and 'Intervention 2a2a2' and 'Intervention 2a2b1' and 'Intervention 2a2b2'. The 'Intervention 2b1a' and 'Intervention 2b1b' groups are further divided into 'Intervention 2b1a1' and 'Intervention 2b1a2' and 'Intervention 2b1b1' and 'Intervention 2b1b2'. The 'Intervention 2b2a' and 'Intervention 2b2b' groups are further divided into 'Intervention 2b2a1' and 'Intervention 2b2a2' and 'Intervention 2b2b1' and 'Intervention 2b2b2'. The 'Control 1a1a' and 'Control 1a1b' groups are further divided into 'Control 1a1a1' and 'Control 1a1a2' and 'Control 1a1b1' and 'Control 1a1b2'. The 'Control 1a2a' and 'Control 1a2b' groups are further divided into 'Control 1a2a1' and 'Control 1a2a2' and 'Control 1a2b1' and 'Control 1a2b2'. The 'Control 1b1a' and 'Control 1b1b' groups are further divided into 'Control 1b1a1' and 'Control 1b1a2' and 'Control 1b1b1' and 'Control 1b1b2'. The 'Control 1b2a' and 'Control 1b2b' groups are further divided into 'Control 1b2a1' and 'Control 1b2a2' and 'Control 1b2b1' and 'Control 1b2b2'. The 'Control 2a1a' and 'Control 2a1b' groups are further divided into 'Control 2a1a1' and 'Control 2a1a2' and 'Control 2a1b1' and 'Control 2a1b2'. The 'Control 2a2a' and 'Control 2a2b' groups are further divided into 'Control 2a2a1' and 'Control 2a2a2' and 'Control 2a2b1' and 'Control 2a2b2'. The 'Control 2b1a' and 'Control 2b1b' groups are further divided into 'Control 2b1a1' and 'Control 2b1a2' and 'Control 2b1b1' and 'Control 2b1b2'. The 'Control 2b2a' and 'Control 2b2b' groups are further divided into 'Control 2b2a1' and 'Control 2b2a2' and 'Control 2b2b1' and 'Control 2b2b2'.

Figure 1 displays the growth rate of the real GDP for 10 Asian countries (China, Hong Kong, Korea, Japan, Malaysia, Singapore, Taiwan, Thailand, Philippines, and Indonesia) from 1990 to 1999. The figure is organized into 10 subplots, one for each country. The y-axis represents the 'Growth rate of real GDP' (ranging from 0 to 10), and the x-axis represents the 'Year' (from 1990 to 1999). A horizontal line at 0 indicates zero growth. A vertical line at 1997 marks the onset of the Asian financial crisis. The data shows a significant decline in growth rates across all countries starting in 1997, with a particularly sharp drop in 1998. The Philippines and Indonesia show the most severe declines, with the Philippines dropping to near zero and Indonesia showing negative growth in 1998. Most countries show a partial recovery in 1999, though growth rates remain lower than pre-crisis levels.

Figure 1 displays the growth rate of the real GDP for 10 Asian countries (China, Hong Kong, Korea, Japan, Malaysia, Singapore, Taiwan, Thailand, Philippines, and Indonesia) from 1990 to 1999. The figure is organized into 10 subplots, one for each country. The y-axis represents the 'Growth rate of real GDP' (ranging from 0 to 10), and the x-axis represents the 'Year' (from 1990 to 1999). A horizontal line at 0 indicates zero growth. A vertical line at 1997 marks the onset of the Asian financial crisis. The data shows a significant decline in growth rates across all countries starting in 1997, with a particularly sharp drop in 1998. The Philippines and Indonesia show the most severe declines, with the Philippines dropping to near zero and Indonesia showing negative growth in 1998. Most countries show a partial recovery in 1999, though growth rates remain lower than pre-crisis levels.

Figure 1 displays the growth rate of the real GDP for 10 Asian countries (China, Hong Kong, Korea, Japan, Malaysia, Singapore, Taiwan, Thailand, Philippines, and Indonesia) from 1990 to 1999. The figure is organized into 10 subplots, one for each country. The y-axis represents the 'Growth rate of real GDP' (ranging from 0 to 10), and the x-axis represents the 'Year' (from 1990 to 1999). A horizontal line at 0 indicates zero growth. A vertical line at 1997 marks the onset of the Asian financial crisis. The data shows a significant decline in growth rates across all countries starting in 1997, with a particularly sharp drop in 1998. The Philippines and Indonesia show the most severe declines, with the Philippines dropping to near zero and Indonesia showing negative growth in 1998. Most countries show a partial recovery in 1999, though growth rates remain lower than pre-crisis levels.

Figure 1 displays the growth rate of the real GDP for 10 Asian countries (China, Hong Kong, Korea, Japan, Malaysia, Singapore, Taiwan, Thailand, Philippines, and Indonesia) from 1990 to 1999. The figure is organized into 10 subplots, one for each country. The y-axis represents the 'Growth rate of real GDP' (ranging from 0 to 10), and the x-axis represents the 'Year' (from 1990 to 1999). A horizontal line at 0 indicates zero growth. A vertical line at 1997 marks the onset of the Asian financial crisis. The data shows a significant decline in growth rates across all countries starting in 1997, with a particularly sharp drop in 1998. The Philippines and Indonesia show the most severe declines, with the Philippines dropping to near zero and Indonesia showing negative growth in 1998. Most countries show a partial recovery in 1999, though growth rates remain lower than pre-crisis levels.

CTT TTT TAT GAT CAA TTA AAC ACT AGA AAG TGC TTA AAA GCC TTT CAC 672
 Leu Phe Tyr Asp Gln Leu Asn Thr Arg Lys Cys Leu Lys Ala Phe His
 210 215 220

AAA TAC AGC AGA CGA TAC GCT CCT TTA AAA ACC CCT AAA GAG GTT TAAAA 722
 Lys Tyr Ser Arg Arg Tyr Ala Pro Leu Lys Thr Pro Lys Glu Val
 225 230 235

AGAGCGGGCT TTATGTTAGA ATAAGTCTTT TTATTCAAAG GAGATTGCAA TGAAT 777

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ser Tyr Pro Pro Pro Pro Asn Pro Thr Gln Glu Thr Gln Gln Asp Phe
 1 5 10 15
 Ile Ile Glu Ala Gln Gln Asp Leu Ile Ile Glu Thr Gln Gln Asp Pro
 20 25 30
 Lys Glu Leu Pro Glu Ser Cys Lys Ile Thr Pro Gln Lys Ile Ser Phe
 35 40 45
 Asn Gln Val Val Phe Lys Lys Ile Lys Arg Lys Leu Asn Arg Phe Ile
 50 55 60
 Gly Ser Ile Leu Ala Arg Thr Glu Val Tyr Lys Asn Leu Val Ala Lys
 65 70 75 80
 Tyr Asp Glu Leu Thr Gly Lys Tyr Glu Ser Leu Leu Ala Lys Glu Ala
 85 90 95
 Asn Ile Lys Glu Thr Phe Trp Glu Arg Arg Ala Asp Ser Glu Lys Glu
 100 105 110
 Ala Phe Phe Leu Glu His Phe Tyr Leu Thr Ser Val Tyr Val Ala Ser
 115 120 125
 Thr Ala Gly Tyr Tyr Ile Thr Pro Lys Gly Ala Lys Thr Phe Ile Glu
 130 135 140
 Ala Thr Glu Arg Phe Lys Ile Ile Glu Pro Val Asp Met Phe Ile Asn
 145 150 155 160
 Asn Pro Thr Tyr His Asp Val Ala Asn Phe Thr Tyr Leu Pro Cys Pro
 165 170 175
 Val Ser Leu Asn Lys His Ala Phe Asn Ser Thr Ile Gln Asn Ala Lys
 180 185 190
 Lys Pro Asp Ile Ser Leu Lys Pro Pro Arg Lys Ser Tyr Phe Asp Asn
 195 200 205
 Leu Phe Tyr Asp Gln Leu Asn Thr Arg Lys Cys Leu Lys Ala Phe His
 210 215 220
 Lys Tyr Ser Arg Arg Tyr Ala Pro Leu Lys Thr Pro Lys Glu Val
 225 230 235

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 50...1252
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AAGTGGAAAA	TTTAGCTAAA	GAAAGAGAAA	AAAGTTTAAA	GGATTAGGC	ATG	ATC	AAT	58								
					Met	Ile	Asn									
					1											
AAG	TTT	AAA	AAT	TTT	GTG	AGC	AAC	TAC	CAG	CAA	TCT	AAC	CAC	TAT	AAA	106
Lys	Phe	Lys	Asn	Phe	Val	Ser	Asn	Tyr	Gln	Gln	Ser	Asn	His	Tyr	Lys	
5						10					15					
GAG	CCT	TTA	GGT	TTT	GGC	ATT	GCC	AGA	GTG	GAT	ATT	GCC	CCT	ATT	TCC	154
Glu	Pro	Leu	Gly	Phe	Gly	Ile	Ala	Arg	Val	Asp	Ile	Ala	Pro	Ile	Ser	
20					25				30						35	
AAA	AAG	ATT	TTA	TGC	GCC	ACT	TAC	CCT	GTT	TTG	AAT	TGG	AAA	GAT	GAA	202
Lys	Lys	Ile	Leu	Cys	Ala	Thr	Tyr	Pro	Val	Leu	Asn	Trp	Lys	Asp	Glu	
			40					45					50			
AAT	TTA	GGC	TCT	TAT	GCG	GTG	TTT	TGC	AAC	TCG	CTT	TCA	AAA	GAA	AAA	250
Asn	Leu	Gly	Ser	Tyr	Ala	Val	Phe	Cys	Asn	Ser	Leu	Ser	Lys	Glu	Lys	
			55					60				65				
ATC	CTA	AAA	GAG	AGC	GCG	AGC	GAG	CGC	GTT	ATT	GAG	ATT	GAT	GAA	AGT	298
Ile	Leu	Lys	Glu	Ser	Ala	Ser	Glu	Arg	Val	Ile	Glu	Ile	Asp	Glu	Ser	
		70					75				80					
TTT	GTG	TTA	AAA	GCG	TTG	GAT	TTT	TAT	ACG	CCC	TTT	TTG	AAT	GAA	GCC	346
Phe	Val	Leu	Lys	Ala	Leu	Asp	Phe	Tyr	Thr	Pro	Phe	Leu	Asn	Glu	Ala	
85						90					95					
TAT	TCT	AAT	AAA	ATG	GCT	CAT	AAA	AAC	ATC	CAA	GTG	GTT	TTA	GAG	CTT	394
Tyr	Ser	Asn	Lys	Met	Ala	His	Lys	Asn	Ile	Gln	Val	Val	Leu	Glu	Leu	
100					105				110					115		
TTA	AAG	GCT	TTA	GAA	GAA	AAT	CGT	TTG	AAA	AAT	AGC	GAT	GGG	GAG	TCT	442
Leu	Lys	Ala	Leu	Glu	Glu	Asn	Arg	Leu	Lys	Asn	Ser	Asp	Gly	Glu	Ser	
			120					125					130			
CTT	TAT	CGC	TTG	GTG	ATC	TTG	TAT	GAA	GAT	AAG	CCT	TGC	GAG	AGC	GTG	490
Leu	Tyr	Arg	Leu	Val	Ile	Leu	Tyr	Glu	Asp	Lys	Pro	Cys	Glu	Ser	Val	
		135					140					145				
GAG	AGC	GCG	TAT	ATG	AAA	CTT	TTA	GCG	CTC	TCT	TTA	GGT	AAA	GCC	CCT	538
Glu	Ser	Ala	Tyr	Met	Lys	Leu	Leu	Ala	Leu	Ser	Leu	Gly	Lys	Ala	Pro	
		150				155						160				
TTG	AGG	AGT	TTG	AAT	TTA	GAG	GGT	ATT	TTT	AAC	CAG	CTT	TCT	AAT	GCG	586

Leu Ala 180	Arg Trp 165	Ser Ser 195	Leu Gly 195	Asn Asn 185	Leu Lys 185	Glu Pro 170	Gly Tyr 170	Ile Glu 170	Phe Leu 190	Asn Glu 190	Gln Trp 175	Leu Leu 195	Ser Arg 195	Asn Met 195	Ala Asn 195	
GCC Ala 180	TGG Trp 165	AGC Ser 195	GGT Gly 195	AAC Asn 185	AAG Lys 185	CCC Pro 170	TAT Tyr 170	GAA Glu 170	TTA Leu 190	GAA Glu 190	TGG Trp 175	CTT Leu 195	AGA Arg 195	ATG Met 195	AAC Asn 195	634
GAA Glu 200	GTG Val 165	GCT Ala 195	TTA Leu 200	AAA Lys 200	ATG Met 200	CGA Arg 170	GAC Asp 170	CAT His 205	TTC Phe 205	CCT Pro 190	AGC Ser 175	ATT Ile 195	GAT Asp 195	TTC Phe 210	ATA Ile 195	682
GAT Asp 215	AAA Lys 165	TTC Phe 195	CCA Pro 215	CGC Arg 215	TAT Tyr 215	TTG Leu 170	ATG Met 170	CAA Gln 220	TTA Leu 220	ATC Ile 190	CCT Pro 175	GAG Glu 225	TTT Phe 225	GAT Asp 215	AAT Asn 215	730
ATC Ile 230	CGC Arg 165	TTA Leu 230	TTG Leu 230	GAT Asp 230	AGC Ser 230	TCA Ser 170	AAA Lys 235	ACG Thr 235	CGC Arg 235	TTT Phe 240	GGG Gly 240	GCG Ala 240	TAT Tyr 240	TTA Leu 240	GGG Gly 240	778
ACT Thr 245	GGA Gly 245	GGT Gly 245	TAT Tyr 245	ACC Thr 245	CAA Gln 250	ATG Met 250	CCT Pro 250	GGG Gly 250	GCT Ala 255	AGT Ser 255	TAT Tyr 255	GTG Val 255	AAT Asn 255	TTT Phe 255	AAC Asn 255	826
GCA Ala 260	GGG Gly 260	GCT Ala 260	ATG Met 260	GGA Gly 265	GTG Val 265	TGC Cys 265	ATG Met 265	AAT Asn 270	GAG Glu 270	GGG Gly 270	CGT Arg 270	ATT Ile 270	TCT Ser 270	TCA Ser 275	TCG Ser 275	874
GTG Val 280	GTG Val 280	GTT Val 280	GGA Gly 280	GCA Ala 280	GGC Gly 280	ACT Thr 285	GAT Asp 285	ATT Ile 285	GGT Gly 285	GGG Gly 285	GGA Gly 285	GCG Ala 290	AGC Ser 290	GTG Val 290	TTA Leu 290	922
GGC Gly 295	GTT Val 295	TTA Leu 295	AGT Ser 295	GGA Gly 295	GGG Gly 295	AAT Asn 300	AAC Asn 300	AAC Asn 300	CCC Pro 300	ATT Ile 300	AGC Ser 300	ATC Ile 300	GGG Gly 305	AAA Lys 305	AAT Asn 305	970
TGT Cys 310	TTG Leu 310	CTA Leu 310	GGG Gly 310	GCT Ala 310	AAT Asn 310	AGC Ser 315	GTT Val 315	ACT Thr 315	GGA Gly 315	ATT Ile 315	AGT Ser 315	CTA Leu 320	GGC Gly 320	GAT Asp 320	GGC Gly 320	1018
TGT Cys 325	ATC Ile 325	GTG Val 325	GAT Asp 325	GCA Ala 325	GGC Gly 330	GTT Val 330	GCG Ala 330	ATA Ile 330	CTA Leu 330	GCC Ala 330	GGG Gly 335	AGC Ser 335	GTG Val 335	ATA Ile 335	GAA Glu 335	1066
ATT Ile 340	GAA Glu 340	GAA Glu 340	AAT Asn 340	GAG Glu 345	TTT Phe 345	AAA Lys 345	AAG Lys 345	CTT Leu 345	TTA Leu 345	GAA Glu 350	GTG Val 350	AAT Asn 350	AGC Ser 350	GCT Ala 350	TTA Leu 355	1114
GAA Glu 360	AAA Lys 360	CAT His 360	GCC Ala 360	AAC Asn 360	AAC Asn 360	CTT Leu 360	TAC Tyr 360	AAA Lys 360	GGC Gly 365	AAA Lys 365	GAA Glu 365	CTT Leu 365	TCC Ser 365	GGA Gly 370	AAA Lys 370	1162
AAT Asn 375	GGC Gly 375	GTG Val 375	CAT His 375	TTT Phe 375	CGT Arg 375	TCC Ser 375	AAT Asn 380	AGT Ser 380	CAG Gln 380	AAT Asn 380	GGC Gly 380	AAG Lys 380	CTG Leu 385	ATT Ile 385	GCT Ala 385	1210
TTT Phe 390	AGG Arg 390	AGC Ser 390	GTG Val 390	AAA Lys 390	AAA Lys 390	ATT Ile 395	GAG Glu 395	TTG Leu 395	AAT Asn 395	CAA Gln 395	AAC Asn 400	CTG Leu 400	CAT His 400	TAAGGATTA		1261

AAAGAATGCT CAAAAAAGT TTGTTATGTC TTGTTTTTTT AGTCTTACAG CTTAGCGGCG 1321
CTGAAGAAAA CAATCAAGCC CAAAAAAC 1350

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Ile	Asn	Lys	Phe	Lys	Asn	Phe	Val	Ser	Asn	Tyr	Gln	Gln	Ser	Asn	1	5	10	15
His	Tyr	Lys	Glu	Pro	Leu	Gly	Phe	Gly	Ile	Ala	Arg	Val	Asp	Ile	Ala	20	25	30	
Pro	Ile	Ser	Lys	Lys	Ile	Leu	Cys	Ala	Thr	Tyr	Pro	Val	Leu	Asn	Trp	35	40	45	
Lys	Asp	Glu	Asn	Leu	Gly	Ser	Tyr	Ala	Val	Phe	Cys	Asn	Ser	Leu	Ser	50	55	60	
Lys	Glu	Lys	Ile	Leu	Lys	Glu	Ser	Ala	Ser	Glu	Arg	Val	Ile	Glu	Ile	65	70	75	80
Asp	Glu	Ser	Phe	Val	Leu	Lys	Ala	Leu	Asp	Phe	Tyr	Thr	Pro	Phe	Leu	85	90	95	
Asn	Glu	Ala	Tyr	Ser	Asn	Lys	Met	Ala	His	Lys	Asn	Ile	Gln	Val	Val	100	105	110	
Leu	Glu	Leu	Leu	Lys	Ala	Leu	Glu	Glu	Asn	Arg	Leu	Lys	Asn	Ser	Asp	115	120	125	
Gly	Glu	Ser	Leu	Tyr	Arg	Leu	Val	Ile	Leu	Tyr	Glu	Asp	Lys	Pro	Cys	130	135	140	
Glu	Ser	Val	Glu	Ser	Ala	Tyr	Met	Lys	Leu	Leu	Ala	Leu	Ser	Leu	Gly	145	150	155	160
Lys	Ala	Pro	Leu	Arg	Ser	Leu	Asn	Leu	Glu	Gly	Ile	Phe	Asn	Gln	Leu	165	170	175	
Ser	Asn	Ala	Ala	Trp	Ser	Gly	Asn	Lys	Pro	Tyr	Glu	Leu	Glu	Trp	Leu	180	185	190	
Arg	Met	Asn	Glu	Val	Ala	Leu	Lys	Met	Arg	Asp	His	Phe	Pro	Ser	Ile	195	200	205	
Asp	Phe	Ile	Asp	Lys	Phe	Pro	Arg	Tyr	Leu	Met	Gln	Leu	Ile	Pro	Glu	210	215	220	
Phe	Asp	Asn	Ile	Arg	Leu	Leu	Asp	Ser	Ser	Lys	Thr	Arg	Phe	Gly	Ala	225	230	235	240
Tyr	Leu	Gly	Thr	Gly	Gly	Tyr	Thr	Gln	Met	Pro	Gly	Ala	Ser	Tyr	Val	245	250	255	
Asn	Phe	Asn	Ala	Gly	Ala	Met	Gly	Val	Cys	Met	Asn	Glu	Gly	Arg	Ile	260	265	270	
Ser	Ser	Ser	Val	Val	Val	Gly	Ala	Gly	Thr	Asp	Ile	Gly	Gly	Gly	Ala	275	280	285	
Ser	Val	Leu	Gly	Val	Leu	Ser	Gly	Gly	Asn	Asn	Asn	Pro	Ile	Ser	Ile	290	295	300	
Gly	Lys	Asn	Cys	Leu	Leu	Gly	Ala	Asn	Ser	Val	Thr	Gly	Ile	Ser	Leu	305	310	315	320
Gly	Asp	Gly	Cys	Ile	Val	Asp	Ala	Gly	Val	Ala	Ile	Leu	Ala	Gly	Ser	325	330	335	
Val	Ile	Glu	Ile	Glu	Glu	Asn	Glu	Phe	Lys	Lys	Leu	Leu	Glu	Val	Asn				

100					105					110					115	
ACC	ATC	ATG	GTA	GCG	AGC	GGT	TTT	CAA	GCT	GAA	AAA	AGC	TTG	CAT	GAC	442
Thr	Ile	Met	Val	Ala	Ser	Gly	Phe	Gln	Ala	Glu	Lys	Ser	Leu	His	Asp	
				120					125					130		
GCC	ATA	GAA	AAG	CAT	AAA	AAC	AAT	TAC	ATT	TTA	ATG	GTA	GAA	GGG	GGT	490
Ala	Ile	Glu	Lys	His	Lys	Asn	Asn	Tyr	Ile	Leu	Met	Val	Glu	Gly	Gly	
			135					140					145			
ATC	CCC	CAA	GGC	ACG	GAA	TAC	TTC	CTC	ACT	CAA	GGC	CCA	AAC	GCT	GAA	538
Ile	Pro	Gln	Gly	Thr	Glu	Tyr	Phe	Leu	Thr	Gln	Gly	Pro	Asn	Ala	Glu	
		150					155					160				
ACG	GGA	GCT	GAA	GAG	TGT	AGG	AAA	GCC	GCT	CAA	TAC	GCA	GCC	GCT	ATT	586
Thr	Gly	Ala	Glu	Glu	Cys	Arg	Lys	Ala	Ala	Gln	Tyr	Ala	Ala	Ala	Ile	
	165					170					175					
TTT	GCC	ATA	GGC	ACA	TGC	TCA	AGT	TTT	GGG	GGC	GTT	CAA	GCG	GCT	TAC	634
Phe	Ala	Ile	Gly	Thr	Cys	Ser	Ser	Phe	Gly	Gly	Val	Gln	Ala	Ala	Tyr	
180					185				190						195	
CCT	AAC	CCC	TCT	AAC	GCG	CAA	CCC	TTG	CAT	AAA	ATC	ATT	GAT	AAA	CCC	682
Pro	Asn	Pro	Ser	Asn	Ala	Gln	Pro	Leu	His	Lys	Ile	Ile	Asp	Lys	Pro	
				200					205					210		
GTG	ATC	AAT	GTT	CCT	GGT	TGC	CCG	CCT	AGT	GAA	AAA	AAT	ATC	GTG	GGT	730
Val	Ile	Asn	Val	Pro	Gly	Cys	Pro	Pro	Ser	Glu	Lys	Asn	Ile	Val	Gly	
			215					220					225			
AAT	GTG	CTT	TAT	TAC	TTG	ATG	TTT	GGG	GCT	CTC	CCT	AAA	TTG	GAT	GCG	778
Asn	Val	Leu	Tyr	Tyr	Leu	Met	Phe	Gly	Ala	Leu	Pro	Lys	Leu	Asp	Ala	
	230						235					240				
TAT	AAC	CGC	CCC	TCT	TGG	GCT	TAT	GGG	AAC	AGG	ATC	CAT	GAT	TTG	TGC	826
Tyr	Asn	Arg	Pro	Ser	Trp	Ala	Tyr	Gly	Asn	Arg	Ile	His	Asp	Leu	Cys	
	245					250					255					
GAA	AGG	AGA	GGG	CAT	TTT	GAT	GCG	GGC	GAA	TTT	GTG	GAG	CAT	TTT	GGC	874
Glu	Arg	Arg	Gly	His	Phe	Asp	Ala	Gly	Glu	Phe	Val	Glu	His	Phe	Gly	
260				265					270					275		
GAT	GAA	AAC	GCT	AAA	AGG	GGC	TTT	TGT	TTG	TAT	AAA	ATG	GGC	TGT	AAA	922
Asp	Glu	Asn	Ala	Lys	Arg	Gly	Phe	Cys	Leu	Tyr	Lys	Met	Gly	Cys	Lys	
			280					285					290			
GGG	CCT	TAC	ACT	TTC	AAC	AAT	TGC	TCC	AAA	CTC	CGC	TTC	AAT	TCA	CAC	970
Gly	Pro	Tyr	Thr	Phe	Asn	Asn	Cys	Ser	Lys	Leu	Arg	Phe	Asn	Ser	His	
			295				300						305			
ACC	TCT	TGG	CCC	ATA	GGT	GCA	GGG	CAT	GGG	TGT	ATA	GGG	TGT	TCT	GAG	1018
Thr	Ser	Trp	Pro	Ile	Gly	Ala	Gly	His	Gly	Cys	Ile	Gly	Cys	Ser	Glu	
		310					315					320				
CCT	AAT	TTT	TGG	GAT	ACG	ATG	AGT	CCT	TTT	GAA	GAG	CCT	TTA	GCG	AAT	1066
Pro	Asn	Phe	Trp	Asp	Thr	Met	Ser	Pro	Phe	Glu	Glu	Pro	Leu	Ala	Asn	
	325					330					335					

CGT TCC ATT AAA ACC GCT TTT GAC GGA TTA GGG GCT GAT AAA GTA GCG 1114
 Arg Ser Ile Lys Thr Ala Phe Asp Gly Leu Gly Ala Asp Lys Val Ala
 340 345 350 355

GAT AAA GTA GGC ACG ACT TTG CTG AGC GCA ACC GCT ATT GGC ATT GTT 1162
 Asp Lys Val Gly Thr Thr Leu Leu Ser Ala Thr Ala Ile Gly Ile Val
 360 365 370

GCG CAT GCG CTC CTT TCT AAA GCG ATC AAA AAC AAA GAG TAAGGGATTA AC 1213
 Ala His Ala Leu Leu Ser Lys Ala Ile Lys Asn Lys Glu
 375 380

ATGTCAAAAA AAATCGTAGT CGATCCTATC ACTAGGATTG AGGGGCATTT AAGGATTGAA 1273
 GTGATCGTAG ATGATGATAA CGTGATCACT G 1304

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Phe Tyr Asp Glu Lys Lys Thr Tyr Gln Lys Ile Glu Glu Arg Leu
 1 5 10 15
 Asp Ile Val Arg Ser Phe Asn Ala His Asn Glu His Lys Asn Leu Gln
 20 25 30
 Asp Glu Phe Lys Gly Ala Gly Ile Ser Arg Arg Asp Leu Leu Lys Trp
 35 40 45
 Ala Gly Met Met Ser Thr Ala Leu Ala Leu Pro Ala Ser Phe Ala Pro
 50 55 60
 Leu Thr Leu Lys Ala Val Glu Val Ala Asn Arg Leu Pro Val Ile Trp
 65 70 75 80
 Leu His Met Ala Glu Cys Thr Gly Cys Ser Glu Ser Leu Leu Arg Ser
 85 90 95
 Ala Asp Pro Thr Ile Asp Ser Ile Ile Phe Asp Tyr Ile Asn Leu Glu
 100 105 110
 Tyr His Glu Thr Ile Met Val Ala Ser Gly Phe Gln Ala Glu Lys Ser
 115 120 125
 Leu His Asp Ala Ile Glu Lys His Lys Asn Asn Tyr Ile Leu Met Val
 130 135 140
 Glu Gly Gly Ile Pro Gln Gly Thr Glu Tyr Phe Leu Thr Gln Gly Pro
 145 150 155 160
 Asn Ala Glu Thr Gly Ala Glu Glu Cys Arg Lys Ala Ala Gln Tyr Ala
 165 170 175
 Ala Ala Ile Phe Ala Ile Gly Thr Cys Ser Ser Phe Gly Gly Val Gln
 180 185 190
 Ala Ala Tyr Pro Asn Pro Ser Asn Ala Gln Pro Leu His Lys Ile Ile
 195 200 205
 Asp Lys Pro Val Ile Asn Val Pro Gly Cys Pro Pro Ser Glu Lys Asn
 210 215 220
 Ile Val Gly Asn Val Leu Tyr Tyr Leu Met Phe Gly Ala Leu Pro Lys
 225 230 235 240
 Leu Asp Ala Tyr Asn Arg Pro Ser Trp Ala Tyr Gly Asn Arg Ile His

GAG Glu	CCT Pro	TTA Leu	GAT Asp	GAA Glu 60	AAT Asn	CTT Leu	TTC Phe	CAA Gln	ACA Thr 65	GCA Ala	AGC Ser	CTT Leu	TCA Ser	AAG Lys 70	CCC Pro	244
CTT Leu	TTT Phe	ATG Met	AAC Asn 75	GCT Ala	AAA Lys	GAG Glu	CAT His	CAA Gln 80	GAT Asp	TTT Phe	TTA Leu	GAC Asp	AAA Lys 85	AAT Asn	TCA Ser	292
TCT Ser	TTG Leu	TAT Tyr 90	GCC Ala	GAT Asp	ACT Thr	CTG Leu	GGC Gly 95	TTG Leu	ATT Ile	AAA Lys	AAC Asn	ACC Thr 100	GCT Ala	TTT Phe	AAG Lys	340
GGG Gly	GAT Asp 105	ATA Ile	ATC Ile	CAT His	AGC Ser	CCT Pro 110	AAA Lys	GAG Glu	CTT Leu	ATA Ile	GAT Asp 115	TGC Cys	TTA Leu	ACC Thr	CAA Gln	388
TTA Leu 120	AAA Lys	GGC Gly	ATG Met	CTC Leu	AAA Lys 125	ACG Thr	CAA Gln	GAT Asp	TTT Phe 130	ATC Ile	CCT Pro	ATT Ile	TTC Phe	ACT Thr	TCT Ser 135	436
AGA Arg	GAG Glu	GCG Ala	TTA Leu	TCC Ser 140	CTT Leu	TCT Ser	TTA Leu	AAA Lys	AAT Asn 145	CCC Pro	TCT Ser	CCA Pro	AGC Ser	GTT Val 150	ATT Ile	484
TTT Phe	AGC Ser	GAT Asp	CTT Leu 155	TCT Ser	AGC Ser	GTT Val	TTG Leu	AGC Ser 160	TGC Cys	ACT Thr	AAA Lys	TTG Leu 165	CCT Pro	TTA Leu	GAG Glu	532
GAC Asp	GCT Ala	AAA Lys 170	TAT Tyr	TTG Leu	GCC Ala	AGT Ser	TTG Leu 175	GAA Glu	AAA Lys	CCC Pro	TCC Ser	ATC Ile 180	AAA Lys	GCC Ala	CCA Pro	580
TTA Leu	AAA Lys 185	AGC Ser	GTG Val	TTT Phe	AAA Lys 190	GAC Asp	ACT Thr	TTC Phe	AAA Lys	AAC Asn	GAT Asp 195	GAA Glu	ATC Ile	ATC Ile	GCC Ala	628
CAG Gln 200	CTA Leu	CCC Pro	TAT Tyr	GAC Asp	CCC Pro 205	ATA Ile	TTG Leu	AAT Asn	TTA Leu 210	TTG Leu	TGC Cys	CAT His	ATT Ile	TTA Leu	CAA Gln 215	676
GAT Asp	GAG Glu	GGG Gly	ATA Ile	GAA Glu 220	TTT Phe	GTT Val	TTT Phe	ATG Met 225	CAT His	GAA Glu	AGC Ser	CGT Arg	TCT Ser	TGT Cys 230	GAA Glu	724
GCG Ala	CTT Leu	TTG Leu	TAT Tyr 235	TAT Tyr	GAA Glu	GCG Ala	CTT Leu 240	TTT Phe	AAA Lys	ACC Thr	CCT Pro	AAA Lys	CGC Arg 245	TTG Leu	ATC Ile	772
ACA Thr	CCC Pro	ACT Thr 250	AAA Lys	AAA Lys	TTC Phe	GTG Val	CTA Leu 255	GAA Glu	AAT Asn	AAT Asn	TTT Phe 260	TCT Ser	ACC Thr	TTT Phe	CCC Pro	820
TTT Phe	AAA Lys 265	GAT Asp	GAA Glu	TTA Leu	GAG Glu	TTT Phe 270	TTA Leu	AGC Ser	GCA Ala	ACC Thr	CCC Pro 275	AAT Asn	TCT Ser	ATC Ile	GTT Val	868
TTG Leu	TAT Tyr	CTC Leu	AGT Ser	TTC Phe	AAG Lys	CGC Arg	CCT Pro	ACA Thr	AGG Arg	TTG Leu	TTA Leu	TTG Leu	CAT His	GCT Ala	AAT Asn	916

280					285					290					295	
GGT TCT TTA AAA ACG CTT TTA AGC GTC AGT TTT GAT TTT AAC AAA ATG	Gly Ser Leu Lys Thr 300	Leu Ser Val Ser 305	Phe Asp Phe Asn Lys Met 310		964											
TTT AAC GCG CTC AAA CAA GAT GAA AAA GCC TCC AGA ATG CTA CAA AAC	Phe Asn Ala Leu Lys 315	Gln Asp Glu Lys 320	Ala Ser Arg Met Leu Gln Asn 325		1012											
TAC GCC ACT AAA TTC CCT GAT TTT TAC GCG CGC ATT GTA GAG CTT TCT	Tyr Ala Thr Lys Phe Pro Asp Phe Tyr Ala Arg Ile Val Glu Leu Ser 330				1060											
AAA TAC GAT CTA GGG GGC GCG AAT TTA TTG GAT TTT TTT TGC ATT TTA	Lys Tyr Asp Leu Gly Gly Ala Asn Leu Leu Asp Phe Phe Cys Ile Leu 345				1108											
GGG TTT GTT TTG GGC TAT AGC GAG GAT TTT TGC ACA CAG AGC GTT ATT	Gly Phe Val Leu Gly Tyr Ser Glu Asp Phe Cys Thr Gln Ser Val Ile 360				1156											
CCT TTG GCT AAA GAA TGC TTA CGC CCT AAA GGC CCT AGG ATT GAT TAT	Pro Leu Ala Lys Glu Cys Leu Arg Pro Lys Gly Pro Arg Ile Asp Tyr 380				1204											
AAA ATC CTT AAA GAC AAT TCT TTG AAA ATG GCT TTA AAC TTT TCA AAG	Lys Ile Leu Lys Asp Asn Ser Leu Lys Met Ala Leu Asn Phe Ser Lys 395				1252											
ATC ATG CAC AGT GCG ATG AGT TTC AGG CTC GCA GGC GTG GAA AAT GAA	Ile Met His Ser Ala Met Ser Phe Arg Leu Ala Gly Val Glu Asn Glu 410				1300											
ATT TTG AGT TTG GGG ATT TTG GAT TCT TTA GCG GAG TTT TTA GGG AAT	Ile Leu Ser Leu Gly Ile Leu Asp Ser Leu Ala Glu Phe Leu Gly Asn 425				1348											
TTC ATT TGG GAT AAC GCG CAA AAT TTT AGC GTT CAA GAA GTA ACG ATC	Phe Ile Trp Asp Asn Ala Gln Asn Phe Ser Val Gln Glu Val Thr Ile 440				1396											
GCT GGG GAT TTC TTT GGC GAA AAA GTG TTT TTG GAT TTG TTT GTG CGG	Ala Gly Asp Phe Phe Gly Glu Lys Val Phe Leu Asp Leu Phe Val Arg 460				1444											
TAT TTC CCT AAA ACC CTA GCC CTT AAA ACG CAT GCA TTT TTG GAT TAT	Tyr Phe Pro Lys Thr Leu Ala Leu Lys Thr His Ala Phe Leu Asp Tyr 475				1492											
GAA TAAGGGCTTA AAAGCGGATG TGCATCATCA GCCCGCCGTC CATGTATT	Glu				1543											

(2) INFORMATION FOR SEQ ID NO:42:

(A) LENGTH: 488 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met	Ala	Cys	Asn	Leu	Gln	Ala	Arg	Phe	Tyr	Ser	Val	Tyr	Lys	Asp	Asn
1				5					10					15	
Thr	Thr	Ser	Phe	Tyr	Leu	Gln	Ala	Ser	Ala	Glu	Thr	Thr	Leu	Glu	Phe
		20						25					30		
Ala	Gln	Lys	Leu	Ser	Glu	Ile	Leu	Pro	Phe	Ser	Leu	Asp	Phe	Ser	Phe
		35					40					45			
Leu	Ser	Leu	Lys	Glu	Ile	Thr	Glu	Pro	Leu	Asp	Glu	Asn	Leu	Phe	Gln
	50					55					60				
Thr	Ala	Ser	Leu	Ser	Lys	Pro	Leu	Phe	Met	Asn	Ala	Lys	Glu	His	Gln
65					70					75					80
Asp	Phe	Leu	Asp	Lys	Asn	Ser	Ser	Leu	Tyr	Ala	Asp	Thr	Leu	Gly	Leu
				85					90					95	
Ile	Lys	Asn	Thr	Ala	Phe	Lys	Gly	Asp	Ile	Ile	His	Ser	Pro	Lys	Glu
		100						105						110	
Leu	Ile	Asp	Cys	Leu	Thr	Gln	Leu	Lys	Gly	Met	Leu	Lys	Thr	Gln	Asp
		115					120					125			
Phe	Ile	Pro	Ile	Phe	Thr	Ser	Arg	Glu	Ala	Leu	Ser	Leu	Ser	Leu	Lys
	130					135					140				
Asn	Pro	Ser	Pro	Ser	Val	Ile	Phe	Ser	Asp	Leu	Ser	Ser	Val	Leu	Ser
145					150					155					160
Cys	Thr	Lys	Leu	Pro	Leu	Glu	Asp	Ala	Lys	Tyr	Leu	Ala	Ser	Leu	Glu
				165					170					175	
Lys	Pro	Ser	Ile	Lys	Ala	Pro	Leu	Lys	Ser	Val	Phe	Lys	Asp	Thr	Phe
			180					185					190		
Lys	Asn	Asp	Glu	Ile	Ile	Ala	Gln	Leu	Pro	Tyr	Asp	Pro	Ile	Leu	Asn
		195					200					205			
Leu	Leu	Cys	His	Ile	Leu	Gln	Asp	Glu	Gly	Ile	Glu	Phe	Val	Phe	Met
	210					215					220				
His	Glu	Ser	Arg	Ser	Cys	Glu	Ala	Leu	Leu	Tyr	Tyr	Glu	Ala	Leu	Phe
225					230					235					240
Lys	Thr	Pro	Lys	Arg	Leu	Ile	Thr	Pro	Thr	Lys	Lys	Phe	Val	Leu	Glu
				245					250					255	
Asn	Asn	Phe	Ser	Thr	Phe	Pro	Phe	Lys	Asp	Glu	Leu	Glu	Phe	Leu	Ser
		260						265					270		
Ala	Thr	Pro	Asn	Ser	Ile	Val	Leu	Tyr	Leu	Ser	Phe	Lys	Arg	Pro	Thr
		275					280						285		
Arg	Leu	Leu	Leu	His	Ala	Asn	Gly	Ser	Leu	Lys	Thr	Leu	Leu	Ser	Val
	290					295					300				
Ser	Phe	Asp	Phe	Asn	Lys	Met	Phe	Asn	Ala	Leu	Lys	Gln	Asp	Glu	Lys
305					310					315					320
Ala	Ser	Arg	Met	Leu	Gln	Asn	Tyr	Ala	Thr	Lys	Phe	Pro	Asp	Phe	Tyr
			325						330					335	
Ala	Arg	Ile	Val	Glu	Leu	Ser	Lys	Tyr	Asp	Leu	Gly	Gly	Ala	Asn	Leu
		340						345					350		
Leu	Asp	Phe	Phe	Cys	Ile	Leu	Gly	Phe	Val	Leu	Gly	Tyr	Ser	Glu	Asp
	355					360						365			
Phe	Cys	Thr	Gln	Ser	Val	Ile	Pro	Leu	Ala	Lys	Glu	Cys	Leu	Arg	Pro
370						375					380				
Lys	Gly	Pro	Arg	Ile	Asp	Tyr	Lys	Ile	Leu	Lys	Asp	Asn	Ser	Leu	Lys

				85					90					95			
Phe	Val	Pro	Asn	Arg	Asn	Ala	Ile	Phe	Ile	Thr	Leu	Leu	His	Ser	Tyr		
			100					105					110				
Ala	Gln	Lys	Leu	Gly	Ala	Ser	Asn	Ile	Ala	Leu	Gly	Val	Ser	Gln	Ala		
		115					120					125					
Asp	Phe	Ser	Gly	Tyr	Pro	Asp	Cys	Lys	Glu	Asp	Phe	Ile	Lys	Ser	Ile		
	130					135					140						
Glu	His	Ala	Leu	Asn	Leu	Gly	Ser	Asn	Thr	Ala	Ile	Lys	Ile	Leu	Thr		
145				150						155					160		
Pro	Leu	Met	Phe	Leu	Asn	Lys	Ala	Gln	Glu	Phe	Gln	Met	Ala	Lys	Asp		
			165					170						175			
Leu	Gly	Val	Leu	Asp	Leu	Val	Ile	Lys	Glu	Thr	His	Thr	Cys	Tyr	Gln		
		180					185						190				
Gly	Glu	Arg	Lys	Ile	Leu	His	Ala	Tyr	Gly	Tyr	Gly	Cys	Asp	Lys	Cys		
	195					200						205					
Pro	Ala	Cys	Gln	Leu	Arg	Lys	Lys	Gly	Phe	Glu	Glu	Phe	Gln	Ala	Asn		
	210					215					220						
Lys	Lys																
225																	

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...1155
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TCCTCTCATG AGCTTTACTT GGTAGGGGGG TCGTGCGCG ATTATTTA ATG GGC ATT	57
Met Gly Ile	
1	
ACC CCA AAA GAT TAC GAT TTA ACC TCA AAC GCT TTA GTC AAT GAA AGC	105
Thr Pro Lys Asp Tyr Asp Leu Thr Ser Asn Ala Leu Val Asn Glu Ser	
5 10 15	
AAA GAG CTT CTT TTA AAG CGC CAT TTT AGG GTG CTA GAA ACC GGT ATC	153
Lys Glu Leu Leu Leu Lys Arg His Phe Arg Val Leu Glu Thr Gly Ile	
20 25 30 35	
AAA CAT GGT ACG ATC ACG GCT CTT AAA AAC CAT CAA AGC TAT GAA ATC	201
Lys His Gly Thr Ile Thr Ala Leu Lys Asn His Gln Ser Tyr Glu Ile	
40 45 50	
ACA ACT TTT AGA ATT GAA AAG GGG CAT ATC AAA CAC CGA AAG CCT AAA	249
Thr Thr Phe Arg Ile Glu Lys Gly His Ile Lys His Arg Lys Pro Lys	
55 60 65	

GAA TTT GGT TTT AGC GTT CAT TTA ACA GAC GAT TTA AAG CGG CGC GAT Glu Leu Val Phe Ser Val His Leu Thr Asp Asp Leu Lys Arg Arg Asp 70 75 80	297
TTT AGC ATG AAT GCG ATC GCT TAT AGC CCT ACA AAA GGG CTG ATT GAT Phe Ser Met Asn Ala Ile Ala Tyr Ser Pro Thr Lys Gly Leu Ile Asp 85 90 95	345
CCT TTT AAA GGG CAG AAT GCG ATT GAA AAT CAA ATG ATT GAA TGC GTG Pro Phe Lys Gly Gln Asn Ala Ile Glu Asn Gln Met Ile Glu Cys Val 100 105 110 115	393
GGG GAA GCG CGA TTA AGG TTT TTT GAA GAC GCT TTA AGG ATT TTA AGA Gly Glu Ala Arg Leu Arg Phe Phe Glu Asp Ala Leu Arg Ile Leu Arg 120 125 130	441
TCG CTG CGA TTC AGT GCA ACT TTA GGC TTT AAG ATA GCG CCA AAC ACC Ser Leu Arg Phe Ser Ala Thr Leu Gly Phe Lys Ile Ala Pro Asn Thr 135 140 145	489
AAA GAA GCG GTT TTT GCG TGT AAG GAT TTG TTA AAA CAC CTT TCT AAA Lys Glu Ala Val Phe Ala Cys Lys Asp Leu Leu Lys His Leu Ser Lys 150 155 160	537
GAA CGC TTA CAA AGT GAA TTG AAT AAG CTT CTT ATG GGG AAA AAC GCC Glu Arg Leu Gln Ser Glu Leu Asn Lys Leu Leu Met Gly Lys Asn Ala 165 170 175	585
TAT GAA GTG GCT AAA GAA TAT CAA GAA ATT TTA GAG TTG GTT ATT CAA Tyr Glu Val Ala Lys Glu Tyr Gln Glu Ile Leu Glu Leu Val Ile Gln 180 185 190 195	633
GAA AAA ATA GAA AAT TTA GGG TTT TTA AAA AAC GCG CCT TTC AAT CTG Glu Lys Ile Glu Asn Leu Gly Phe Leu Lys Asn Ala Pro Phe Asn Leu 200 205 210	681
GAA TTA AGA TTG TTA GGG TTT TTT AAG CAT CAA AAA AGT TTA GAA AGT Glu Leu Arg Leu Leu Gly Phe Phe Lys His Gln Lys Ser Leu Glu Ser 215 220 225	729
TTA CGC TAC CCT AAA AAA ACG ATC GTT TTA TTT TCC AAA GCT AAA GAA Leu Arg Tyr Pro Lys Lys Thr Ile Val Leu Phe Ser Lys Ala Lys Glu 230 235 240	777
TGC CAT AAA TCT TTT TTA AAT ATT CAT AAC AAA ACA GAG TTA AAA TTT Cys His Lys Ser Phe Leu Asn Ile His Asn Lys Thr Glu Leu Lys Phe 245 250 255	825
TTA TTG AAA AAC TAC GAT TTA GAG CCT TTT AAT TTG GCT TTA GAT TTT Leu Leu Lys Asn Tyr Asp Leu Glu Pro Phe Asn Leu Ala Leu Asp Phe 260 265 270 275	873
TAT GCG CTC AAA AAC CCC AAA CAT GCT TTA AAA ATT AAA GGC TTG TTA Tyr Ala Leu Lys Asn Pro Lys His Ala Leu Lys Ile Lys Gly Leu Leu 280 285 290	921
AAA GAA ATC TTT GAT TCT AAC GAG CCT TTT AAA AAA GAA CAC TTG GCC Lys Glu Ile Phe Asp Ser Asn Glu Pro Phe Lys Lys Glu His Leu Ala 969	

090327 091504
"090327 091504"

295	300	305	
CTT AAG GGC GGT GCG CTT CAA AGC TTG GGT TAC CAG CAC CAA AAA ATC			1017
Leu Lys Gly Gly Ala Leu Gln Ser Leu Gly Tyr Gln His Gln Lys Ile			
310	315	320	
GGC GAA ATT TTA AAC GCA TGC TTA GAT TTA GTC ATC GCT AAC CCT AAA			1065
Gly Glu Ile Leu Asn Ala Cys Leu Asp Leu Val Ile Ala Asn Pro Lys			
325	330	335	
AAT AAC GCT TTA GAA TGG CTG ATT GAA TGG GTT AAG GGT CAT TAT TTA			1113
Asn Asn Ala Leu Glu Trp Leu Ile Glu Trp Val Lys Gly His Tyr Leu			
340	345	350	355
CCT AAT GAT ACT ATA AAT CTT TCG CCA ATA GGC AGA AGA AAT TAAAAACAG			1164
Pro Asn Asp Thr Ile Asn Leu Ser Pro Ile Gly Arg Arg Asn			
360	365		
AGAAAACATG ATAACGATGA ATGCGATTCA ATGGCCT			1201

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met	Gly	Ile	Thr	Pro	Lys	Asp	Tyr	Asp	Leu	Thr	Ser	Asn	Ala	Leu	Val
1				5					10					15	
Asn	Glu	Ser	Lys	Glu	Leu	Leu	Leu	Lys	Arg	His	Phe	Arg	Val	Leu	Glu
			20					25					30		
Thr	Gly	Ile	Lys	His	Gly	Thr	Ile	Thr	Ala	Leu	Lys	Asn	His	Gln	Ser
		35					40					45			
Tyr	Glu	Ile	Thr	Thr	Phe	Arg	Ile	Glu	Lys	Gly	His	Ile	Lys	His	Arg
	50					55					60				
Lys	Pro	Lys	Glu	Leu	Val	Phe	Ser	Val	His	Leu	Thr	Asp	Asp	Leu	Lys
65				70						75				80	
Arg	Arg	Asp	Phe	Ser	Met	Asn	Ala	Ile	Ala	Tyr	Ser	Pro	Thr	Lys	Gly
			85					90						95	
Leu	Ile	Asp	Pro	Phe	Lys	Gly	Gln	Asn	Ala	Ile	Glu	Asn	Gln	Met	Ile
			100					105					110		
Glu	Cys	Val	Gly	Glu	Ala	Arg	Leu	Arg	Phe	Phe	Glu	Asp	Ala	Leu	Arg
		115					120					125			
Ile	Leu	Arg	Ser	Leu	Arg	Phe	Ser	Ala	Thr	Leu	Gly	Phe	Lys	Ile	Ala
	130					135					140				
Pro	Asn	Thr	Lys	Glu	Ala	Val	Phe	Ala	Cys	Lys	Asp	Leu	Leu	Lys	His
145				150						155				160	
Leu	Ser	Lys	Glu	Arg	Leu	Gln	Ser	Glu	Leu	Asn	Lys	Leu	Leu	Met	Gly
			165					170						175	
Lys	Asn	Ala	Tyr	Glu	Val	Ala	Lys	Glu	Tyr	Gln	Glu	Ile	Leu	Glu	Leu
		180						185					190		
Val	Ile	Gln	Glu	Lys	Ile	Glu	Asn	Leu	Gly	Phe	Leu	Lys	Asn	Ala	Pro
		195					200					205			

Phe Asn Leu Glu Leu Arg Leu Leu Gly Phe Phe Lys His Gln Lys Ser
 210 215 220
 Leu Glu Ser Leu Arg Tyr Pro Lys Lys Thr Ile Val Leu Phe Ser Lys
 225 230 235 240
 Ala Lys Glu Cys His Lys Ser Phe Leu Asn Ile His Asn Lys Thr Glu
 245 250 255
 Leu Lys Phe Leu Leu Lys Asn Tyr Asp Leu Glu Pro Phe Asn Leu Ala
 260 265 270
 Leu Asp Phe Tyr Ala Leu Lys Asn Pro Lys His Ala Leu Lys Ile Lys
 275 280 285
 Gly Leu Leu Lys Glu Ile Phe Asp Ser Asn Glu Pro Phe Lys Lys Glu
 290 295 300
 His Leu Ala Leu Lys Gly Gly Ala Leu Gln Ser Leu Gly Tyr Gln His
 305 310 315 320
 Gln Lys Ile Gly Glu Ile Leu Asn Ala Cys Leu Asp Leu Val Ile Ala
 325 330 335
 Asn Pro Lys Asn Asn Ala Leu Glu Trp Leu Ile Glu Trp Val Lys Gly
 340 345 350
 His Tyr Leu Pro Asn Asp Thr Ile Asn Leu Ser Pro Ile Gly Arg Arg
 355 360 365
 Asn

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 50...340
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TTTCCCCTA TATCAAAGC CATCATCAAG AAGTTTAAAG GCTCAAAGC ATG ATT TTT	58
Met Ile Phe	
1	
TCC ACT CTT ATT AAT GCG ATA GCG GTG ATT TTA AGC TCG CTC ATT ACG	106
Ser Thr Leu Ile Asn Ala Ile Ala Val Ile Leu Ser Ser Leu Ile Thr	
5 10 15	
ATT TAT ATG TGG ATA GTA ATC ATT TAT TCG CTT ATC AGT TTC GTG CAG	154
Ile Tyr Met Trp Ile Val Ile Ile Tyr Ser Leu Ile Ser Phe Val Gln	
20 25 30 35	
CCT AAC CCC AAT AAC CCC ATC ATG CAA ATT CTC GCT CGC TTG TGT GAG	202
Pro Asn Pro Asn Asn Pro Ile Met Gln Ile Leu Ala Arg Leu Cys Glu	
40 45 50	
CCG GTG TTT TAT TTT TTA CGC TCT AGA TTC AAG CTG GTG TTT AAC GGG	250

ATC GCT CTC AAA TTT GGC AAT TAT TAC TTG AAC CAT TTG AAA AAA GAA	1443
Ile Ala Leu Lys Phe Gly Asn Tyr Tyr Leu Asn His Leu Lys Lys Glu	
460 465 470	
TTC AAC CAC CCC CTT TTT GTC GCC TAC GCT TAT AAC GCT GGG CCT GGG	1491
Phe Asn His Pro Leu Phe Val Ala Tyr Ala Tyr Asn Ala Gly Pro Gly	
475 480 485 490	
TTT TTA AGG AGG TGG TTA GAA AGT TCC AAA CGA TTT AAA GAA AAA AAT	1539
Phe Leu Arg Arg Trp Leu Glu Ser Ser Lys Arg Phe Lys Glu Lys Asn	
495 500 505	
CAT TTT GAG CCA TGG CTT AGC ATG GAG CTT ATG CCT TAT AGC GAG ACT	1587
His Phe Glu Pro Trp Leu Ser Met Glu Leu Met Pro Tyr Ser Glu Thr	
510 515 520	
CGC ATG TAT GGC TTT AGG GTC ATG CTC AAT TAC TTG ATT TAT CAA GAA	1635
Arg Met Tyr Gly Phe Arg Val Met Leu Asn Tyr Leu Ile Tyr Gln Glu	
525 530 535	
ATT TTT GGG AAT TTC ATC CCT ATT GAT GGA TTT TTA GAA CAA ACT CTT	1683
Ile Phe Gly Asn Phe Ile Pro Ile Asp Gly Phe Leu Glu Gln Thr Leu	
540 545 550	
AAC TCA AAG GAC AAA CCA TGATTAAAAA ATGCCTTTTTT CCTGCTGCGG GCTATGGC	1739
Asn Ser Lys Asp Lys Pro	
555 560	
A	1740

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Arg Phe Phe Thr Leu Phe Phe Ile Gly Met Leu Gly Val Gly Phe	
1 5 10 15	
Ser Gln Thr Glu Leu Asn Leu Lys Asp Leu Glu Lys Lys Pro Ala Gly	
20 25 30	
Ile Val Arg Asp Tyr Tyr Leu Trp Arg Tyr Ile Ser Asp Lys Lys Thr	
35 40 45	
Ser Leu Glu Asn Ala Lys Lys Ala Tyr Glu Leu Thr Gln Asn Lys Asn	
50 55 60	
Asn Ala Leu Gln Lys Ala Met Gln Glu Lys Gly Ser Asp Asn Ala Glu	
65 70 75 80	
Lys Asn Pro Asp Val Lys Leu Pro Glu Asp Ile Tyr Cys Lys Gln Thr	
85 90 95	
Ala Leu Glu Ser Met Leu Glu Thr Thr Asp Thr Phe Gln Ala Ser Cys	
100 105 110	
Ile Ala Ile Ala Leu Lys Ser Lys Ile Arg Asp Phe Asp Lys Ile Pro	
115 120 125	

(A) LENGTH: 770 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 16...738
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TAAAAAGAAG GACAA ATG ATG CCA TTT GAA GCT GTA ATC GGG CTA GAA GTC	51
Met Met Pro Phe Glu Ala Val Ile Gly Leu Glu Val	
1 5 10	
CAT GTC CAA CTC AAC ACC AAA ACC AAA ATC TTT TGC TCT TGC TCT ACA	99
His Val Gln Leu Asn Thr Lys Thr Lys Ile Phe Cys Ser Cys Ser Thr	
15 20 25	
AGC TTT GGA GAA TCC CCT AAT TCT AAC ACC TGC CCT GTG TGT TTG GGT	147
Ser Phe Gly Glu Ser Pro Asn Ser Asn Thr Cys Pro Val Cys Leu Gly	
30 35 40	
TTA CCG GGA GCT TTG CCG GTA TTG AAT AAA GAA GTG GTT AAA AAA GCC	195
Leu Pro Gly Ala Leu Pro Val Leu Asn Lys Glu Val Val Lys Lys Ala	
45 50 55 60	
ATC CAA TTA GGC ACA GCC ATT GAA GCC AAT ATC AAC CAA TAT TCT ATT	243
Ile Gln Leu Gly Thr Ala Ile Glu Ala Asn Ile Asn Gln Tyr Ser Ile	
65 70 75	
TTT GCG AGG AAA AAT TAT TTT TAC CCT GAT TTG CCT AAG GCT TAT CAA	291
Phe Ala Arg Lys Asn Tyr Phe Tyr Pro Asp Leu Pro Lys Ala Tyr Gln	
80 85 90	
ATT TCG CAG TTT GAA GTC CCT ATT GTG AGC GAT GGG AAA TTA GAG ATT	339
Ile Ser Gln Phe Glu Val Pro Ile Val Ser Asp Gly Lys Leu Glu Ile	
95 100 105	
GAC ACT AAA GAG GGT GCA AAA ATC GTG CGT ATT GAA AGG GCC CAC ATG	387
Asp Thr Lys Glu Gly Ala Lys Ile Val Arg Ile Glu Arg Ala His Met	
110 115 120	
GAA GAA GAC GCC GGT AAA AAT ATC CAT GAG GGC AGT TAT TCT TTA GTG	435
Glu Glu Asp Ala Gly Lys Asn Ile His Glu Gly Ser Tyr Ser Leu Val	
125 130 135 140	
GAT TTG AAC CGC GCT TGC ACC CCT TTA TTA GAA ATT GTC AGT AAG CCG	483
Asp Leu Asn Arg Ala Cys Thr Pro Leu Leu Glu Ile Val Ser Lys Pro	
145 150 155	
GAC ATG CGA AAT AGT GAA GAA GCT ATA GCG TAT TTG AAA AAG CTC CAT	531
Asp Met Arg Asn Ser Glu Glu Ala Ile Ala Tyr Leu Lys Lys Leu His	
160 165 170	

GCT ATC GTG CGT TTT ATA GGG ATT TCT GAT GCG AAC ATG CAA GAG GGG	579
Ala Ile Val Arg Phe Ile Gly Ile Ser Asp Ala Asn Met Gln Glu Gly	
175 180 185	
AAT TTC AGG TGC GAT GCG AAC GTG TCC ATT AGA CCC AAA GGC GAT GAA	627
Asn Phe Arg Cys Asp Ala Asn Val Ser Ile Arg Pro Lys Gly Asp Glu	
190 195 200	
AAG CTT TAT ACG AGA GTA GAG ATT AAA AAT CTA AAT AGC TTT AGA TTC	675
Lys Leu Tyr Thr Arg Val Glu Ile Lys Asn Leu Asn Ser Phe Arg Phe	
205 210 215 220	
ATT GCT AAA GCG ATT GAA TAC GAG ATA GAG CGC CAA AGC GCG GAC GTG	723
Ile Ala Lys Ala Ile Glu Tyr Glu Ile Glu Arg Gln Ser Ala Asp Val	
225 230 235	
GGA GAA CGG GCG CTA TAATGAAGAG GTGGTTCAAG AAACGCGCCT TT	770
Gly Glu Arg Ala Leu	
240	

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Met Pro Phe Glu Ala Val Ile Gly Leu Glu Val His Val Gln Leu	
1 5 10 15	
Asn Thr Lys Thr Lys Ile Phe Cys Ser Cys Ser Thr Ser Phe Gly Glu	
20 25 30	
Ser Pro Asn Ser Asn Thr Cys Pro Val Cys Leu Gly Leu Pro Gly Ala	
35 40 45	
Leu Pro Val Leu Asn Lys Glu Val Val Lys Lys Ala Ile Gln Leu Gly	
50 55 60	
Thr Ala Ile Glu Ala Asn Ile Asn Gln Tyr Ser Ile Phe Ala Arg Lys	
65 70 75 80	
Asn Tyr Phe Tyr Pro Asp Leu Pro Lys Ala Tyr Gln Ile Ser Gln Phe	
85 90 95	
Glu Val Pro Ile Val Ser Asp Gly Lys Leu Glu Ile Asp Thr Lys Glu	
100 105 110	
Gly Ala Lys Ile Val Arg Ile Glu Arg Ala His Met Glu Glu Asp Ala	
115 120 125	
Gly Lys Asn Ile His Glu Gly Ser Tyr Ser Leu Val Asp Leu Asn Arg	
130 135 140	
Ala Cys Thr Pro Leu Leu Glu Ile Val Ser Lys Pro Asp Met Arg Asn	
145 150 155 160	
Ser Glu Glu Ala Ile Ala Tyr Leu Lys Lys Leu His Ala Ile Val Arg	
165 170 175	
Phe Ile Gly Ile Ser Asp Ala Asn Met Gln Glu Gly Asn Phe Arg Cys	
180 185 190	
Asp Ala Asn Val Ser Ile Arg Pro Lys Gly Asp Glu Lys Leu Tyr Thr	

	195		200		205
Arg	Val	Glu	Ile	Lys	Asn
	210				215
Ile	Glu	Tyr	Glu	Ile	Glu
225			230		235
Leu					

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...444
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ATGGGAGTGG ATTGA ATG CAA GAA ATT GAA ATT TTT TGC GAT GGC TCT TCT	51
Met Gln Glu Ile Glu Ile Phe Cys Asp Gly Ser Ser	
1 5 10	
TTA GGC AAT CCC GGG CCA GGC GGT TAT GCG GCG ATT TTA CGC TAT AAA	99
Leu Gly Asn Pro Gly Pro Gly Gly Tyr Ala Ala Ile Leu Arg Tyr Lys	
15 20 25	
GAT AAA GAA AAA ACC ATC AGT GGG GGC GAA GAA TTC ACC ACG AAT AAC	147
Asp Lys Glu Lys Thr Ile Ser Gly Gly Glu Glu Phe Thr Thr Asn Asn	
30 35 40	
CGC ATG GAA TTA AGA GCG CTC AAT GAA GCG TTA AAA ATT TTG AAA CGC	195
Arg Met Glu Leu Arg Ala Leu Asn Glu Ala Leu Lys Ile Leu Lys Arg	
45 50 55 60	
CCA TGC CGT ATC ACG CTT TAT AGC GAT TCG CAA TAC GTG TGC CAA GCG	243
Pro Cys Arg Ile Thr Leu Tyr Ser Asp Ser Gln Tyr Val Cys Gln Ala	
65 70 75	
ATC AAT GTG TGG CTA GCT AAC TGG CAA AAA AAG AAT TTT TCT AAA GTT	291
Ile Asn Val Trp Leu Ala Asn Trp Gln Lys Lys Asn Phe Ser Lys Val	
80 85 90	
AAA AAT GTG GAT TTA TGG AAA GAA TTT TTA GAA GTC TCT AAA GGG CAT	339
Lys Asn Val Asp Leu Trp Lys Glu Phe Leu Glu Val Ser Lys Gly His	
95 100 105	
TCT ATT GTG GCT GTT TGG ATC AAG GGG CAT AAC GGG CAT GCC GAG AAT	387
Ser Ile Val Ala Val Trp Ile Lys Gly His Asn Gly His Ala Glu Asn	
110 115 120	

GAA CGA TGC GAT AGC CTC GCT AAA TTA GAG GCG CAA AAA CGG GTC AAA 435
 Glu Arg Cys Asp Ser Leu Ala Lys Leu Glu Ala Gln Lys Arg Val Lys
 125 130 135 140

ACG ACC ACT TAAAGGGAAA AATGATGAAA AACAAACGCT CTCAAAACAG CCC 487
 Thr Thr Thr

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Gln	Glu	Ile	Glu	Ile	Phe	Cys	Asp	Gly	Ser	Ser	Leu	Gly	Asn	Pro
1				5					10					15	
Gly	Pro	Gly	Gly	Tyr	Ala	Ala	Ile	Leu	Arg	Tyr	Lys	Asp	Lys	Glu	Lys
			20					25					30		
Thr	Ile	Ser	Gly	Gly	Glu	Glu	Phe	Thr	Thr	Asn	Asn	Arg	Met	Glu	Leu
		35					40					45			
Arg	Ala	Leu	Asn	Glu	Ala	Leu	Lys	Ile	Leu	Lys	Arg	Pro	Cys	Arg	Ile
		50				55					60				
Thr	Leu	Tyr	Ser	Asp	Ser	Gln	Tyr	Val	Cys	Gln	Ala	Ile	Asn	Val	Trp
65					70					75				80	
Leu	Ala	Asn	Trp	Gln	Lys	Lys	Asn	Phe	Ser	Lys	Val	Lys	Asn	Val	Asp
			85					90					95		
Leu	Trp	Lys	Glu	Phe	Leu	Glu	Val	Ser	Lys	Gly	His	Ser	Ile	Val	Ala
			100					105					110		
Val	Trp	Ile	Lys	Gly	His	Asn	Gly	His	Ala	Glu	Asn	Glu	Arg	Cys	Asp
		115					120					125			
Ser	Leu	Ala	Lys	Leu	Glu	Ala	Gln	Lys	Arg	Val	Lys	Thr	Thr	Thr	
		130					135				140				

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 48...1181
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

215										220					225					
CAA	AAG	CTC	CCC	ATT	GGC	TTA	GGT	CAA	GGG	CTA	TAC	GCT	AAA	TTA	GAC	776				
Gln	Lys	Leu	Pro	Ile	Gly	Leu	Gly	Gln	Gly	Leu	Tyr	Ala	Lys	Leu	Asp					
230					235					240										
GCT	AAA	ATC	GCT	GAA	GCG	ATG	ATG	GGG	CTT	AAT	GGG	GTG	AAA	GCG	GTT	824				
Ala	Lys	Ile	Ala	Glu	Ala	Met	Met	Gly	Leu	Asn	Gly	Val	Lys	Ala	Val					
245					250					255										
GAA	ATA	GGC	AAG	GGG	GTA	GAA	AGC	TCT	TTA	TTA	AAA	GGC	TCA	GAG	TAT	872				
Glu	Ile	Gly	Lys	Gly	Val	Glu	Ser	Ser	Leu	Leu	Lys	Gly	Ser	Glu	Tyr					
260					265					270					275					
AAT	GAT	TTA	ATG	GAT	CAA	AAG	GGG	TTT	TTG	AGC	AAT	CGT	AGC	GGA	GGG	920				
Asn	Asp	Leu	Met	Asp	Gln	Lys	Gly	Phe	Leu	Ser	Asn	Arg	Ser	Gly	Gly					
280					285					290										
GTT	TTA	GGG	GGC	ATG	AGC	AAT	GGG	GAA	GAA	ATC	ATT	GTT	AGA	GTG	CAT	968				
Val	Leu	Gly	Gly	Met	Ser	Asn	Gly	Glu	Glu	Ile	Ile	Val	Arg	Val	His					
295					300					305										
TTC	AAA	CCC	ACG	CCA	AGC	ATT	TTC	CAA	CCT	CAA	CGA	ACC	ATA	GAC	ATT	1016				
Phe	Lys	Pro	Thr	Pro	Ser	Ile	Phe	Gln	Pro	Gln	Arg	Thr	Ile	Asp	Ile					
310					315					320										
AAT	GGC	AAT	GAG	TGC	GAA	TGC	TTG	TTA	AAG	GGC	AGG	CAT	GAT	CCT	TGC	1064				
Asn	Gly	Asn	Glu	Cys	Glu	Cys	Leu	Leu	Lys	Gly	Arg	His	Asp	Pro	Cys					
325					330					335										
ATT	GCG	ATT	AGA	GGG	AGC	GTG	GTG	TGC	GAG	AGT	TTG	TTA	GCG	TTG	GTG	1112				
Ile	Ala	Ile	Arg	Gly	Ser	Val	Val	Cys	Glu	Ser	Leu	Leu	Ala	Leu	Val					
340					345					350					355					
TTG	GCT	GAT	ATG	GTA	TTA	CTC	AAT	TTG	ACT	TCA	AAA	ATA	GAG	TAT	TTA	1160				
Leu	Ala	Asp	Met	Val	Leu	Leu	Asn	Leu	Thr	Ser	Lys	Ile	Glu	Tyr	Leu					
360					365					370										
AAA	ACG	ATT	TAT	AAT	GAG	AAT	TAAACGAAAT	TGGATACAAT	CAGCTTAAAA	AGGA	1215									
Lys	Thr	Ile	Tyr	Asn	Glu	Asn														
375																				
TA															1217					

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met	Arg	Leu	Ser	Ser	Ala	Ser	Lys	Thr	Glu	Gly	Ser	Gln	Met	Asn	Thr
1				5					10					15	

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 20...535
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TCATTGTGCC TGAAGCCAC ATG CGC TAC ATG CTC ATC AAC GAT TAT TAC AAG	52
Met Arg Tyr Met Leu Ile Asn Asp Tyr Tyr Lys	
1 5 10	
GTG TTT TTG GGC GAA AAA GAT AAG GAT TTG TAT GTG AAG CGC TTG GAA	100
Val Phe Leu Gly Glu Lys Asp Lys Asp Leu Tyr Val Lys Arg Leu Glu	
15 20 25	
AAA ATC ACG CCT AAA ATC TAT CTG GCG AGC GTG TTT TTA GAG AAA CAC	148
Lys Ile Thr Pro Lys Ile Tyr Leu Ala Ser Val Phe Leu Glu Lys His	
30 35 40	
ACC CCT TTA AAA AGT CTT TTA GAA AAA ATC CCT AAG GGA AAA AAA GAG	196
Thr Pro Leu Lys Ser Leu Leu Glu Lys Ile Pro Lys Gly Lys Lys Glu	
45 50 55	
ACT ATC ACC TAT CAT AAC CCT TGT CAT GCC AAA AAA ACC CTA AAC GCT	244
Thr Ile Thr Tyr His Asn Pro Cys His Ala Lys Lys Thr Leu Asn Ala	
60 65 70 75	
CAC AAA GAA GTG CGC AAC TTG CTC AAT TTG CAT TAT GAA ATT AAA GAA	292
His Lys Glu Val Arg Asn Leu Leu Asn Leu His Tyr Glu Ile Lys Glu	
80 85 90	
ATG CCG GAC AAT TGT TGC GGT TTT GGG GGG ATT ACG ATG CAA ACA CAA	340
Met Pro Asp Asn Cys Cys Gly Phe Gly Gly Ile Thr Met Gln Thr Gln	
95 100 105	
AAG GCG GGA TTT TCT TTA AAA GTG GGG CTT CTT AGG GCT AAA GAA ATC	388
Lys Ala Gly Phe Ser Leu Lys Val Gly Leu Leu Arg Ala Lys Glu Ile	
110 115 120	
ATA GAC ACC AAA GCT GCA ATT TTG AGC GCT GAA TGC GGG GCA TGC CAT	436
Ile Asp Thr Lys Ala Ala Ile Leu Ser Ala Glu Cys Gly Ala Cys His	
125 130 135	
ATG CAA TTA AAC AAC GCT TTA AAG TCT TTA GAC GAC CCT AAC ACT CCG	484
Met Gln Leu Asn Asn Ala Leu Lys Ser Leu Asp Asp Pro Asn Thr Pro	
140 145 150 155	
CCA TTT TTG CAC CCT TTA GAA CTC ATC GCT AAA GCC TTA AAA AGC GCT	532
Pro Phe Leu His Pro Leu Glu Leu Ile Ala Lys Ala Leu Lys Ser Ala	
160 165 170	
GAA TAAAAAGCCT TTTTAACCCC ATTCTCCAAC ATCTTTTAT ATAATACAGA GCT	588
Glu	

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 172 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```

Met Arg Tyr Met Leu Ile Asn Asp Tyr Tyr Lys Val Phe Leu Gly Glu
 1      5      10      15
Lys Asp Lys Asp Leu Tyr Val Lys Arg Leu Glu Lys Ile Thr Pro Lys
 20      25      30
Ile Tyr Leu Ala Ser Val Phe Leu Glu Lys His Thr Pro Leu Lys Ser
 35      40      45
Leu Leu Glu Lys Ile Pro Lys Gly Lys Lys Glu Thr Ile Thr Tyr His
 50      55      60
Asn Pro Cys His Ala Lys Lys Thr Leu Asn Ala His Lys Glu Val Arg
 65      70      75      80
Asn Leu Leu Asn Leu His Tyr Glu Ile Lys Glu Met Pro Asp Asn Cys
 85      90      95
Cys Gly Phe Gly Gly Ile Thr Met Gln Thr Gln Lys Ala Gly Phe Ser
100      105      110
Leu Lys Val Gly Leu Leu Arg Ala Lys Glu Ile Ile Asp Thr Lys Ala
115      120      125
Ala Ile Leu Ser Ala Glu Cys Gly Ala Cys His Met Gln Leu Asn Asn
130      135      140
Ala Leu Lys Ser Leu Asp Asp Pro Asn Thr Pro Pro Phe Leu His Pro
145      150      155      160
Leu Glu Leu Ile Ala Lys Ala Leu Lys Ser Ala Glu
165      170

```

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 30...317
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```

GGCGTTAAAG CTCTGTATTA TATAAAAAG ATG TTG GAG AAT GGG GTT AAA AAG      53
                Met Leu Glu Asn Gly Val Lys Lys
                1                5

GCT TTT TAT TCA GCG CTT TTT AAG GCT TTA GCG ATG AGT TCT AAA GGG      101
Ala Phe Tyr Ser Ala Leu Phe Lys Ala Leu Ala Met Ser Ser Lys Gly
10      15      20

```

TGC	AAA	AAT	GGC	GGA	GTG	TTA	GGG	TCG	TCT	AAA	GAC	TTT	AAA	GCG	TTG	149
Cys	Lys	Asn	Gly	Gly	Val	Leu	Gly	Ser	Ser	Lys	Asp	Phe	Lys	Ala	Leu	
25					30					35					40	
TTT	AAT	TGC	ATA	TGG	CAT	GCC	CCG	CAT	TCA	GCG	CTC	AAA	ATT	GCA	GCT	197
Phe	Asn	Cys	Ile	Trp	His	Ala	Pro	His	Ser	Ala	Leu	Lys	Ile	Ala	Ala	
			45						50					55		
TTG	GTG	TCT	ATG	ATT	TCT	TTA	GCC	CTA	AGA	AGC	CCC	ACT	TTT	AAA	GAA	245
Leu	Val	Ser	Met	Ile	Ser	Leu	Ala	Leu	Arg	Ser	Pro	Thr	Phe	Lys	Glu	
			60					65					70			
AAT	CCC	GCC	TTT	TGT	GTT	TGC	ATC	GTA	ATC	CCC	CCA	AAA	CCG	CAA	CAA	293
Asn	Pro	Ala	Phe	Cys	Val	Cys	Ile	Val	Ile	Pro	Pro	Lys	Pro	Gln	Gln	
		75					80					85				
TTG	TCC	GGC	ATT	TCT	TTA	ATT	TCA	TAATGCAAAT				TGAGCAACCT			TTTGCATTCT	347
Leu	Ser	Gly	Ile	Ser	Leu	Ile	Ser									
	90					95										
TAC																350

095007-0501

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met	Met	Ile	Phe	Ile	Asp	Ala	Cys	Phe	Arg	Lys	Glu	Thr	Pro	Tyr	Thr	1	5	10	15
Pro	Ile	Trp	Met	Met	Arg	Gln	Ala	Gly	Arg	Tyr	Leu	Ser	Glu	Tyr	Gln	20	25	30	
Glu	Ser	Arg	Lys	Lys	Ala	Gly	Ser	Phe	Leu	Glu	Leu	Cys	Lys	Asn	Ser	35	40	45	
Asp	Leu	Ala	Thr	Glu	Val	Thr	Leu	Gln	Pro	Val	Glu	Ile	Leu	Gly	Val	50	55	60	
Asp	Ala	Ala	Ile	Leu	Phe	Ser	Asp	Ile	Leu	Val	Val	Pro	Leu	Glu	Met	65	70	75	80
Gly	Leu	Asn	Leu	Glu	Phe	Ile	Pro	Lys	Lys	Gly	Pro	His	Phe	Leu	Glu	85	90	95	
Thr	Ile	Thr	Asp	Leu	Lys	Ser	Val	Glu	Ser	Leu	Lys	Val	Gly	Ala	Tyr	100	105	110	
Lys	Gln	Leu	Asn	Tyr	Val	Tyr	Asp	Thr	Ile	Ser	Gln	Thr	Arg	Gln	Lys	115	120	125	
Leu	Ser	Arg	Glu	Lys	Ala	Leu	Ile	Gly	Phe	Cys	Gly	Ser	Pro	Trp	Thr	130	135	140	
Leu	Ala	Thr	Tyr	Met	Ile	Glu	Gly	Glu	Gly	Ser	Lys	Ser	Tyr	Ala	Lys	145	150	155	160
Ser	Lys	Lys	Met	Leu	Tyr	Ser	Glu	Pro	Glu	Val	Leu	Lys	Ala	Leu	Leu	165	170	175	
Glu	Lys	Leu	Ser	Leu	Glu	Leu	Ile	Glu	Tyr	Leu	Ser	Leu	Gln	Ile	Gln	180	185	190	
Ala	Gly	Val	Asn	Ala	Val	Met	Ile	Phe	Asp	Ser	Trp	Ala	Ser	Ala	Leu	195	200	205	
Glu	Lys	Glu	Ala	Tyr	Leu	Lys	Phe	Ser	Trp	Asp	Tyr	Leu	Lys	Lys	Ile	210	215	220	
Ser	Lys	Glu	Leu	Lys	Lys	Arg	Tyr	Ala	His	Ile	Pro	Val	Ile	Leu	Phe	225	230	235	240
Pro	Lys	Gly	Ile	Gly	Ala	Tyr	Leu	Asp	Ser	Ile	Asp	Gly	Glu	Phe	Asp	245	250	255	
Val	Phe	Gly	Val	Asp	Trp	Gly	Thr	Pro	Leu	Thr	Ala	Ala	Lys	Lys	Ile	260	265	270	
Leu	Gly	Gly	Lys	Tyr	Val	Leu	Gln	Gly	Asn	Leu	Glu	Pro	Thr	Arg	Leu	275	280	285	
Tyr	Asp	Lys	Asn	Ala	Leu	Glu	Gly	Val	Glu	Thr	Ile	Leu	Lys	Val		290	295	300	
Met	Gly	Asn	Gln	Gly	His	Ile	Phe	Asn	Leu	Gly	His	Gly	Met	Leu	Pro	305	310	315	320
Asp	Leu	Pro	Arg	Glu	Asn	Ala	Lys	Tyr	Leu	Val	Gln	Leu	Val	His	Ala	325	330	335	
Lys	Thr	Arg	Arg													340			

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...732
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TAGACGACTA TGTGCATTAA GGGAATGAAA ATG ATA CGA AAA ATT TTA ATA GGA	54
Met Ile Arg Lys Ile Leu Ile Gly	
1 5	
CTT TTT TTG AGT TTT TTG AGC ATG GAA GCT GGC GAA AAA GTG TAT GCG	102
Leu Phe Leu Ser Phe Leu Ser Met Glu Ala Gly Glu Lys Val Tyr Ala	
10 15 20	
ATT TTC AAT GTG AAA GCG ACA CAA GAT TCC AAA CTC ACC TTA GAC AGC	150
Ile Phe Asn Val Lys Ala Thr Gln Asp Ser Lys Leu Thr Leu Asp Ser	
25 30 35 40	
ACA GGA ATT GTG GAT AGC ATT AAG GTT ACT GAG GGG AGC GTG GTC AAA	198
Thr Gly Ile Val Asp Ser Ile Lys Val Thr Glu Gly Ser Val Val Lys	
45 50 55	
AAG GGC GAT GTT TTG TTG CTT TTA TAT AAT CAA GAC AAA CAG GCT CAA	246
Lys Gly Asp Val Leu Leu Leu Leu Tyr Asn Gln Asp Lys Gln Ala Gln	
60 65 70	
AGC GAT TCC ACC GAA CAA CAA CTC ATT TTC GCT AAA AAG CAA TAC CAA	294
Ser Asp Ser Thr Glu Gln Gln Leu Ile Phe Ala Lys Lys Gln Tyr Gln	
75 80 85	
CGA TAC AGC AAA ATT GGG GGC GCT GTG GAT AAA AAC ACT CTA GAG GGT	342
Arg Tyr Ser Lys Ile Gly Gly Ala Val Asp Lys Asn Thr Leu Glu Gly	
90 95 100	
TAT GAG TTC ACT TAC AGG CGC TTG GAG TCT GAT TAC GCT TAT TCT ATT	390
Tyr Glu Phe Thr Tyr Arg Arg Leu Glu Ser Asp Tyr Ala Tyr Ser Ile	
105 110 115 120	
GCG GTA TTG AAT AAA ACC ATT TTA AGA GCC CCT TTT GAT GGC GTG ATA	438
Ala Val Leu Asn Lys Thr Ile Leu Arg Ala Pro Phe Asp Gly Val Ile	
125 130 135	
GCG AGT AAA AAC ATT CAA GTG GGC GAA GGG GTG AGC GCG AAT AAC ACG	486
Ala Ser Lys Asn Ile Gln Val Gly Glu Gly Val Ser Ala Asn Asn Thr	
140 145 150	
GTG TTA TTG AGA TTA GTC AGC CAT GCT AGG AAA TTA GTT ATT GAA TTT	534
Val Leu Leu Arg Leu Val Ser His Ala Arg Lys Leu Val Ile Glu Phe	

155	160	165	
GAT TCT AAA TAT ATT AAT GCG GTC AAA GTA GGG GAC ACT TAC ACC TAT			582
Asp Ser Lys Tyr Ile Asn Ala Val Lys Val Gly Asp Thr Tyr Thr Tyr			
170	175	180	
TCT ATA GAC GGG GAT TCT AAT CAG CAT GAA GCT AAA ATC ACT AAG ATT			630
Ser Ile Asp Gly Asp Ser Asn Gln His Glu Ala Lys Ile Thr Lys Ile			
185	190	195	200
TAC CCC ACG GTT GAT GAA AAC ACC AGG AAA GTG AGC GCT GAA GCC CTT			678
Tyr Pro Thr Val Asp Glu Asn Thr Arg Lys Val Ser Ala Glu Ala Leu			
205	210	215	
TTA TCT AAG CCT ATG GCA GTG GGG CTT TTT GGC GAT GGG TTT ATC CAA			726
Leu Ser Lys Pro Met Ala Val Gly Leu Phe Gly Asp Gly Phe Ile Gln			
220	225	230	
ACG AAA TAATAGGATA TTTTGATGTA TAAAACAGCG ATTA			766
Thr Lys			

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Ile	Arg	Lys	Ile	Leu	Ile	Gly	Leu	Phe	Leu	Ser	Phe	Leu	Ser	Met
1				5				10						15	
Glu	Ala	Gly	Glu	Lys	Val	Tyr	Ala	Ile	Phe	Asn	Val	Lys	Ala	Thr	Gln
			20					25					30		
Asp	Ser	Lys	Leu	Thr	Leu	Asp	Ser	Thr	Gly	Ile	Val	Asp	Ser	Ile	Lys
		35					40					45			
Val	Thr	Glu	Gly	Ser	Val	Val	Lys	Lys	Gly	Asp	Val	Leu	Leu	Leu	Leu
		50				55					60				
Tyr	Asn	Gln	Asp	Lys	Gln	Ala	Gln	Ser	Asp	Ser	Thr	Glu	Gln	Gln	Leu
65					70					75					80
Ile	Phe	Ala	Lys	Lys	Gln	Tyr	Gln	Arg	Tyr	Ser	Lys	Ile	Gly	Gly	Ala
			85						90					95	
Val	Asp	Lys	Asn	Thr	Leu	Glu	Gly	Tyr	Glu	Phe	Thr	Tyr	Arg	Arg	Leu
			100					105					110		
Glu	Ser	Asp	Tyr	Ala	Tyr	Ser	Ile	Ala	Val	Leu	Asn	Lys	Thr	Ile	Leu
		115					120					125			
Arg	Ala	Pro	Phe	Asp	Gly	Val	Ile	Ala	Ser	Lys	Asn	Ile	Gln	Val	Gly
		130				135					140				
Glu	Gly	Val	Ser	Ala	Asn	Asn	Thr	Val	Leu	Leu	Arg	Leu	Val	Ser	His
145					150					155					160
Ala	Arg	Lys	Leu	Val	Ile	Glu	Phe	Asp	Ser	Lys	Tyr	Ile	Asn	Ala	Val
			165						170					175	
Lys	Val	Gly	Asp	Thr	Tyr	Thr	Tyr	Ser	Ile	Asp	Gly	Asp	Ser	Asn	Gln

ATG GTG TTA AGC TTA CTC ATT GTG CCG GTG TTT TAT CGT TTG CTC GCT 493
Met Val Leu Ser Leu Leu Ile Val Pro Val Phe Tyr Arg Leu Leu Ala
130 135 140

CCC ATA GAC GAC AAA ATC AAG CGG TTT TAT CAA AAC CAA AAA ACT TTA 541
Pro Ile Asp Asp Lys Ile Lys Arg Phe Tyr Gln Asn Gln Lys Thr Leu
145 150 155 160

GAA TGAAAAAAT TGCTTTCATT TTGGCTTTAT GGGTGGGCTT GTTAGGGGCG TTTGAG 600
Glu

CCTAAAAAAA GTCATATTTA TTTTGGGGCT 630

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Ile Leu Ala Ala Leu Tyr Glu Ser Ile Leu Glu Pro Phe Ile Ile
1 5 10 15
Met Val Thr Met Pro Leu Ser Phe Ser Gly Ala Phe Phe Ala Leu Gly
20 25 30
Leu Val His Gln Pro Leu Ser Met Phe Ser Met Ile Gly Leu Ile Leu
35 40 45
Leu Ile Gly Met Val Gly Lys Asn Ala Thr Leu Leu Ile Asp Val Ala
50 55 60
Asn Glu Glu Arg Lys Lys Gly Leu Asn Ile Gln Glu Ala Ile Leu Phe
65 70 75 80
Ala Gly Lys Thr Arg Leu Arg Pro Ile Leu Met Thr Thr Ile Ala Met
85 90 95
Val Cys Gly Met Leu Pro Leu Ala Leu Ala Ser Gly Asp Gly Ala Ala
100 105 110
Met Lys Ser Pro Ile Gly Ile Ala Met Ser Gly Gly Leu Met Ile Ser
115 120 125
Met Val Leu Ser Leu Leu Ile Val Pro Val Phe Tyr Arg Leu Leu Ala
130 135 140
Pro Ile Asp Asp Lys Ile Lys Arg Phe Tyr Gln Asn Gln Lys Thr Leu
145 150 155 160
Glu

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...945
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TAAAAGGTTT TTACAAAC	ATG ATA AAA AGC CAA AAA GAA TAT TTA GAA AGA	51
	Met Ile Lys Ser Gln Lys Glu Tyr Leu Glu Arg	
	1 5 10	
ATT GCA TAT TTA AAC ACC CTA TCG CAC CAT TAT TAC AAC CTT GAT GAA	99	
Ile Ala Tyr Leu Asn Thr Leu Ser His His Tyr Tyr Asn Leu Asp Glu		
	15 20 25	
CCC ATC GTA AGC GAT GCG ATC TAT GAT GAA CTT TAC CAA GAA TTG AAA	147	
Pro Ile Val Ser Asp Ala Ile Tyr Asp Glu Leu Tyr Gln Glu Leu Lys		
	30 35 40	
GCT TAT GAA GAA AAA AAC CCT AAT GGC ATT CAA GCT AAT TCC CCT ACC	195	
Ala Tyr Glu Glu Lys Asn Pro Asn Gly Ile Gln Ala Asn Ser Pro Thr		
	45 50 55	
CAA AAA GTG GGG GCT ACT ACC ACC AAT TCG TTC AAT AAA AAC CCC CAT	243	
Gln Lys Val Gly Ala Thr Thr Thr Asn Ser Phe Asn Lys Asn Pro His		
	60 65 70 75	
TTA ATG CGG ATG TGG AGC TTA GAT GAT GTG TTC AAT CAA AGC GAA TTG	291	
Leu Met Arg Met Trp Ser Leu Asp Asp Val Phe Asn Gln Ser Glu Leu		
	80 85 90	
CAA GCG TGG TTG CAA CGC ATT TTA AAA GCC TAT CCT AGT GCT TCG TTC	339	
Gln Ala Trp Leu Gln Arg Ile Leu Lys Ala Tyr Pro Ser Ala Ser Phe		
	95 100 105	
GTG TGT TCG CCC AAA CTT GAT GGG GTT TCG CTC AAT CTT TTG TAT CAA	387	
Val Cys Ser Pro Lys Leu Asp Gly Val Ser Leu Asn Leu Leu Tyr Gln		
	110 115 120	
CAT GGC AAG CTA GTG AAG GCG ACC ACT AGG GGC AAC GGC TTA GAA GGA	435	
His Gly Lys Leu Val Lys Ala Thr Thr Arg Gly Asn Gly Leu Glu Gly		
	125 130 135	
GAA TTA GTT AGC GCA AAC GCT AAA CAC ATC GCT AAT ATC CCC CAC GCT	483	
Glu Leu Val Ser Ala Asn Ala Lys His Ile Ala Asn Ile Pro His Ala		
	140 145 150 155	
ATC GCT TAT AAT GGA GAA ATA GAA ATC AGG GGC GAA GTG ATC ATT TCT	531	
Ile Ala Tyr Asn Gly Glu Ile Glu Ile Arg Gly Glu Val Ile Ile Ser		
	160 165 170	
AAA AAG GAT TTT GAC GCT TTG AAT CAA GAG CGC TTA AAC GCT AAT GAA	579	
Lys Lys Asp Phe Asp Ala Leu Asn Gln Glu Arg Leu Asn Ala Asn Glu		
	175 180 185	
CCC CTA TTC GCT AAC CCC AGA AAC GCC GCA TCA GGG AGT TTG AGG CAA	627	

Pro	Leu	Phe	Ala	Asn	Pro	Arg	Asn	Ala	Ala	Ser	Gly	Ser	Leu	Arg	Gln		
	190						195					200					
CTT	GAT	AGC	GAA	ATC	ACT	AAA	AAG	CGT	AAA	TTG	CAA	TTC	ATT	CCT	TGG	675	
Leu	Asp	Ser	Glu	Ile	Thr	Lys	Lys	Arg	Lys	Leu	Gln	Phe	Ile	Pro	Trp		
	205					210				215							
GGC	GTG	GGC	AAG	CAT	TCT	TTA	AAT	TTT	TTA	AGC	TTT	AAG	GAG	TGT	TTG	723	
Gly	Val	Gly	Lys	His	Ser	Leu	Asn	Phe	Leu	Ser	Phe	Lys	Glu	Cys	Leu		
	220				225					230					235		
GAT	TTT	ATC	GTC	TCG	TTA	GGT	TTT	AGC	GCC	ATT	CAA	TAC	TTA	AGC	CTA	771	
Asp	Phe	Ile	Val	Ser	Leu	Gly	Phe	Ser	Ala	Ile	Gln	Tyr	Leu	Ser	Leu		
				240					245					250			
AAC	AAA	AAC	CAC	CAA	GAA	ATA	GAA	GAC	AAT	TAC	CAC	ACC	CTA	ATT	AGA	819	
Asn	Lys	Asn	His	Gln	Glu	Ile	Glu	Asp	Asn	Tyr	His	Thr	Leu	Ile	Arg		
			255					260					265				
GAA	AGG	GAG	GGC	TTT	TTT	GCC	CTT	TTA	GAC	GGC	ATG	GTG	ATC	GTT	GTG	867	
Glu	Arg	Glu	Gly	Phe	Phe	Ala	Leu	Leu	Asp	Gly	Met	Val	Ile	Val	Val		
		270					275					280					
AAT	GAA	TTA	AAT	ATT	CAA	AAG	GAG	CTA	GGC	TAC	ACG	CAA	AAA	TCC	CCT	915	
Asn	Glu	Leu	Asn	Ile	Gln	Lys	Glu	Leu	Gly	Tyr	Thr	Gln	Lys	Ser	Pro		
	285					290				295							
AAA	TNG	CTT	GCG	CTT	ATA	AAT	TCC	CGG	CTT	TAGAAAAACA CACCAAAATT					GTA	968	
Lys	Xaa	Leu	Ala	Leu	Ile	Asn	Ser	Arg	Leu								
	300				305												
GGAGTCATTA ACCAAGTGGG GCGCASSGGG CGATCACAC																1007	

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met	Ile	Lys	Ser	Gln	Lys	Glu	Tyr	Leu	Glu	Arg	Ile	Ala	Tyr	Leu	Asn		
1				5				10						15			
Thr	Leu	Ser	His	His	Tyr	Tyr	Asn	Leu	Asp	Glu	Pro	Ile	Val	Ser	Asp		
			20					25					30				
Ala	Ile	Tyr	Asp	Glu	Leu	Tyr	Gln	Glu	Leu	Lys	Ala	Tyr	Glu	Glu	Lys		
			35				40					45					
Asn	Pro	Asn	Gly	Ile	Gln	Ala	Asn	Ser	Pro	Thr	Gln	Lys	Val	Gly	Ala		
			50			55				60							
Thr	Thr	Thr	Asn	Ser	Phe	Asn	Lys	Asn	Pro	His	Leu	Met	Arg	Met	Trp		
			65		70				75					80			
Ser	Leu	Asp	Asp	Val	Phe	Asn	Gln	Ser	Glu	Leu	Gln	Ala	Trp	Leu	Gln		
			85					90					95				
Arg	Ile	Leu	Lys	Ala	Tyr	Pro	Ser	Ala	Ser	Phe	Val	Cys	Ser	Pro	Lys		

Leu	Asp	Gly	Val	Ser	Leu	Asn	Leu	Tyr	Gln	His	Gly	Lys	Leu	Val	
		115					120				125				
Lys	Ala	Thr	Thr	Arg	Gly	Asn	Gly	Leu	Glu	Gly	Glu	Leu	Val	Ser	Ala
		130				135					140				
Asn	Ala	Lys	His	Ile	Ala	Asn	Ile	Pro	His	Ala	Ile	Ala	Tyr	Asn	Gly
					150					155					160
Glu	Ile	Glu	Ile	Arg	Gly	Glu	Val	Ile	Ile	Ser	Lys	Lys	Asp	Phe	Asp
				165				170						175	
Ala	Leu	Asn	Gln	Glu	Arg	Leu	Asn	Ala	Asn	Glu	Pro	Leu	Phe	Ala	Asn
		180					185						190		
Pro	Arg	Asn	Ala	Ala	Ser	Gly	Ser	Leu	Arg	Gln	Leu	Asp	Ser	Glu	Ile
		195					200					205			
Thr	Lys	Lys	Arg	Lys	Leu	Gln	Phe	Ile	Pro	Trp	Gly	Val	Gly	Lys	His
		210				215					220				
Ser	Leu	Asn	Phe	Leu	Ser	Phe	Lys	Glu	Cys	Leu	Asp	Phe	Ile	Val	Ser
					230					235					240
Leu	Gly	Phe	Ser	Ala	Ile	Gln	Tyr	Leu	Ser	Leu	Asn	Lys	Asn	His	Gln
				245						250				255	
Glu	Ile	Glu	Asp	Asn	Tyr	His	Thr	Leu	Ile	Arg	Glu	Arg	Glu	Gly	Phe
			260					265					270		
Phe	Ala	Leu	Leu	Asp	Gly	Met	Val	Ile	Val	Val	Asn	Glu	Leu	Asn	Ile
		275					280					285			
Gln	Lys	Glu	Leu	Gly	Tyr	Thr	Gln	Lys	Ser	Pro	Lys	Xaa	Leu	Ala	Leu
		290				295					300				
Ile	Asn	Ser	Arg	Leu											
305															

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 937 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 44...880
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGCTTTAGA	TTAGATGCAG	AAAAAGACGC	CCAACTTTAT	GGC	ATG	AAT	ATT	TTT		55
					Met	Asn	Ile	Phe		
					1					
AAG ATC CGA	GAA ATT ATC	CAT TAT GAC	GGG GAG GTT	ACA GAG ATT	CTT					103
Lys Ile Arg	Glu Ile Ile	His Tyr Asp	Gly Glu Val	Thr Glu Ile	Leu					
5		10		15	20					
GGG GGG AGC	GAT GGC GTG	ATG CTC GGG	TTT CTT AGC	GTT AGG GGC	GAG					151
Gly Gly Ser	Asp Gly Val	Met Leu Gly	Phe Leu Ser	Val Arg Gly	Glu					
	25		30		35					

265

270

275

ACG CTT TCA TAAATTTAAT TTTTGTTTTA ATTTAAAGGG ATAAAACATG CGAAGTCAT 929
 Thr Leu Ser

TTTTGCAC

937

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Asn Ile Phe Lys Ile Arg Glu Ile Ile His Tyr Asp Gly Glu Val
 1 5 10 15
 Thr Glu Ile Leu Gly Gly Ser Asp Gly Val Met Leu Gly Phe Leu Ser
 20 25 30
 Val Arg Gly Glu Ser Ile Pro Leu Val Asp Val Lys Arg Trp Leu His
 35 40 45
 Tyr Asn Ala Asn Asp Pro Ser Arg Asp Leu Lys Glu Cys Ser Val Lys
 50 55 60
 Asp Asp His Asn Leu Val Ile Val Cys His Phe Ser Asn His Ser Ile
 65 70 75 80
 Ala Leu Lys Val Leu Lys Ile Glu Arg Ile Ile His Lys Asn Trp Thr
 85 90 95
 Glu Ile Ser Ala Gly Asp Lys Gln Gly Ile Asn Glu Glu Gly Lys Leu
 100 105 110
 Ser Ala Ile Thr Arg Phe Asp Glu Glu Arg Val Val Gln Ile Leu Asp
 115 120 125
 Val Glu Lys Met Ile Ser Asp Val Phe Pro Ser Leu Lys Asp Leu Asp
 130 135 140
 Asp Leu Thr Leu Arg Cys Ile Glu Ala Ile Gln Ser Gln Lys Leu Ile
 145 150 155 160
 Leu Ile Ala Glu Asp Ser Leu Ser Ala Leu Lys Thr Leu Glu Lys Ile
 165 170 175
 Val Gln Thr Leu Glu Leu Arg Tyr Leu Ala Phe Pro Asn Gly Arg Glu
 180 185 190
 Leu Leu Asp Tyr Leu Tyr Glu Lys Glu His Tyr Gln Gln Val Gly Val
 195 200 205
 Val Ile Thr Asp Leu Glu Met Pro Asn Ile Ser Gly Phe Glu Val Leu
 210 215 220
 Lys Thr Ile Lys Ala Asp His Arg Thr Glu His Leu Pro Val Ile Ile
 225 230 235 240
 Asn Ser Ser Met Ser Asp Ser Asn Arg Gln Leu Ala Gln Ser Leu
 245 250 255
 Glu Ala Asp Gly Phe Val Val Lys Ser Asn Ile Leu Glu Ile His Glu
 260 265 270
 Met Leu Lys Lys Thr Leu Ser
 275

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 21...593
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATAATTTAAA AGGATACGAT	ATG AAA CAA CTA TTT TTG ATC ATT GGA GCC	50
	Met Lys Gln Leu Phe Leu Ile Ile Gly Ala	
	1 5 10	
CCA GGG AGT GGT AAA ACC ACT GAT GCA GAG CTT ATC GCT AAA AAT AAC		98
Pro Gly Ser Gly Lys Thr Thr Asp Ala Glu Leu Ile Ala Lys Asn Asn		
	15 20 25	
AGC GAA ACA ATC GCT CAT TTT TCT ACC GGG GAT TTA CTC AGG GCT GAG		146
Ser Glu Thr Ile Ala His Phe Ser Thr Gly Asp Leu Leu Arg Ala Glu		
	30 35 40	
AGC GCT AAA AAG ACC GAG CGA GGC TTA TTG ATT GAA AAA TTC ACT TCT		194
Ser Ala Lys Lys Thr Glu Arg Gly Leu Leu Ile Glu Lys Phe Thr Ser		
	45 50 55	
CAA GGC GAA TTA GTG CCT TTA GAA ATT GTG GTA GAA ACG ATC CTT TCA		242
Gln Gly Glu Leu Val Pro Leu Glu Ile Val Val Glu Thr Ile Leu Ser		
	60 65 70	
GCG ATT AAA AGC TCT GGT AAA GGG ATC ATT TTA ATT GAT GGT TAT CCT		290
Ala Ile Lys Ser Ser Gly Lys Gly Ile Ile Leu Ile Asp Gly Tyr Pro		
	75 80 85 90	
AGG AGC GTG GAA CAA ATG CAG GCT TTG GAT AAG GAA TTG AAC GCT CAA		338
Arg Ser Val Glu Gln Met Gln Ala Leu Asp Lys Glu Leu Asn Ala Gln		
	95 100 105	
AAC GAA GTG ATC TTA AAA AGC GTG ATT GAA GTA GAA GTG AGT GAA AAC		386
Asn Glu Val Ile Leu Lys Ser Val Ile Glu Val Glu Val Ser Glu Asn		
	110 115 120	
ACT GCT AAA GAA AGG GTT TTA GGG CGC TCT AGG GGG GCT GAT GAT AAT		434
Thr Ala Lys Glu Arg Val Leu Gly Arg Ser Arg Gly Ala Asp Asp Asn		
	125 130 135	
GAA AAG GTG TTT CAT AAC CGC ATG CGG GTG TTT TTG GAT CCG TTG GGC		482
Glu Lys Val Phe His Asn Arg Met Arg Val Phe Leu Asp Pro Leu Gly		
	140 145 150	
GAG ATC CAA AAT TTT TAC AAG AAT AAG AAG GTG TAT AAA GCG ATC GAT		530
Glu Ile Gln Asn Phe Tyr Lys Asn Lys Lys Val Tyr Lys Ala Ile Asp		

155	160	165	170	
GGG GAG AGG AGC ATT GAA GAG ATT GTG GGC GAA ATG CAA GAG TAT ATC				578
Gly Glu Arg Ser Ile Glu Glu Ile Val Gly Glu Met Gln Glu Tyr Ile				
	175	180	185	
TTG TCT TTC GGT AAT TAAAATGCAC TCTCAAGGAG AATAGCTGTG ATTTCTG				630
Leu Ser Phe Gly Asn				
	190			

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met	Lys	Gln	Leu	Phe	Leu	Ile	Ile	Gly	Ala	Pro	Gly	Ser	Gly	Lys	Thr
1				5				10					15		
Thr	Asp	Ala	Glu	Leu	Ile	Ala	Lys	Asn	Asn	Ser	Glu	Thr	Ile	Ala	His
			20					25					30		
Phe	Ser	Thr	Gly	Asp	Leu	Leu	Arg	Ala	Glu	Ser	Ala	Lys	Lys	Thr	Glu
		35					40					45			
Arg	Gly	Leu	Leu	Ile	Glu	Lys	Phe	Thr	Ser	Gln	Gly	Glu	Leu	Val	Pro
	50					55					60				
Leu	Glu	Ile	Val	Val	Glu	Thr	Ile	Leu	Ser	Ala	Ile	Lys	Ser	Ser	Gly
65					70					75					80
Lys	Gly	Ile	Ile	Leu	Ile	Asp	Gly	Tyr	Pro	Arg	Ser	Val	Glu	Gln	Met
				85					90					95	
Gln	Ala	Leu	Asp	Lys	Glu	Leu	Asn	Ala	Gln	Asn	Glu	Val	Ile	Leu	Lys
			100					105					110		
Ser	Val	Ile	Glu	Val	Glu	Val	Ser	Glu	Asn	Thr	Ala	Lys	Glu	Arg	Val
		115					120					125			
Leu	Gly	Arg	Ser	Arg	Gly	Ala	Asp	Asp	Asn	Glu	Lys	Val	Phe	His	Asn
	130					135					140				
Arg	Met	Arg	Val	Phe	Leu	Asp	Pro	Leu	Gly	Glu	Ile	Gln	Asn	Phe	Tyr
145					150					155					160
Lys	Asn	Lys	Lys	Val	Tyr	Lys	Ala	Ile	Asp	Gly	Glu	Arg	Ser	Ile	Glu
				165					170					175	
Glu	Ile	Val	Gly	Glu	Met	Gln	Glu	Tyr	Ile	Leu	Ser	Phe	Gly	Asn	
			180					185					190		

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...717
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AGT TAC CCC CCC CCC CCC AAT CCC ACA CAA GAA ACG CAA CAA GAT TTT	48
Ser Tyr Pro Pro Pro Pro Asn Pro Thr Gln Glu Thr Gln Gln Asp Phe	
1 5 10 15	
ATT ATT GAA GCA CAA CAA GAT TTG ATT ATT GAA ACG CAA CAA GAC CCC	96
Ile Ile Glu Ala Gln Gln Asp Leu Ile Ile Glu Thr Gln Gln Asp Pro	
20 25 30	
AAA GAA CTA CCT GAG TCT TGC AAA ATA ACG CCC CAA AAA ATC TCT TTT	144
Lys Glu Leu Pro Glu Ser Cys Lys Ile Thr Pro Gln Lys Ile Ser Phe	
35 40 45	
AAC CAA GTG GTT TTT AAA AAA ATT AAA AGA AAA CTC AAC CGC TTC ATT	192
Asn Gln Val Val Phe Lys Lys Ile Lys Arg Lys Leu Asn Arg Phe Ile	
50 55 60	
GGA AGC ATT TTA GCT CGG ACA GAA GTG TAT AAG AAT CTC GTG GCA AAA	240
Gly Ser Ile Leu Ala Arg Thr Glu Val Tyr Lys Asn Leu Val Ala Lys	
65 70 75 80	
TAC GAT GAA CTC ACA GGA AAA TAC GAA TCA TTA TTG GCA AAA GAG GCA	288
Tyr Asp Glu Leu Thr Gly Lys Tyr Glu Ser Leu Leu Ala Lys Glu Ala	
85 90 95	
AAC ATC AAA GAG ACC TTT TGG GAA AGG CGT GCT GAT AGC GAA AAA GAA	336
Asn Ile Lys Glu Thr Phe Trp Glu Arg Arg Ala Asp Ser Glu Lys Glu	
100 105 110	
GCC TTT TTT TTA GAG CAT TTT TAC CTC ACT AGC GTG TAT GTG GCT TCT	384
Ala Phe Phe Leu Glu His Phe Tyr Leu Thr Ser Val Tyr Val Ala Ser	
115 120 125	
ACA GCA GGA TAC TAT ATC ACG CCT AAG GGC GCT AAA ACC TTT ATA GAA	432
Thr Ala Gly Tyr Tyr Ile Thr Pro Lys Gly Ala Lys Thr Phe Ile Glu	
130 135 140	
GCC ACG GAG CGT TTT AAA ATC ATA GAG CCG GTG GAT ATG TTC ATA AAC	480
Ala Thr Glu Arg Phe Lys Ile Ile Glu Pro Val Asp Met Phe Ile Asn	
145 150 155 160	
AAC CCC ACT TAC CAT GAT GTG GCT AAT TTT ACC TAT TTG CCT TGC CCT	528
Asn Pro Thr Tyr His Asp Val Ala Asn Phe Thr Tyr Leu Pro Cys Pro	
165 170 175	
GTT TCT TTA AAC AAG CAT GCT TTC AAT AGC ACC ATT CAA AAT GCA AAA	576
Val Ser Leu Asn Lys His Ala Phe Asn Ser Thr Ile Gln Asn Ala Lys	
180 185 190	
AAG CCT GAC ATT TCA TTA AAA CCC CCT AGA AAA TCC TAT TTT GAT AAT	624
Lys Pro Asp Ile Ser Leu Lys Pro Pro Arg Lys Ser Tyr Phe Asp Asn	
195 200 205	

CTT TTT TAT GAT CAA TTA AAC ACT AGA AAG TGC TTA AAA GCC TTT CAC 672
 Leu Phe Tyr Asp Gln Leu Asn Thr Arg Lys Cys Leu Lys Ala Phe His
 210 215 220

AAA TAC AGC AGA CGA TAC GCT CCT TTA AAA ACC CCT AAA GAG GTT TAAAA 722
 Lys Tyr Ser Arg Arg Tyr Ala Pro Leu Lys Thr Pro Lys Glu Val
 225 230 235

AGAGCGGGCT TTATGTTAGA ATAAGTCTTT TTATTCAAAG GAGATTGCAA TGAAT 777

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ser	Tyr	Pro	Pro	Pro	Pro	Asn	Pro	Thr	Gln	Glu	Thr	Gln	Gln	Asp	Phe	1	5	10	15
Ile	Ile	Glu	Ala	Gln	Gln	Asp	Leu	Ile	Ile	Glu	Thr	Gln	Gln	Asp	Pro	20	25	30	
Lys	Glu	Leu	Pro	Glu	Ser	Cys	Lys	Ile	Thr	Pro	Gln	Lys	Ile	Ser	Phe	35	40	45	
Asn	Gln	Val	Val	Phe	Lys	Lys	Ile	Lys	Arg	Lys	Leu	Asn	Arg	Phe	Ile	50	55	60	
Gly	Ser	Ile	Leu	Ala	Arg	Thr	Glu	Val	Tyr	Lys	Asn	Leu	Val	Ala	Lys	65	70	75	80
Tyr	Asp	Glu	Leu	Thr	Gly	Lys	Tyr	Glu	Ser	Leu	Leu	Ala	Lys	Glu	Ala	85	90	95	
Asn	Ile	Lys	Glu	Thr	Phe	Trp	Glu	Arg	Arg	Ala	Asp	Ser	Glu	Lys	Glu	100	105	110	
Ala	Phe	Phe	Leu	Glu	His	Phe	Tyr	Leu	Thr	Ser	Val	Tyr	Val	Ala	Ser	115	120	125	
Thr	Ala	Gly	Tyr	Tyr	Ile	Thr	Pro	Lys	Gly	Ala	Lys	Thr	Phe	Ile	Glu	130	135	140	
Ala	Thr	Glu	Arg	Phe	Lys	Ile	Ile	Glu	Pro	Val	Asp	Met	Phe	Ile	Asn	145	150	155	160
Asn	Pro	Thr	Tyr	His	Asp	Val	Ala	Asn	Phe	Thr	Tyr	Leu	Pro	Cys	Pro	165	170	175	
Val	Ser	Leu	Asn	Lys	His	Ala	Phe	Asn	Ser	Thr	Ile	Gln	Asn	Ala	Lys	180	185	190	
Lys	Pro	Asp	Ile	Ser	Leu	Lys	Pro	Pro	Arg	Lys	Ser	Tyr	Phe	Asp	Asn	195	200	205	
Leu	Phe	Tyr	Asp	Gln	Leu	Asn	Thr	Arg	Lys	Cys	Leu	Lys	Ala	Phe	His	210	215	220	
Lys	Tyr	Ser	Arg	Arg	Tyr	Ala	Pro	Leu	Lys	Thr	Pro	Lys	Glu	Val		225	230	235	

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 50...1252
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AAGTGGAAAA	TTTAGCTAAA	GAAAGAGAAA	AAAGTTTAAA	GGATTAGGC	ATG	ATC	AAT	58
					Met	Ile	Asn	
					1			
AAG	TTT	AAA	AAT	TTT	GTG	AGC	AAC	106
Lys	Phe	Lys	Asn	Phe	Val	Ser	Asn	
5					10			
GAG	CCT	TTA	GGT	TTT	GGC	ATT	GCC	154
Glu	Pro	Leu	Gly	Phe	Gly	Ile	Ala	
20					25			
AAA	AAG	ATT	TTA	TGC	GCC	ACT	TAC	202
Lys	Lys	Ile	Leu	Cys	Ala	Thr	Tyr	
				40				
AAT	TTA	GGC	TCT	TAT	GCG	GTG	TTT	250
Asn	Leu	Gly	Ser	Tyr	Ala	Val	Phe	
		55				60		
ATC	CTA	AAA	GAG	AGC	GCG	AGC	GAG	298
Ile	Leu	Lys	Glu	Ser	Ala	Ser	Glu	
		70				75		
TTT	GTG	TTA	AAA	GCG	TTG	GAT	TTT	346
Phe	Val	Leu	Lys	Ala	Leu	Asp	Phe	
85					90			
TAT	TCT	AAT	AAA	ATG	GCT	CAT	AAA	394
Tyr	Ser	Asn	Lys	Met	Ala	His	Lys	
100					105			
TTA	AAG	GCT	TTA	GAA	GAA	AAT	CGT	442
Leu	Lys	Ala	Leu	Glu	Glu	Asn	Arg	
				120				
CTT	TAT	CGC	TTG	GTG	ATC	TTG	TAT	490
Leu	Tyr	Arg	Leu	Val	Ile	Leu	Tyr	
			135					
GAG	AGC	GCG	TAT	ATG	AAA	CTT	TTA	538
Glu	Ser	Ala	Tyr	Met	Lys	Leu	Leu	
		150				155		
TTG	AGG	AGT	TTG	AAT	TTA	GAG	GGT	586

	340		345		350										
Ser	Ala	Leu	Glu	Lys	His	Ala	Asn	Asn	Leu	Tyr	Lys	Gly	Lys	Glu	Leu
	355						360					365			
Ser	Gly	Lys	Asn	Gly	Val	His	Phe	Arg	Ser	Asn	Ser	Gln	Asn	Gly	Lys
	370					375					380				
Leu	Ile	Ala	Phe	Arg	Ser	Val	Lys	Lys	Ile	Glu	Leu	Asn	Gln	Asn	Leu
385					390					395					400
His															

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 50...1201
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TTATTTTAT	TATGTTAAGA	TAATGAAAAT	TTCTAATTAA	GGAGTGGTC	ATG	TTC	TAC	58								
					Met	Phe	Tyr									
					1											
GAT	GAA	AAA	AAG	ACC	TAT	CAA	AAG	ATT	GAA	GAA	CGC	CTT	GAT	ATA	GTC	106
Asp	Glu	Lys	Lys	Thr	Tyr	Gln	Lys	Ile	Glu	Glu	Arg	Leu	Asp	Ile	Val	
5						10					15					
CGT	TCG	TTT	AAC	GCT	CAC	AAC	GAG	CAT	AAA	AAC	TTG	CAA	GAC	GAG	TTT	154
Arg	Ser	Phe	Asn	Ala	His	Asn	Glu	His	Lys	Asn	Leu	Gln	Asp	Glu	Phe	
20					25					30					35	
AAA	GGG	GCG	GGC	ATT	TCT	AGG	CGC	GAT	TTA	TTG	AAG	TGG	GCG	GGC	ATG	202
Lys	Gly	Ala	Gly	Ile	Ser	Arg	Arg	Asp	Leu	Leu	Lys	Trp	Ala	Gly	Met	
				40					45					50		
ATG	AGC	ACA	GCG	TTA	GCC	TTG	CCG	GCT	AGT	TTT	GCT	CCC	TTG	ACT	TTG	250
Met	Ser	Thr	Ala	Leu	Ala	Leu	Pro	Ala	Ser	Phe	Ala	Pro	Leu	Thr	Leu	
			55					60					65			
AAG	GCG	GTG	GAA	GTG	GCT	AAC	AGA	TTG	CCC	GTG	ATT	TGG	TTG	CAC	ATG	298
Lys	Ala	Val	Glu	Val	Ala	Asn	Arg	Leu	Pro	Val	Ile	Trp	Leu	His	Met	
		70					75					80				
GCA	GAA	TGC	ACC	GGT	TGT	AGC	GAA	AGT	TTG	TTA	AGG	AGC	GCA	GAC	CCC	346
Ala	Glu	Cys	Thr	Gly	Cys	Ser	Glu	Ser	Leu	Leu	Arg	Ser	Ala	Asp	Pro	
	85					90					95					
ACC	ATT	GAT	AGC	ATT	ATC	TTT	GAT	TAC	ATC	AAC	CTA	GAA	TAC	CAT	GAG	394
Thr	Ile	Asp	Ser	Ile	Ile	Phe	Asp	Tyr	Ile	Asn	Leu	Glu	Tyr	His	Glu	

CGT TCC ATT AAA ACC GCT TTT GAC GGA TTA GGG GCT GAT AAA GTA GCG 1114
 Arg Ser Ile Lys Thr Ala Phe Asp Gly Leu Gly Ala Asp Lys Val Ala
 340 345 350 355

GAT AAA GTA GGC ACG ACT TTG CTG AGC GCA ACC GCT ATT GGC ATT GTT 1162
 Asp Lys Val Gly Thr Thr Leu Leu Ser Ala Thr Ala Ile Gly Ile Val
 360 365 370

GCG CAT GCG CTC CTT TCT AAA GCG ATC AAA AAC AAA GAG TAAGGGATTA AC 1213
 Ala His Ala Leu Leu Ser Lys Ala Ile Lys Asn Lys Glu
 375 380

ATGTCAAAAA AAATCGTAGT CGATCCTATC ACTAGGATTG AGGGGCATTT AAGGATTGAA 1273
 GTGATCGTAG ATGATGATAA CGTGATCACT G 1304

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Phe Tyr Asp Glu Lys Lys Thr Tyr Gln Lys Ile Glu Glu Arg Leu
 1 5 10 15
 Asp Ile Val Arg Ser Phe Asn Ala His Asn Glu His Lys Asn Leu Gln
 20 25 30
 Asp Glu Phe Lys Gly Ala Gly Ile Ser Arg Arg Asp Leu Leu Lys Trp
 35 40 45
 Ala Gly Met Met Ser Thr Ala Leu Ala Leu Pro Ala Ser Phe Ala Pro
 50 55 60
 Leu Thr Leu Lys Ala Val Glu Val Ala Asn Arg Leu Pro Val Ile Trp
 65 70 75 80
 Leu His Met Ala Glu Cys Thr Gly Cys Ser Glu Ser Leu Leu Arg Ser
 85 90 95
 Ala Asp Pro Thr Ile Asp Ser Ile Ile Phe Asp Tyr Ile Asn Leu Glu
 100 105 110
 Tyr His Glu Thr Ile Met Val Ala Ser Gly Phe Gln Ala Glu Lys Ser
 115 120 125
 Leu His Asp Ala Ile Glu Lys His Lys Asn Asn Tyr Ile Leu Met Val
 130 135 140
 Glu Gly Gly Ile Pro Gln Gly Thr Glu Tyr Phe Leu Thr Gln Gly Pro
 145 150 155 160
 Asn Ala Glu Thr Gly Ala Glu Glu Cys Arg Lys Ala Ala Gln Tyr Ala
 165 170 175
 Ala Ala Ile Phe Ala Ile Gly Thr Cys Ser Ser Phe Gly Gly Val Gln
 180 185 190
 Ala Ala Tyr Pro Asn Pro Ser Asn Ala Gln Pro Leu His Lys Ile Ile
 195 200 205
 Asp Lys Pro Val Ile Asn Val Pro Gly Cys Pro Pro Ser Glu Lys Asn
 210 215 220
 Ile Val Gly Asn Val Leu Tyr Tyr Leu Met Phe Gly Ala Leu Pro Lys
 225 230 235 240
 Leu Asp Ala Tyr Asn Arg Pro Ser Trp Ala Tyr Gly Asn Arg Ile His

	75	80	85	
AGC TTG ATG GAA CGC AAG AGT TTT AGC CAA CTT TTA AGC CCA AAA GCC				344
Ser Leu Met Glu Arg Lys Ser Phe Ser Gln Leu Leu Ser Pro Lys Ala				
	90	95	100	
TGG ATT GAT CAG ATG AAA GCG TAT TTT CTT ATC AGC GGC AAA CCC CAC				392
Trp Ile Asp Gln Met Lys Ala Tyr Phe Leu Ile Ser Gly Lys Pro His				
	105	110	115	
ACT AAA GGA GCG TAT AAC CCT ATC CAA CTC GTG GCT TAT TCC ACT TTG				440
Thr Lys Gly Ala Tyr Asn Pro Ile Gln Leu Val Ala Tyr Ser Thr Leu				
	120	125	130	
ATT GTT TTG ATC GTG TTG ATG AGT TTG AGC GGG ATG GTG CTG TAT TAT				488
Ile Val Leu Ile Val Leu Met Ser Leu Ser Gly Met Val Leu Tyr Tyr				
	135	140	145	150
AAT GTC TAT CAT GCG GGG CTT GGA GCG TTT TTA GGA AGC GCT TTT AAG				536
Asn Val Tyr His Ala Gly Leu Gly Ala Phe Leu Gly Ser Ala Phe Lys				
	155	160	165	
TGG TTT GAA ACG CTT TGT GGA GGG TTA GCG AAT GTT CGT TTC ATC CAC				584
Trp Phe Glu Thr Leu Cys Gly Gly Leu Ala Asn Val Arg Phe Ile His				
	170	175	180	
CAC TTA GCG ACT TGG GGG TTT ATT TTG TTT GTC CCT GTG CAT GTT TAT				632
His Leu Ala Thr Trp Gly Phe Ile Leu Phe Val Pro Val His Val Tyr				
	185	190	195	
ATG GTG TTT TTC CAT TCT ATC AGG TAT GAA AGT TCG GGG GCG GAT TCT				680
Met Val Phe Phe His Ser Ile Arg Tyr Glu Ser Ser Gly Ala Asp Ser				
	200	205	210	
ATG ATT AAT GGC TAT GGT TAT ACC AAA GAA TGAGTCAAAA AATCCTAATT CTA				733
Met Ile Asn Gly Tyr Gly Tyr Thr Lys Glu				
	215	220		
GGTATTGGCA ATATCCTTTT TGGCGATGAA GGGATTGGGG TGCATTTAGC CCACTACCTC				793
AAAAAAAAATT TTCTTT				810

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met	Asp	Lys	Met	Asn	Lys	Val	Val	Leu	His	Lys	Glu	Tyr	Ser	Gly	Phe
1				5				10						15	
Val	Arg	Phe	Phe	His	Trp	Val	Arg	Ala	Leu	Ser	Ile	Phe	Ala	Leu	Ile
			20					25					30		
Ala	Thr	Gly	Phe	Tyr	Ile	Ala	Tyr	Pro	Phe	Leu	Gln	Pro	Asn	Ser	Ser

280	285	290	295	
GGT TCT TTA AAA ACG CTT TTA AGC GTC AGT TTT GAT TTT AAC AAA ATG				964
Gly Ser Leu Lys Thr Leu Leu Ser Val Ser Phe Asp Phe Asn Lys Met	300	305	310	
TTT AAC GCG CTC AAA CAA GAT GAA AAA GCC TCC AGA ATG CTA CAA AAC				1012
Phe Asn Ala Leu Lys Gln Asp Glu Lys Ala Ser Arg Met Leu Gln Asn	315	320	325	
TAC GCC ACT AAA TTC CCT GAT TTT TAC GCG CGC ATT GTA GAG CTT TCT				1060
Tyr Ala Thr Lys Phe Pro Asp Phe Tyr Ala Arg Ile Val Glu Leu Ser	330	335	340	
AAA TAC GAT CTA GGG GGC GCG AAT TTA TTG GAT TTT TTT TGC ATT TTA				1108
Lys Tyr Asp Leu Gly Gly Ala Asn Leu Leu Asp Phe Phe Cys Ile Leu	345	350	355	
GGG TTT GTT TTG GGC TAT AGC GAG GAT TTT TGC ACA CAG AGC GTT ATT				1156
Gly Phe Val Leu Gly Tyr Ser Glu Asp Phe Cys Thr Gln Ser Val Ile	360	365	370	
CCT TTG GCT AAA GAA TGC TTA CGC CCT AAA GGC CCT AGG ATT GAT TAT				1204
Pro Leu Ala Lys Glu Cys Leu Arg Pro Lys Gly Pro Arg Ile Asp Tyr	380	385	390	
AAA ATC CTT AAA GAC AAT TCT TTG AAA ATG GCT TTA AAC TTT TCA AAG				1252
Lys Ile Leu Lys Asp Asn Ser Leu Lys Met Ala Leu Asn Phe Ser Lys	395	400	405	
ATC ATG CAC AGT GCG ATG AGT TTC AGG CTC GCA GGC GTG GAA AAT GAA				1300
Ile Met His Ser Ala Met Ser Phe Arg Leu Ala Gly Val Glu Asn Glu	410	415	420	
ATT TTG AGT TTG GGG ATT TTG GAT TCT TTA GCG GAG TTT TTA GGG AAT				1348
Ile Leu Ser Leu Gly Ile Leu Asp Ser Leu Ala Glu Phe Leu Gly Asn	425	430	435	
TTC ATT TGG GAT AAC GCG CAA AAT TTT AGC GTT CAA GAA GTA ACG ATC				1396
Phe Ile Trp Asp Asn Ala Gln Asn Phe Ser Val Gln Glu Val Thr Ile	440	445	450	
GCT GGG GAT TTC TTT GGC GAA AAA GTG TTT TTG GAT TTG TTT GTG CGG				1444
Ala Gly Asp Phe Phe Gly Glu Lys Val Phe Leu Asp Leu Phe Val Arg	460	465	470	
TAT TTC CCT AAA ACC CTA GCC CTT AAA ACG CAT GCA TTT TTG GAT TAT				1492
Tyr Phe Pro Lys Thr Leu Ala Leu Lys Thr His Ala Phe Leu Asp Tyr	475	480	485	
GAA TAAGGGCTTA AAAGCGGATG TGCATCATCA GCCCGCCGTC CATGTATT				1543
Glu				

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 488 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met	Ala	Cys	Asn	Leu	Gln	Ala	Arg	Phe	Tyr	Ser	Val	Tyr	Lys	Asp	Asn
1				5					10					15	
Thr	Thr	Ser	Phe	Tyr	Leu	Gln	Ala	Ser	Ala	Glu	Thr	Thr	Leu	Glu	Phe
			20					25					30		
Ala	Gln	Lys	Leu	Ser	Glu	Ile	Leu	Pro	Phe	Ser	Leu	Asp	Phe	Ser	Phe
		35					40					45			
Leu	Ser	Leu	Lys	Glu	Ile	Thr	Glu	Pro	Leu	Asp	Glu	Asn	Leu	Phe	Gln
	50					55					60				
Thr	Ala	Ser	Leu	Ser	Lys	Pro	Leu	Phe	Met	Asn	Ala	Lys	Glu	His	Gln
65					70					75					80
Asp	Phe	Leu	Asp	Lys	Asn	Ser	Ser	Leu	Tyr	Ala	Asp	Thr	Leu	Gly	Leu
			85						90					95	
Ile	Lys	Asn	Thr	Ala	Phe	Lys	Gly	Asp	Ile	Ile	His	Ser	Pro	Lys	Glu
			100					105					110		
Leu	Ile	Asp	Cys	Leu	Thr	Gln	Leu	Lys	Gly	Met	Leu	Lys	Thr	Gln	Asp
		115					120					125			
Phe	Ile	Pro	Ile	Phe	Thr	Ser	Arg	Glu	Ala	Leu	Ser	Leu	Ser	Leu	Lys
	130					135					140				
Asn	Pro	Ser	Pro	Ser	Val	Ile	Phe	Ser	Asp	Leu	Ser	Ser	Val	Leu	Ser
145					150					155					160
Cys	Thr	Lys	Leu	Pro	Leu	Glu	Asp	Ala	Lys	Tyr	Leu	Ala	Ser	Leu	Glu
			165						170					175	
Lys	Pro	Ser	Ile	Lys	Ala	Pro	Leu	Lys	Ser	Val	Phe	Lys	Asp	Thr	Phe
			180					185					190		
Lys	Asn	Asp	Glu	Ile	Ile	Ala	Gln	Leu	Pro	Tyr	Asp	Pro	Ile	Leu	Asn
		195					200					205			
Leu	Leu	Cys	His	Ile	Leu	Gln	Asp	Glu	Gly	Ile	Glu	Phe	Val	Phe	Met
	210					215					220				
His	Glu	Ser	Arg	Ser	Cys	Glu	Ala	Leu	Leu	Tyr	Tyr	Glu	Ala	Leu	Phe
225					230					235					240
Lys	Thr	Pro	Lys	Arg	Leu	Ile	Thr	Pro	Thr	Lys	Lys	Phe	Val	Leu	Glu
			245						250					255	
Asn	Asn	Phe	Ser	Thr	Phe	Pro	Phe	Lys	Asp	Glu	Leu	Glu	Phe	Leu	Ser
			260					265					270		
Ala	Thr	Pro	Asn	Ser	Ile	Val	Leu	Tyr	Leu	Ser	Phe	Lys	Arg	Pro	Thr
		275					280					285			
Arg	Leu	Leu	Leu	His	Ala	Asn	Gly	Ser	Leu	Lys	Thr	Leu	Leu	Ser	Val
	290					295					300				
Ser	Phe	Asp	Phe	Asn	Lys	Met	Phe	Asn	Ala	Leu	Lys	Gln	Asp	Glu	Lys
305					310					315					320
Ala	Ser	Arg	Met	Leu	Gln	Asn	Tyr	Ala	Thr	Lys	Phe	Pro	Asp	Phe	Tyr
			325						330					335	
Ala	Arg	Ile	Val	Glu	Leu	Ser	Lys	Tyr	Asp	Leu	Gly	Gly	Ala	Asn	Leu
			340					345					350		
Leu	Asp	Phe	Phe	Cys	Ile	Leu	Gly	Phe	Val	Leu	Gly	Tyr	Ser	Glu	Asp
		355					360					365			
Phe	Cys	Thr	Gln	Ser	Val	Ile	Pro	Leu	Ala	Lys	Glu	Cys	Leu	Arg	Pro
	370					375					380				
Lys	Gly	Pro	Arg	Ile	Asp	Tyr	Lys	Ile	Leu	Lys	Asp	Asn	Ser	Leu	Lys

385		390		395		400
Met	Ala	Leu	Asn	Phe	Ser	Lys
			405			
Leu	Ala	Gly	Val	Glu	Asn	Glu
			420			
Leu	Ala	Glu	Phe	Leu	Gly	Asn
			435			
Ser	Val	Gln	Glu	Val	Thr	Ile
			450			
Phe	Leu	Asp	Leu	Phe	Val	Arg
			465			
Thr	His	Ala	Phe	Leu	Asp	Tyr
			485			

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 17...694
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TTTTTAAGGA ATTTTG ATG GAA CAA AAA ATT TGC GTG ATC GGT TTT AGC GGC	52
Met Glu Gln Lys Ile Cys Val Ile Gly Phe Ser Gly	
1 5 10	
GGG CAA GAC AGC ACC ACT TTA GCC GTG TGG GCG AAA AAG CGT TTT AAA	100
Gly Gln Asp Ser Thr Thr Leu Ala Val Trp Ala Lys Lys Arg Phe Lys	
15 20 25	
AAA GTC TGT TTA GTG GGG TTT GAT TAT GCG CAA AAA CAC TCT GTG GAA	148
Lys Val Cys Leu Val Gly Phe Asp Tyr Ala Gln Lys His Ser Val Glu	
30 35 40	
TTA GAA TGC GCT CAA AAA ATC GCT TCT CTT TTA CAA CTC CCT TAT GAA	196
Leu Glu Cys Ala Gln Lys Ile Ala Ser Leu Leu Gln Leu Pro Tyr Glu	
45 50 55 60	
ATC ATC CCA TTA GAT TTT TTA GAA AAT ATC ACC CGC TCT GCG CTT TTT	244
Ile Ile Pro Leu Asp Phe Leu Glu Asn Ile Thr Arg Ser Ala Leu Phe	
65 70 75	
AAA AAC TCT AAC GAT TTA ATA GGG CAT TCG CAT GCG CAA AAT AAA GAT	292
Lys Asn Ser Asn Asp Leu Ile Gly His Ser His Ala Gln Asn Lys Asp	
80 85 90	
TTA CCC AAT TCT TTT GTG CCT AAT CGT AAC GCT ATT TTT ATC ACC CTT	340
Leu Pro Asn Ser Phe Val Pro Asn Arg Asn Ala Ile Phe Ile Thr Leu	

95	100	105	
TTG CAT TCT TAC GCG CAA AAA CTA GGG GCT AGC AAT ATC GCT TTA GGA			388
Leu His Ser Tyr Ala Gln Lys Leu Gly Ala Ser Asn Ile Ala Leu Gly			
110	115	120	
GTT TCG CAA GCG GAT TTT AGC GGC TAT CCG GAT TGT AAA GAA GAT TTT			436
Val Ser Gln Ala Asp Phe Ser Gly Tyr Pro Asp Cys Lys Glu Asp Phe			
125	130	135	140
ATT AAA AGC ATC GAG CAT GCC TTA AAT TTA GGA TCA AAC ACG GCG ATT			484
Ile Lys Ser Ile Glu His Ala Leu Asn Leu Gly Ser Asn Thr Ala Ile			
145	150	155	
AAA ATC CTA ACG CCT TTA ATG TTT TTG AAT AAA GCG CAA GAA TTT CAA			532
Lys Ile Leu Thr Pro Leu Met Phe Leu Asn Lys Ala Gln Glu Phe Gln			
160	165	170	
ATG GCT AAA GAT TTG GGC GTC TTG GAT TTA GTC ATC AAA GAA ACG CAC			580
Met Ala Lys Asp Leu Gly Val Leu Asp Leu Val Ile Lys Glu Thr His			
175	180	185	
ACC TGC TAT CAA GGA GAG CGA AAG ATT TTG CAT GCT TAT GGT TAT GGT			628
Thr Cys Tyr Gln Gly Glu Arg Lys Ile Leu His Ala Tyr Gly Tyr Gly			
190	195	200	
TGC GAT AAA TGC CCG GCA TGC CAA TTG AGA AAA AAA GGC TTT GAA GAG			676
Cys Asp Lys Cys Pro Ala Cys Gln Leu Arg Lys Lys Gly Phe Glu Glu			
205	210	215	220
TTT CAA GCT AAT AAA AAA TAAGGTTTTT TAAAAAACCA A			715
Phe Gln Ala Asn Lys Lys			
225			

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met	Glu	Gln	Lys	Ile	Cys	Val	Ile	Gly	Phe	Ser	Gly	Gly	Gln	Asp	Ser
1				5					10					15	
Thr	Thr	Leu	Ala	Val	Trp	Ala	Lys	Lys	Arg	Phe	Lys	Lys	Val	Cys	Leu
		20						25					30		
Val	Gly	Phe	Asp	Tyr	Ala	Gln	Lys	His	Ser	Val	Glu	Leu	Glu	Cys	Ala
		35					40					45			
Gln	Lys	Ile	Ala	Ser	Leu	Leu	Gln	Leu	Pro	Tyr	Glu	Ile	Ile	Pro	Leu
		50				55					60				
Asp	Phe	Leu	Glu	Asn	Ile	Thr	Arg	Ser	Ala	Leu	Phe	Lys	Asn	Ser	Asn
65				70					75					80	
Asp	Leu	Ile	Gly	His	Ser	His	Ala	Gln	Asn	Lys	Asp	Leu	Pro	Asn	Ser

Phe Asn Leu Glu Leu Arg Leu Leu Gly Phe Phe Lys His Gln Lys Ser
 210 215 220
 Leu Glu Ser Leu Arg Tyr Pro Lys Lys Thr Ile Val Leu Phe Ser Lys
 225 230 235 240
 Ala Lys Glu Cys His Lys Ser Phe Leu Asn Ile His Asn Lys Thr Glu
 245 250 255
 Leu Lys Phe Leu Leu Lys Asn Tyr Asp Leu Glu Pro Phe Asn Leu Ala
 260 265 270
 Leu Asp Phe Tyr Ala Leu Lys Asn Pro Lys His Ala Leu Lys Ile Lys
 275 280 285
 Gly Leu Leu Lys Glu Ile Phe Asp Ser Asn Glu Pro Phe Lys Lys Glu
 290 295 300
 His Leu Ala Leu Lys Gly Gly Ala Leu Gln Ser Leu Gly Tyr Gln His
 305 310 315 320
 Gln Lys Ile Gly Glu Ile Leu Asn Ala Cys Leu Asp Leu Val Ile Ala
 325 330 335
 Asn Pro Lys Asn Asn Ala Leu Glu Trp Leu Ile Glu Trp Val Lys Gly
 340 345 350
 His Tyr Leu Pro Asn Asp Thr Ile Asn Leu Ser Pro Ile Gly Arg Arg
 355 360 365
 Asn

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 50...340
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TTTTCCCCTA TATCCAAAGC CATCATCAAG AAGTTTAAAG GCTCAAAGC ATG ATT TTT	58
Met Ile Phe	
1	
TCC ACT CTT ATT AAT GCG ATA GCG GTG ATT TTA AGC TCG CTC ATT ACG	106
Ser Thr Leu Ile Asn Ala Ile Ala Val Ile Leu Ser Ser Leu Ile Thr	
5 10 15	
ATT TAT ATG TGG ATA GTA ATC ATT TAT TCG CTT ATC AGT TTC GTG CAG	154
Ile Tyr Met Trp Ile Val Ile Ile Tyr Ser Leu Ile Ser Phe Val Gln	
20 25 30 35	
CCT AAC CCC AAT AAC CCC ATC ATG CAA ATT CTC GCT CGC TTG TGT GAG	202
Pro Asn Pro Asn Asn Pro Ile Met Gln Ile Leu Ala Arg Leu Cys Glu	
40 45 50	
CCG GTG TTT TAT TTT TTA CGC TCT AGA TTC AAG CTG GTG TTT AAC GGG	250

Pro Val Phe Tyr Phe Leu Arg Ser Arg Phe Lys Leu Val Phe Asn Gly
55 60 65

TTG GAT TTC TCT CCT TTA GTG GTG GTC ATT GTT TTG AAA TTC TTG GAT 298
Leu Asp Phe Ser Pro Leu Val Val Val Ile Val Leu Lys Phe Leu Asp
70 75 80

CTC ACG CTC ATT CAG TGG CTT TTC ATG CTC GCT AAA AAC CTT TAAAGAAAA 349
Leu Thr Leu Ile Gln Trp Leu Phe Met Leu Ala Lys Asn Leu
85 90 95

TCATGCGTTT T 360

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met Ile Phe Ser Thr Leu Ile Asn Ala Ile Ala Val Ile Leu Ser Ser
1 5 10 15
Leu Ile Thr Ile Tyr Met Trp Ile Val Ile Ile Tyr Ser Leu Ile Ser
20 25 30
Phe Val Gln Pro Asn Pro Asn Asn Pro Ile Met Gln Ile Leu Ala Arg
35 40 45
Leu Cys Glu Pro Val Phe Tyr Phe Leu Arg Ser Arg Phe Lys Leu Val
50 55 60
Phe Asn Gly Leu Asp Phe Ser Pro Leu Val Val Val Ile Val Leu Lys
65 70 75 80
Phe Leu Asp Leu Thr Leu Ile Gln Trp Leu Phe Met Leu Ala Lys Asn
85 90 95
Leu

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...1701
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

(A) LENGTH: 770 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 16...738
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TAAAAAGAAG GACAA ATG ATG CCA TTT GAA GCT GTA ATC GGG CTA GAA GTC	51
Met Met Pro Phe Glu Ala Val Ile Gly Leu Glu Val	
1 5 10	
CAT GTC CAA CTC AAC ACC AAA ACC AAA ATC TTT TGC TCT TGC TCT ACA	99
His Val Gln Leu Asn Thr Lys Thr Lys Ile Phe Cys Ser Cys Ser Thr	
15 20 25	
AGC TTT GGA GAA TCC CCT AAT TCT AAC ACC TGC CCT GTG TGT TTG GGT	147
Ser Phe Gly Glu Ser Pro Asn Ser Asn Thr Cys Pro Val Cys Leu Gly	
30 35 40	
TTA CCG GGA GCT TTG CCG GTA TTG AAT AAA GAA GTG GTT AAA AAA GCC	195
Leu Pro Gly Ala Leu Pro Val Leu Asn Lys Glu Val Val Lys Lys Ala	
45 50 55 60	
ATC CAA TTA GGC ACA GCC ATT GAA GCC AAT ATC AAC CAA TAT TCT ATT	243
Ile Gln Leu Gly Thr Ala Ile Glu Ala Asn Ile Asn Gln Tyr Ser Ile	
65 70 75	
TTT GCG AGG AAA AAT TAT TTT TAC CCT GAT TTG CCT AAG GCT TAT CAA	291
Phe Ala Arg Lys Asn Tyr Phe Tyr Pro Asp Leu Pro Lys Ala Tyr Gln	
80 85 90	
ATT TCG CAG TTT GAA GTC CCT ATT GTG AGC GAT GGG AAA TTA GAG ATT	339
Ile Ser Gln Phe Glu Val Pro Ile Val Ser Asp Gly Lys Leu Glu Ile	
95 100 105	
GAC ACT AAA GAG GGT GCA AAA ATC GTG CGT ATT GAA AGG GCC CAC ATG	387
Asp Thr Lys Glu Gly Ala Lys Ile Val Arg Ile Glu Arg Ala His Met	
110 115 120	
GAA GAA GAC GCC GGT AAA AAT ATC CAT GAG GGC AGT TAT TCT TTA GTG	435
Glu Glu Asp Ala Gly Lys Asn Ile His Glu Gly Ser Tyr Ser Leu Val	
125 130 135 140	
GAT TTG AAC CGC GCT TGC ACC CCT TTA TTA GAA ATT GTC AGT AAG CCG	483
Asp Leu Asn Arg Ala Cys Thr Pro Leu Leu Glu Ile Val Ser Lys Pro	
145 150 155	
GAC ATG CGA AAT AGT GAA GAA GCT ATA GCG TAT TTG AAA AAG CTC CAT	531
Asp Met Arg Asn Ser Glu Glu Ala Ile Ala Tyr Leu Lys Lys Leu His	
160 165 170	

GCT ATC GTG CGT TTT ATA GGG ATT TCT GAT GCG AAC ATG CAA GAG GGG	579
Ala Ile Val Arg Phe Ile Gly Ile Ser Asp Ala Asn Met Gln Glu Gly	
175 180 185	
AAT TTC AGG TGC GAT GCG AAC GTG TCC ATT AGA CCC AAA GGC GAT GAA	627
Asn Phe Arg Cys Asp Ala Asn Val Ser Ile Arg Pro Lys Gly Asp Glu	
190 195 200	
AAG CTT TAT ACG AGA GTA GAG ATT AAA AAT CTA AAT AGC TTT AGA TTC	675
Lys Leu Tyr Thr Arg Val Glu Ile Lys Asn Leu Asn Ser Phe Arg Phe	
205 210 215 220	
ATT GCT AAA GCG ATT GAA TAC GAG ATA GAG CGC CAA AGC GCG GAC GTG	723
Ile Ala Lys Ala Ile Glu Tyr Glu Ile Glu Arg Gln Ser Ala Asp Val	
225 230 235	
GGA GAA CGG GCG CTA TAATGAAGAG GTGGTTCAAG AAACGCGCCT TT	770
Gly Glu Arg Ala Leu	
240	

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Met Pro Phe Glu Ala Val Ile Gly Leu Glu Val His Val Gln Leu	
1 5 10 15	
Asn Thr Lys Thr Lys Ile Phe Cys Ser Cys Ser Thr Ser Phe Gly Glu	
20 25 30	
Ser Pro Asn Ser Asn Thr Cys Pro Val Cys Leu Gly Leu Pro Gly Ala	
35 40 45	
Leu Pro Val Leu Asn Lys Glu Val Val Lys Lys Ala Ile Gln Leu Gly	
50 55 60	
Thr Ala Ile Glu Ala Asn Ile Asn Gln Tyr Ser Ile Phe Ala Arg Lys	
65 70 75 80	
Asn Tyr Phe Tyr Pro Asp Leu Pro Lys Ala Tyr Gln Ile Ser Gln Phe	
85 90 95	
Glu Val Pro Ile Val Ser Asp Gly Lys Leu Glu Ile Asp Thr Lys Glu	
100 105 110	
Gly Ala Lys Ile Val Arg Ile Glu Arg Ala His Met Glu Glu Asp Ala	
115 120 125	
Gly Lys Asn Ile His Glu Gly Ser Tyr Ser Leu Val Asp Leu Asn Arg	
130 135 140	
Ala Cys Thr Pro Leu Leu Glu Ile Val Ser Lys Pro Asp Met Arg Asn	
145 150 155 160	
Ser Glu Glu Ala Ile Ala Tyr Leu Lys Lys Leu His Ala Ile Val Arg	
165 170 175	
Phe Ile Gly Ile Ser Asp Ala Asn Met Gln Glu Gly Asn Phe Arg Cys	
180 185 190	
Asp Ala Asn Val Ser Ile Arg Pro Lys Gly Asp Glu Lys Leu Tyr Thr	

	195		200		205
Arg	Val	Glu	Ile	Lys	Asn
	210		215		220
Ile	Glu	Tyr	Glu	Ile	Glu
225		230		235	
Leu					

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...444
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ATGGGAGTGG	ATTGA	ATG	CAA	GAA	ATT	GAA	ATT	TTT	TGC	GAT	GGC	TCT	TCT	51
		Met	Gln	Glu	Ile	Glu	Ile	Phe	Cys	Asp	Gly	Ser	Ser	
		1				5					10			
TTA	GGC	AAT	CCC	GGG	CCA	GGC	GGT	TAT	GCG	GCG	ATT	TTA	CGC	99
Leu	Gly	Asn	Pro	Gly	Pro	Gly	Gly	Tyr	Ala	Ala	Ile	Leu	Arg	
	15					20						25		
GAT	AAA	GAA	AAA	ACC	ATC	AGT	GGG	GGC	GAA	GAA	TTC	ACC	ACG	147
Asp	Lys	Glu	Lys	Thr	Ile	Ser	Gly	Gly	Glu	Glu	Phe	Thr	Thr	
	30					35					40			
CGC	ATG	GAA	TTA	AGA	GCG	CTC	AAT	GAA	GCG	TTA	AAA	ATT	TTG	195
Arg	Met	Glu	Leu	Arg	Ala	Leu	Asn	Glu	Ala	Leu	Lys	Ile	Leu	
45					50				55				60	
CCA	TGC	CGT	ATC	ACG	CTT	TAT	AGC	GAT	TCG	CAA	TAC	GTG	TGC	243
Pro	Cys	Arg	Ile	Thr	Leu	Tyr	Ser	Asp	Ser	Gln	Tyr	Val	Cys	
			65					70					75	
ATC	AAT	GTG	TGG	CTA	GCT	AAC	TGG	CAA	AAA	AAG	AAT	TTT	TCT	291
Ile	Asn	Val	Trp	Leu	Ala	Asn	Trp	Gln	Lys	Lys	Asn	Phe	Ser	
		80					85					90		
AAA	AAT	GTG	GAT	TTA	TGG	AAA	GAA	TTT	TTA	GAA	GTC	TCT	AAA	339
Lys	Asn	Val	Asp	Leu	Trp	Lys	Glu	Phe	Leu	Glu	Val	Ser	Lys	
	95					100						105		
TCT	ATT	GTG	GCT	GTT	TGG	ATC	AAG	GGG	CAT	AAC	GGG	CAT	GCC	387
Ser	Ile	Val	Ala	Val	Trp	Ile	Lys	Gly	His	Asn	Gly	His	Ala	
	110					115					120			

GAA CGA TGC GAT AGC CTC GCT AAA TTA GAG GCG CAA AAA CGG GTC AAA 435
 Glu Arg Cys Asp Ser Leu Ala Lys Leu Glu Ala Gln Lys Arg Val Lys
 125 130 135 140

ACG ACC ACT TAAAGGGAAA AATGATGAAA AACAAACGCT CTCAAAACAG CCC 487
 Thr Thr Thr

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Gln	Glu	Ile	Glu	Ile	Phe	Cys	Asp	Gly	Ser	Ser	Leu	Gly	Asn	Pro
1				5					10					15	
Gly	Pro	Gly	Gly	Tyr	Ala	Ala	Ile	Leu	Arg	Tyr	Lys	Asp	Lys	Glu	Lys
			20					25					30		
Thr	Ile	Ser	Gly	Gly	Glu	Glu	Phe	Thr	Thr	Asn	Asn	Arg	Met	Glu	Leu
		35					40					45			
Arg	Ala	Leu	Asn	Glu	Ala	Leu	Lys	Ile	Leu	Lys	Arg	Pro	Cys	Arg	Ile
	50					55				60					
Thr	Leu	Tyr	Ser	Asp	Ser	Gln	Tyr	Val	Cys	Gln	Ala	Ile	Asn	Val	Trp
65					70					75				80	
Leu	Ala	Asn	Trp	Gln	Lys	Lys	Asn	Phe	Ser	Lys	Val	Lys	Asn	Val	Asp
			85					90					95		
Leu	Trp	Lys	Glu	Phe	Leu	Glu	Val	Ser	Lys	Gly	His	Ser	Ile	Val	Ala
			100					105					110		
Val	Trp	Ile	Lys	Gly	His	Asn	Gly	His	Ala	Glu	Asn	Glu	Arg	Cys	Asp
		115				120					125				
Ser	Leu	Ala	Lys	Leu	Glu	Ala	Gln	Lys	Arg	Val	Lys	Thr	Thr	Thr	
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 48...1181
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

215	220	225	
CAA AAG CTC CCC ATT GGC TTA GGT CAA GGG CTA TAC GCT AAA TTA GAC			776
Gln Lys Leu Pro Ile Gly Leu Gly Gln Gly Leu Tyr Ala Lys Leu Asp			
230	235	240	
GCT AAA ATC GCT GAA GCG ATG ATG GGG CTT AAT GGG GTG AAA GCG GTT			824
Ala Lys Ile Ala Glu Ala Met Met Gly Leu Asn Gly Val Lys Ala Val			
245	250	255	
GAA ATA GGC AAG GGG GTA GAA AGC TCT TTA TTA AAA GGC TCA GAG TAT			872
Glu Ile Gly Lys Gly Val Glu Ser Ser Leu Leu Lys Gly Ser Glu Tyr			
260	265	270	275
AAT GAT TTA ATG GAT CAA AAG GGG TTT TTG AGC AAT CGT AGC GGA GGG			920
Asn Asp Leu Met Asp Gln Lys Gly Phe Leu Ser Asn Arg Ser Gly Gly			
280	285	290	
GTT TTA GGG GGC ATG AGC AAT GGG GAA GAA ATC ATT GTT AGA GTG CAT			968
Val Leu Gly Gly Met Ser Asn Gly Glu Glu Ile Ile Val Arg Val His			
295	300	305	
TTC AAA CCC ACG CCA AGC ATT TTC CAA CCT CAA CGA ACC ATA GAC ATT			1016
Phe Lys Pro Thr Pro Ser Ile Phe Gln Pro Gln Arg Thr Ile Asp Ile			
310	315	320	
AAT GGC AAT GAG TGC GAA TGC TTG TTA AAG GGC AGG CAT GAT CCT TGC			1064
Asn Gly Asn Glu Cys Glu Cys Leu Leu Lys Gly Arg His Asp Pro Cys			
325	330	335	
ATT GCG ATT AGA GGG AGC GTG GTG TGC GAG AGT TTG TTA GCG TTG GTG			1112
Ile Ala Ile Arg Gly Ser Val Val Cys Glu Ser Leu Leu Ala Leu Val			
340	345	350	355
TTG GCT GAT ATG GTA TTA CTC AAT TTG ACT TCA AAA ATA GAG TAT TTA			1160
Leu Ala Asp Met Val Leu Leu Asn Leu Thr Ser Lys Ile Glu Tyr Leu			
360	365	370	
AAA ACG ATT TAT AAT GAG AAT TAAACGAAAT TGGATACAAT CAGCTTAAAA AGGA			1215
Lys Thr Ile Tyr Asn Glu Asn			
375			
TA			1217

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 378 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met	Arg	Leu	Ser	Ser	Ala	Ser	Lys	Thr	Glu	Gly	Ser	Gln	Met	Asn	Thr
1				5					10					15	

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 20...535
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TCATTGTGCC TGAAGCCAC ATG CGC TAC ATG CTC ATC AAC GAT TAT TAC AAG	52
Met Arg Tyr Met Leu Ile Asn Asp Tyr Tyr Lys	
1 5 10	
GTG TTT TTG GGC GAA AAA GAT AAG GAT TTG TAT GTG AAG CGC TTG GAA	100
Val Phe Leu Gly Glu Lys Asp Lys Asp Leu Tyr Val Lys Arg Leu Glu	
15 20 25	
AAA ATC ACG CCT AAA ATC TAT CTG GCG AGC GTG TTT TTA GAG AAA CAC	148
Lys Ile Thr Pro Lys Ile Tyr Leu Ala Ser Val Phe Leu Glu Lys His	
30 35 40	
ACC CCT TTA AAA AGT CTT TTA GAA AAA ATC CCT AAG GGA AAA AAA GAG	196
Thr Pro Leu Lys Ser Leu Leu Glu Lys Ile Pro Lys Gly Lys Lys Glu	
45 50 55	
ACT ATC ACC TAT CAT AAC CCT TGT CAT GCC AAA AAA ACC CTA AAC GCT	244
Thr Ile Thr Tyr His Asn Pro Cys His Ala Lys Lys Thr Leu Asn Ala	
60 65 70 75	
CAC AAA GAA GTG CGC AAC TTG CTC AAT TTG CAT TAT GAA ATT AAA GAA	292
His Lys Glu Val Arg Asn Leu Leu Asn Leu His Tyr Glu Ile Lys Glu	
80 85 90	
ATG CCG GAC AAT TGT TGC GGT TTT GGG GGG ATT ACG ATG CAA ACA CAA	340
Met Pro Asp Asn Cys Cys Gly Phe Gly Gly Ile Thr Met Gln Thr Gln	
95 100 105	
AAG GCG GGA TTT TCT TTA AAA GTG GGG CTT CTT AGG GCT AAA GAA ATC	388
Lys Ala Gly Phe Ser Leu Lys Val Gly Leu Leu Arg Ala Lys Glu Ile	
110 115 120	
ATA GAC ACC AAA GCT GCA ATT TTG AGC GCT GAA TGC GGG GCA TGC CAT	436
Ile Asp Thr Lys Ala Ala Ile Leu Ser Ala Glu Cys Gly Ala Cys His	
125 130 135	
ATG CAA TTA AAC AAC GCT TTA AAG TCT TTA GAC GAC CCT AAC ACT CCG	484
Met Gln Leu Asn Asn Ala Leu Lys Ser Leu Asp Asp Pro Asn Thr Pro	
140 145 150 155	
CCA TTT TTG CAC CCT TTA GAA CTC ATC GCT AAA GCC TTA AAA AGC GCT	532
Pro Phe Leu His Pro Leu Glu Leu Ile Ala Lys Ala Leu Lys Ser Ala	
160 165 170	
GAA TAAAAAGCCT TTTTAACCCC ATTCTCCAAC ATCTTTTAT ATAATACAGA GCT	588
Glu	

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met Arg Tyr Met Leu Ile Asn Asp Tyr Tyr Lys Val Phe Leu Gly Glu
1 5 10 15
Lys Asp Lys Asp Leu Tyr Val Lys Arg Leu Glu Lys Ile Thr Pro Lys
20 25 30
Ile Tyr Leu Ala Ser Val Phe Leu Glu Lys His Thr Pro Leu Lys Ser
35 40 45
Leu Leu Glu Lys Ile Pro Lys Gly Lys Lys Glu Thr Ile Thr Tyr His
50 55 60
Asn Pro Cys His Ala Lys Lys Thr Leu Asn Ala His Lys Glu Val Arg
65 70 75 80
Asn Leu Leu Asn Leu His Tyr Glu Ile Lys Glu Met Pro Asp Asn Cys
85 90 95
Cys Gly Phe Gly Gly Ile Thr Met Gln Thr Gln Lys Ala Gly Phe Ser
100 105 110
Leu Lys Val Gly Leu Leu Arg Ala Lys Glu Ile Ile Asp Thr Lys Ala
115 120 125
Ala Ile Leu Ser Ala Glu Cys Gly Ala Cys His Met Gln Leu Asn Asn
130 135 140
Ala Leu Lys Ser Leu Asp Asp Pro Asn Thr Pro Pro Phe Leu His Pro
145 150 155 160
Leu Glu Leu Ile Ala Lys Ala Leu Lys Ser Ala Glu
165 170

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 30...317
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGCGTTAAAG CTCTGTATTA TATAAAAAG ATG TTG GAG AAT GGG GTT AAA AAG
Met Leu Glu Asn Gly Val Lys Lys
1 5
GCT TTT TAT TCA GCG CTT TTT AAG GCT TTA GCG ATG AGT TCT AAA GGG
Ala Phe Tyr Ser Ala Leu Phe Lys Ala Leu Ala Met Ser Ser Lys Gly
10 15 20

53

101

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met Leu Glu Asn Gly Val Lys Lys Ala Phe Tyr Ser Ala Leu Phe Lys
1 5 10 15
Ala Leu Ala Met Ser Ser Lys Gly Cys Lys Asn Gly Gly Val Leu Gly
20 25 30
Ser Ser Lys Asp Phe Lys Ala Leu Phe Asn Cys Ile Trp His Ala Pro
35 40 45
His Ser Ala Leu Lys Ile Ala Ala Leu Val Ser Met Ile Ser Leu Ala
50 55 60
Leu Arg Ser Pro Thr Phe Lys Glu Asn Pro Ala Phe Cys Val Cys Ile
65 70 75 80
Val Ile Pro Pro Lys Pro Gln Gln Leu Ser Gly Ile Ser Leu Ile Ser
85 90 95

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 69...1718
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TCATCATCTC CACTTCTAAT TTAACCTCTA ACGCCCTTAA CGCAATTGAG CAAATCAGAA 60
GCACAGGA ATG GGG ATT GAC ATT GAT GAA ATC ACT GAA GAG GAT TTT ATC 110
Met Gly Ile Asp Ile Asp Glu Ile Thr Glu Glu Asp Phe Ile
1 5 10
TAT TCT CGC ATT GAT TGG GAA AAG TTT GAT CCC ACA AAA ACG CAA GAC 158
Tyr Ser Arg Ile Asp Trp Glu Lys Phe Asp Pro Thr Lys Thr Gln Asp
15 20 25 30
GAA ATC CCC TTA TGC GAT AAG AAA AAG CCG CGC TCG CAT CAA ACA GAA 206
Glu Ile Pro Leu Cys Asp Lys Lys Lys Pro Arg Ser His Gln Thr Glu
35 40 45
GCC ATA AAC GCC ACT AAA GAG TAT TTT TCT GAC CCT AAA AAC GCT AGA 254
Ala Ile Asn Ala Thr Lys Glu Tyr Phe Ser Asp Pro Lys Asn Ala Arg

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 933 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met Thr Gln Ala Trp Leu Met Lys Pro Leu Leu Lys Lys Lys Ser Lys
 1 5 10 15
 Ser Leu Glu Ala Met Met Ala Thr Asn His Asn Asp Glu Lys Thr Leu
 20 25 30
 Phe Asp Ala Ile Leu Leu Gln Asp Leu Ala Asp Ala Met Tyr Asn Val
 35 40 45
 Met Pro Thr Lys Leu Gly Asp Arg Asn Tyr Trp Glu Asn Phe Thr Lys
 50 55 60
 Lys Thr Gly Asn Ile Ala Arg Thr Leu Asn Asn Arg Leu Lys Ile Ile
 65 70 75 80
 Phe Asp Lys Asn Pro Glu Phe Phe His Gly Phe Leu Asp Ser Leu Arg
 85 90 95
 Glu Asn Ile His Gln Asn Ile Lys Glu Asp Glu Ala Leu Asp Met Ile
 100 105 110
 Thr Ser His Ile Ile Thr Lys Pro Ile Phe Asp Ala Leu Phe Gly Asp
 115 120 125
 Asn Ile Lys Asn Pro Ile Ala Lys Ala Leu Asp Lys Met Val Glu Lys
 130 135 140
 Leu Ser Thr Leu Gly Leu Glu Gly Glu Thr Lys Asp Leu Lys Asn Leu
 145 150 155 160
 Tyr Glu Ser Val Lys Thr Glu Ala Leu His Ala Lys Ser Gln Lys Ser
 165 170 175
 Gln Gln Glu Leu Ile Lys Asn Leu Tyr Asn Thr Phe Phe Lys Glu Ala
 180 185 190
 Phe Lys Lys Gln Ser Glu Lys Leu Gly Ile Val Tyr Thr Pro Ile Glu
 195 200 205
 Val Val Asp Phe Ile Leu Arg Ala Thr Asn Gly Ile Leu Lys Lys His
 210 215 220
 Phe Asn Thr Asp Phe Asn Asp Gln Ser Ile Thr Ile Phe Asp Pro Phe
 225 230 235 240
 Thr Gly Thr Gly Ser Phe Ile Ala Arg Leu Leu Ser Lys Glu Asn Ala
 245 250 255
 Leu Ile Ser Asp Glu Ala Leu Lys Glu Lys Phe Gln Lys Asn Leu Phe
 260 265 270
 Ala Phe Asp Ile Val Leu Leu Ser Tyr Tyr Ile Ala Leu Ile Asn Ile
 275 280 285
 Thr Gln Ala Ala Gln Asn Arg Asp Gly Ser Leu Asn Asn Phe Lys Asn
 290 295 300
 Ile Ala Leu Thr Asp Ser Leu Asp Tyr Leu Glu Glu Lys Thr Asn Lys
 305 310 315 320
 Gly Val Leu Pro Leu Tyr Glu Asp Leu Lys Glu Asn Lys Gly Ile Lys
 325 330 335
 Asp Thr Leu Ala Asn Gln Asn Ile Arg Val Ile Ile Gly Asn Pro Pro
 340 345 350

Tyr	Ser	Ala	Gly	Ala	Lys	Ser	Gln	Asn	Asp	Asn	Asn	Gln	Asn	Leu	Ser	355	360	365
His	Pro	Lys	Leu	Glu	Lys	Leu	Val	Tyr	Glu	Lys	Tyr	Gly	Lys	Asn	Ser	370	375	380
Thr	Ser	Arg	Ser	Val	Gly	Lys	Thr	Thr	Arg	Asp	Thr	Leu	Ile	Gln	Ser	385	390	395
Ile	Arg	Met	Ala	Ser	Asp	Val	Val	Lys	Asp	Arg	Gly	Val	Ile	Gly	Phe	405	410	415
Val	Val	Asn	Gly	Gly	Phe	Ile	Asp	Ser	Lys	Ser	Ala	Asp	Gly	Phe	Arg	420	425	430
Lys	Cys	Val	Ala	Lys	Glu	Phe	Ser	His	Leu	Tyr	Val	Leu	Asn	Leu	Arg	435	440	445
Gly	Asn	Gln	Arg	Thr	Ser	Gly	Glu	Val	Ser	Lys	Lys	Glu	Gly	Gly	Lys	450	455	460
Ile	Phe	Asp	Ser	Gly	Ser	Arg	Ala	Thr	Val	Ala	Ile	Ile	Phe	Phe	Val	465	470	475
Lys	Asp	Lys	Ser	Thr	Pro	Asp	Asn	Thr	Ile	Phe	Tyr	Tyr	Glu	Val	Glu	485	490	495
Asp	Tyr	Leu	Lys	Arg	Glu	Ala	Lys	Leu	Asn	Trp	Leu	Ala	Asn	Phe	Glu	500	505	510
Asn	Leu	Asp	Phe	Val	Pro	Phe	Glu	Lys	Ile	Thr	Pro	Asn	Asp	Lys	Gly	515	520	525
Asp	Trp	Ile	Asn	Gln	Arg	Asn	Asp	Ala	Phe	Glu	Lys	Leu	Ile	Pro	Leu	530	535	540
Lys	Arg	Asp	Lys	Thr	Leu	Gln	Asn	Asp	Ser	Val	Phe	Asp	Ile	Asn	Ser	545	550	555
Leu	Gly	Val	Val	Ser	Gly	Arg	Asp	Pro	Trp	Val	Tyr	Asn	Phe	Ser	Pro	565	570	575
Asn	Ile	Leu	Thr	Gln	Ser	Val	Gln	Lys	Cys	Ile	Asp	Thr	Tyr	Asn	Ala	580	585	590
Asp	Leu	Lys	Arg	Phe	Asn	Ala	Arg	Phe	Arg	Glu	Ala	Phe	Lys	Gln	Arg	595	600	605
Ala	Gln	Ser	Val	Lys	Ala	Gly	Asp	Leu	Tyr	Lys	Gln	Leu	Asn	Asp	Lys	610	615	620
Glu	Ile	Thr	Thr	Asp	Lys	Thr	Lys	Ile	Ala	Trp	Thr	Asp	Gly	Leu	Lys	625	630	635
Asn	Lys	Leu	Ile	Lys	Asn	Lys	Ser	Ala	Arg	Glu	Ser	Ser	Glu	Glu	Arg	645	650	655
Val	Arg	Leu	Ala	Leu	Tyr	Arg	Pro	Phe	Asn	Lys	Gln	Trp	Leu	Tyr	Trp	660	665	670
Asp	Lys	Asp	Trp	Ile	Asn	Arg	Gln	Arg	Glu	Phe	Ser	Lys	Ile	Phe	Pro	675	680	685
Asp	Lys	Asp	Ala	Gln	Asn	Val	Val	Ile	Asn	Thr	Gly	Val	Gly	Asn	Gly	690	695	700
Lys	Asp	Phe	Ser	Ala	Leu	Val	Ser	Asp	Phe	Ile	Ser	Asp	Tyr	Ser	Leu	705	710	715
Ile	Ser	Pro	Asn	Gln	Ala	Tyr	Pro	Leu	Tyr	Tyr	Tyr	Asp	Asp	Leu	Gly	725	730	735
Asn	Arg	His	Tyr	Ala	Ile	Ser	Gly	Tyr	Cys	Leu	Asn	Leu	Phe	Arg	Arg	740	745	750
His	Tyr	Gly	Asp	Asn	Leu	Ile	Ala	Glu	Glu	Glu	Ile	Phe	Tyr	Tyr	Ile	755	760	765
Tyr	Ala	Ile	Phe	His	His	Lys	Gly	Tyr	Leu	Glu	Lys	Tyr	Lys	Asn	Ser	770	775	780
Leu	Ala	Lys	Glu	Ala	Pro	Arg	Ile	Ala	Leu	Ser	Glu	Asp	Phe	Lys	Glu	785	790	795
Leu	Ser	Val	Leu	Gly	Lys	Glu	Leu	Ala	Glu	Leu	His	Leu	Asn	Tyr	Glu	805	810	815

Ser Gly Glu Met His Asp Asn Ile Lys Tyr Thr Thr Leu Met Asn Ala
820 825 830
Glu Ile Glu Gly Tyr Tyr Asp Val Asp Lys Met Thr Lys Lys Gly Asp
835 840 845
Cys Ile Ile Tyr Asn Gln Asn Ile Ala Ile Thr Lys Ile Pro Lys Lys
850 855 860
Ala Phe Asp Tyr Val Ile Asn Gly Lys Ser Ala Ile Asp Trp Val Ile
865 870 875 880
Glu Arg Tyr Gln Lys Thr Met Asp Lys Glu Ser Leu Ile Glu Asn Asn
885 890 895
Pro Asn Asp Tyr Ala Gly Gly Lys Tyr Val Phe Glu Leu Leu Cys Arg
900 905 910
Val Ile Thr Leu Ser Val Lys Ser Val Asp Leu Ile Glu Lys Ile Ser
915 920 925
Glu Lys Arg Phe Glu
930

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 24...1370
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

AAGATCAGCG AAAAGAGGTT TGA GTG ATT ACA TCG CTT GGG GGT GTG GAA TAT	53
Val Ile Thr Ser Leu Gly Gly Val Glu Tyr	
1 5 10	
TTT GAA AGG CAA TGT CTT GCT TTC TTA AAA AAT CCA CAA ACT AAT CCA	101
Phe Glu Arg Gln Cys Leu Ala Phe Leu Lys Asn Pro Gln Thr Asn Pro	
15 20 25	
CAA AAT GAG CAA TAC ATT CCA GGA GTG TTT TCG TAT CAA GAA AAC AAA	149
Gln Asn Glu Gln Tyr Ile Pro Gly Val Phe Ser Tyr Gln Glu Asn Lys	
30 35 40	
ATT TCT TTT TCT TTT TTG GTT TTA GGA GAA ATT GAA GAG ATC CAC TCT	197
Ile Ser Phe Ser Phe Leu Val Leu Gly Glu Ile Glu Glu Ile His Ser	
45 50 55	
TTG CAA TAC CAA ACG CTC TAT ATT GTG GAT AAC AAA AAA AGA TAC ACT	245
Leu Gln Tyr Gln Thr Leu Tyr Ile Val Asp Asn Lys Lys Arg Tyr Thr	
60 65 70	
CTT TAC AAG CTT TAT GAT CGC ATT ATT TTG GGT CAT ACT TTA GGG TAT	293
Leu Tyr Lys Leu Tyr Asp Arg Ile Ile Leu Gly His Thr Leu Gly Tyr	
75 80 85 90	

TCT Ser	GCA Ala	CCA Pro	ATC Ile	ACG Thr 95	CTC Leu	TAT Tyr	TAT Tyr	GAA Glu	TGG Trp 100	CTG Leu	TTT Phe	GAT Asp	GAT Asp	TGG Trp 105	ATC Ile	341
GAT Asp	CCA Pro	GAA Glu	AAA Lys 110	ATT Ile	ATG Met	GGC Gly	GAT Asp	CGT Arg 115	TTT Phe	GTT Val	TGT Cys	AGG Arg	ACA Thr 120	AAT Asn	TAT Tyr	389
TTA Leu	GAA Glu	AGT Ser 125	TTT Phe	TTT Phe	ACG Thr	ACC Thr	AAG Lys 130	AAG Lys	CAT His	TTG Leu	CTA Leu	CCT Pro 135	GAT Asp	ACA Thr	TTA Leu	437
TTT Phe	AAA Lys 140	GTA Val	GAT Asp	GAA Glu	AGT Ser	GGG Gly 145	TGT Cys	GAA Glu	AGT Ser	TAT Tyr	CAT His 150	GAG Glu	AAT Asn	AAC Asn	GAT Asp	485
AAG Lys 155	GAC Asp	TTT Phe	ATC Ile	CTA Leu	CAA Gln 160	TCA Ser	TTT Phe	TAT Tyr	ATT Ile	CAA Gln 165	AAT Asn	GAT Asp	TTT Phe	TTA Leu	TCC Ser 170	533
CAA Gln	AGA Arg	TAT Tyr	GAA Glu	AAA Lys 175	GAC Asp	AAG Lys	ATA Ile	AAA Lys	GCA Ala 180	AAA Lys	TCT Ser	AAT Asn	TTG Leu	ATT Ile	CCT Pro 185	581
AAA Lys	AGA Arg	CAG Gln	AAT Asn 190	CGT Arg	TTA Leu	TTA Leu	ACT Thr	TAT Tyr 195	CAA Gln	TTT Phe	GAT Asp	TTG Leu	TCT Ser	TTG Leu	GAA Glu	629
TGC Cys	AAT Asn 205	ATA Ile	ATT Ile	TTT Phe	GAA Glu	ACC Thr	CTT Leu	GAA Glu	AAA Lys	TTA Leu	GCA Ala	CTT Leu 215	ATT Ile	GCT Ala	GGA Gly	677
GCG Ala	ATT Ile 220	AAA Lys	AAC Asn	TTT Phe	TTT Phe	ATT Ile 225	TTG Leu	ATT Ile	TAT Tyr	GCT Ala	CAT His 230	TCT Ser	AAT Asn	TTT Phe	GAC Asp	725
ATC Ile 235	CAA Gln	ATT Ile	GAC Asp	TAT Tyr	ATC Ile 240	CAA Gln	TTC Phe	AAG Lys	CTT Leu	TCT Ser 245	AAT Asn	AAA Lys	GAC Asp	ATT Ile	ACA Thr 250	773
GCA Ala	ATA Ile	AGA Arg	AAC Asn	ACT Thr 255	TAC Tyr	AAA Lys	AAA Lys	GAT Asp	AAA Lys 260	AAG Lys	TCT Ser	ATG Met	GAG Glu	ATA Ile 265	GAT Asp	821
CTT Leu	TAT Tyr	GGG Gly	ATT Ile 270	GCT Ala	ATA Ile	AAT Asn	TTC Phe	CAA Gln 275	CGG Arg	ATA Ile	GAC Asp	AAT Asn	TTT Phe 280	TCT Ser	GTA Val	869
ATA Ile	CTT Leu	GAA Glu 285	AAA Lys	TGG Trp	ATT Ile	GTT Val	TTT Phe 290	TAT Tyr	ATC Ile	AAA Lys	GAC Asp	AAT Asn 295	AGA Arg	GAT Asp	TTC Phe	917
CAA Gln 300	CTT Leu	GCA Ala	AGT Ser	ATT Ile	TTA Leu	GAC Asp 305	ATT Ile	ATT Ile	AAT Asn	AAA Lys	AAA Lys 310	GAT Asp	CCA Pro	ATT Ile	ATT Ile	965
CAC His	TTG Leu	TAT Tyr	TTG Leu	GAC Asp	ATG Met	TTT Phe	GTA Val	TTG Leu	ATT Ile	AGC Ser	ATG Met	ATT Ile	GAA Glu	AGT Ser	TTT Phe	1013

Arg	Ile	Ile	Leu	Gly	His	Thr	Leu	Gly	Tyr	Ser	Ala	Pro	Ile	Thr	Leu
				85					90					95	
Tyr	Tyr	Glu	Trp	Leu	Phe	Asp	Asp	Trp	Ile	Asp	Pro	Glu	Lys	Ile	Met
			100					105					110		
Gly	Asp	Arg	Phe	Val	Cys	Arg	Thr	Asn	Tyr	Leu	Glu	Ser	Phe	Phe	Thr
		115					120					125			
Thr	Lys	Lys	His	Leu	Leu	Pro	Asp	Thr	Leu	Phe	Lys	Val	Asp	Glu	Ser
	130					135					140				
Gly	Cys	Glu	Ser	Tyr	His	Glu	Asn	Asn	Asp	Lys	Asp	Phe	Ile	Leu	Gln
145					150					155					160
Ser	Phe	Tyr	Ile	Gln	Asn	Asp	Phe	Leu	Ser	Gln	Arg	Tyr	Glu	Lys	Asp
				165					170					175	
Lys	Ile	Lys	Ala	Lys	Ser	Asn	Leu	Ile	Pro	Lys	Arg	Gln	Asn	Arg	Leu
			180					185					190		
Leu	Thr	Tyr	Gln	Phe	Asp	Leu	Ser	Leu	Glu	Cys	Asn	Ile	Ile	Phe	Glu
		195					200					205			
Thr	Leu	Glu	Lys	Leu	Ala	Leu	Ile	Ala	Gly	Ala	Ile	Lys	Asn	Phe	Phe
	210					215					220				
Ile	Leu	Ile	Tyr	Ala	His	Ser	Asn	Phe	Asp	Ile	Gln	Ile	Asp	Tyr	Ile
225					230					235					240
Gln	Phe	Lys	Leu	Ser	Asn	Lys	Asp	Ile	Thr	Ala	Ile	Arg	Asn	Thr	Tyr
				245					250					255	
Lys	Lys	Asp	Lys	Lys	Ser	Met	Glu	Ile	Asp	Leu	Tyr	Gly	Ile	Ala	Ile
			260					265					270		
Asn	Phe	Gln	Arg	Ile	Asp	Asn	Phe	Ser	Val	Ile	Leu	Glu	Lys	Trp	Ile
		275					280						285		
Val	Phe	Tyr	Ile	Lys	Asp	Asn	Arg	Asp	Phe	Gln	Leu	Ala	Ser	Ile	Leu
	290					295					300				
Asp	Ile	Ile	Asn	Lys	Lys	Asp	Pro	Ile	Ile	His	Leu	Tyr	Leu	Asp	Met
305				310						315					320
Phe	Val	Leu	Ile	Ser	Met	Ile	Glu	Ser	Phe	Leu	Lys	Lys	Pro	Gln	Gln
				325					330					335	
Thr	Lys	Leu	His	Glu	Lys	Leu	Ser	Glu	Phe	Phe	Lys	Ile	Ser	Leu	Ser
			340					345					350		
Arg	Thr	Lys	Cys	Asp	Gln	Thr	Lys	Asn	Tyr	Phe	Asn	Asp	Lys	Cys	Gln
		355					360					365			
Glu	Asp	Leu	Ile	Gln	Gln	Ile	Val	Asp	Cys	Arg	Asn	Ser	Leu	Ala	His
	370					375					380				
Gly	Arg	Ser	Leu	Lys	Leu	Asp	Thr	Asn	Lys	Ala	Thr	Asp	Ile	Ser	His
385				390						395					400
Ala	Phe	Ile	Asp	Phe	Lys	Gln	Ile	Val	Ile	Glu	Phe	Phe	Phe	Gly	Glu
				405					410					415	
Ile	Gly	Leu	Ser	Asp	Phe	Ile	Thr	Asn	Asn	Phe	Gly	Phe	Leu	Asn	Lys
			420					425					430		
Val	Lys	Le													

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

-109-

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...1302
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTAAATGAAT TTAAAAGGAA AAAT ATG GCA GTA AGA TTT GGG ATT ATC TTT	51
Met Ala Val Arg Phe Gly Ile Ile Phe	
1 5	
ATA TCT GAC TCT ATT GAT GAT TAT AAA GCC AAA CAA TTA AGA TCA ATT	99
Ile Ser Asp Ser Ile Asp Asp Tyr Lys Ala Lys Gln Leu Arg Ser Ile	
10 15 20 25	
TTA GAA CGC AAG AAA GAG TGT AAT TTT ATA TGG TTT AAT GAA TCA AGT	147
Leu Glu Arg Lys Lys Glu Cys Asn Phe Ile Trp Phe Asn Glu Ser Ser	
30 35 40	
GCT ATA ATT CAC AAT ACT CCT AAA GTT TTT GAA GGA GAG AGT TTT TTT	195
Ala Ile Ile His Asn Thr Pro Lys Val Phe Glu Gly Glu Ser Phe Phe	
45 50 55	
GAT CAT CTT TTC GTT AGT GCA AAA ATT ACT GCT TTT GTG GTA TCC ACA	243
Asp His Leu Phe Val Ser Ala Lys Ile Thr Ala Phe Val Val Ser Thr	
60 65 70	
AAC GAA TCA GAT ACA ATA TTC AAT TTA AAA AAC TAC TTG CTA GTA TTA	291
Asn Glu Ser Asp Thr Ile Phe Asn Leu Lys Asn Tyr Leu Leu Val Leu	
75 80 85	
GCC AAA AAT CTC AAT AAT AGA GAT ATT TGG TAT TGT GAA AAC ACT ATT	339
Ala Lys Asn Leu Asn Asn Arg Asp Ile Trp Tyr Cys Glu Asn Thr Ile	
90 95 100 105	
TGC GAT AAA AAA GGC ACT TAT AAT ATA GAA ATA GAA TTA GTG AGC AAT	387
Cys Asp Lys Lys Gly Thr Tyr Asn Ile Glu Ile Glu Leu Val Ser Asn	
110 115 120	
GCT AAT GAT TTT AGA GGA GTG TTT GGA GAA GTG TTA GGT ATA GTC AAA	435
Ala Asn Asp Phe Arg Gly Val Phe Gly Glu Val Leu Gly Ile Val Lys	
125 130 135	
GAC ACT TTC GGT GAT TTA CTG CAA CTT CTT ACA AAT TTA AAG AAC AAG	483
Asp Thr Phe Gly Asp Leu Leu Gln Leu Leu Thr Asn Leu Lys Asn Lys	
140 145 150	
GAA ATT GAA TTT AAT TTT CAT AAA AAA ATT AAT TAC GGA TTG CCT TTT	531
Glu Ile Glu Phe Asn Phe His Lys Lys Ile Asn Tyr Gly Leu Pro Phe	
155 160 165	
GGG ATT ATC TTT ATC GCT AGC AAC TCT GAC AAC CCT ATT GAT ATT GAC	579
Gly Ile Ile Phe Ile Ala Ser Asn Ser Asp Asn Pro Ile Asp Ile Asp	
170 175 180 185	
AAT AAA ACC AAA AAG TTA AAA TCA TGC TTT CGT GAT GAT GAG AGT AAC	627

Asn	Lys	Thr	Lys	Lys 190	Leu	Lys	Ser	Cys	Phe 195	Arg	Asp	Asp	Glu	Ser 200	Asn	
TGT Cys	TTT Phe	ATT Ile	GAC Asp 205	TGC Cys	CCA Pro	ATT Ile	ACA Thr	ATT Ile 210	GAG Glu	GAT Asp	TAT Tyr	TTA Leu 215	ATT Ile	TTA Leu	GAT Asp	675
AAT Asn	CTA Leu	AAA Lys 220	AGC Ser	TGT Cys	TTT Phe	GTA Val 225	ATC Ile	CAA Gln	AAT Asn	AAG Lys	CCA Pro 230	AAT Asn 230	GTA Val	ACA Thr	TTA Leu	723
TTT Phe	GAT Asp 235	AAC Asn	GAC Asp	GAG Glu	AAC Asn	GAT Asp 240	AGA Arg	CCA Pro	TTC Phe	AAT Asn	TTA Leu 245	AAG Lys	CGA Arg	TAC Tyr	TTG Leu	771
TTA Leu 250	GGA Gly	TTG Leu	AAA Lys	GAA Glu	AAG Lys 255	TTA Leu	GGG Gly	TTT Phe	GAG Glu	CCA Pro 260	ACG Thr	GGT Gly	ATT Ile	TTC Phe	TAT Tyr 265	819
TGC Cys	GAA Glu	AAC Asn	GCA Ala 270	AAC Asn	ACA Thr	CAC His	AAA Lys	ATT Ile	GAA Glu 275	TTG Leu	ATT Ile	GGT Gly	AAT Asn 280	GAT Asp	TCT Ser	867
GAT Asp	TTC Phe	AGA Arg	GAG Glu 285	GTA Val	TTA Leu	CTT Leu	GAA Glu	TTT Phe 290	TCA Ser	GAG Glu	AAT Asn	ATA Ile 295	CCA Pro	AAA Lys	GCC Ala	915
CCT Pro	AAT Asn 300	GAA Glu	CTA Leu	CCA Pro	CAA Gln	TTT Phe 305	CTT Leu	ACA Thr	AAC Asn	TTT Phe	AAA Lys 310	AAT Asn 310	TCA Ser	AAA Lys	ATC Ile	963
CCC Pro	AAT Asn 315	GGA Gly	AAC Asn	ATT Ile	TCA Ser	TTT Phe 320	TCG Ser	CCA Pro	CCA Pro	AAA Lys 325	AAT Asn 325	TCT Ser	CCA Pro	TCA Ser	ATT Ile	1011
TCT Ser 330	TCA Ser	TAT Tyr	GCT Ala	TTA Leu	TCT Ser 335	GAT Asp	AAG Lys	ATT Ile	AAA Lys	AGA Arg 340	GAA Glu	GTA Val	AGA Arg	GAT Asp	ACC Thr 345	1059
TTT Phe	GAT Asp	CGC Arg	TAT Tyr 350	TTG Leu	TGG Trp	CAT His	GGT Gly	TAT Tyr 355	TCT Ser 355	AAA Lys	ATT Ile	CCA Pro	CAG Gln	GAG Glu 360	AAA Lys	1107
AGG Arg	ATA Ile	GCC Ala 365	AAA Lys	ATA Ile	AAA Lys	GAG Glu	CAA Gln	GTG Val 370	AAG Lys	GAA Glu	GAA Glu	ATT Ile 375	AAA Lys 375	CTA Leu	AAT Asn	1155
CCT Pro	TCT Ser	TTT Phe 380	CGT Arg	AAT Asn	TAT Tyr	AGA Arg 385	GTA Val	GAC Asp	TCT Ser	GAA Glu	CAA Gln	AAC Asn 390	CGC Arg	AAG Lys	ATC Ile	1203
AAT Asn	GAA Glu 395	ATT Ile	GCT Ala	GAG Glu	GGT Gly	TTA Leu 400	AAA Lys	AGT Ser	GGT Gly	AAG Lys	ATA Ile 405	ATT Ile	GGT Gly	AAA Lys	AAG Lys	1251
GTT Val 410	ATT Ile	GCT Ala	AAT Asn	GCG Ala	TTC Phe 415	GAT Asp	CTA Leu	AAT Asn	GCT Ala 420	AGC Ser	TTA Leu	TTG Leu	TTT Phe	TAT Tyr 425	TAC Tyr	1299

TCC TGATGATTTA AAGAATTTAA AGGAACGATT ATTTATAGAT ATT
Ser

1345

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met	Ala	Val	Arg	Phe	Gly	Ile	Ile	Phe	Ile	Ser	Asp	Ser	Ile	Asp	Asp
1				5				10					15		
Tyr	Lys	Ala	Lys	Gln	Leu	Arg	Ser	Ile	Leu	Glu	Arg	Lys	Lys	Glu	Cys
		20					25					30			
Asn	Phe	Ile	Trp	Phe	Asn	Glu	Ser	Ser	Ala	Ile	Ile	His	Asn	Thr	Pro
	35					40					45				
Lys	Val	Phe	Glu	Gly	Glu	Ser	Phe	Phe	Asp	His	Leu	Phe	Val	Ser	Ala
	50				55					60					
Lys	Ile	Thr	Ala	Phe	Val	Val	Ser	Thr	Asn	Glu	Ser	Asp	Thr	Ile	Phe
	65				70					75				80	
Asn	Leu	Lys	Asn	Tyr	Leu	Leu	Val	Leu	Ala	Lys	Asn	Leu	Asn	Asn	Arg
			85					90					95		
Asp	Ile	Trp	Tyr	Cys	Glu	Asn	Thr	Ile	Cys	Asp	Lys	Lys	Gly	Thr	Tyr
		100					105					110			
Asn	Ile	Glu	Ile	Glu	Leu	Val	Ser	Asn	Ala	Asn	Asp	Phe	Arg	Gly	Val
	115					120					125				
Phe	Gly	Glu	Val	Leu	Gly	Ile	Val	Lys	Asp	Thr	Phe	Gly	Asp	Leu	Leu
	130				135					140					
Gln	Leu	Leu	Thr	Asn	Leu	Lys	Asn	Lys	Glu	Ile	Glu	Phe	Asn	Phe	His
	145				150					155				160	
Lys	Lys	Ile	Asn	Tyr	Gly	Leu	Pro	Phe	Gly	Ile	Ile	Phe	Ile	Ala	Ser
			165					170						175	
Asn	Ser	Asp	Asn	Pro	Ile	Asp	Ile	Asp	Asn	Lys	Thr	Lys	Lys	Leu	Lys
		180					185					190			
Ser	Cys	Phe	Arg	Asp	Asp	Glu	Ser	Asn	Cys	Phe	Ile	Asp	Cys	Pro	Ile
	195					200					205				
Thr	Ile	Glu	Asp	Tyr	Leu	Ile	Leu	Asp	Asn	Leu	Lys	Ser	Cys	Phe	Val
	210				215					220					
Ile	Gln	Asn	Lys	Pro	Asn	Val	Thr	Leu	Phe	Asp	Asn	Asp	Glu	Asn	Asp
	225				230					235				240	
Arg	Pro	Phe	Asn	Leu	Lys	Arg	Tyr	Leu	Leu	Gly	Leu	Lys	Glu	Lys	Leu
			245					250						255	
Gly	Phe	Glu	Pro	Thr	Gly	Ile	Phe	Tyr	Cys	Glu	Asn	Ala	Asn	Thr	His
		260					265						270		
Lys	Ile	Glu	Leu	Ile	Gly	Asn	Asp	Ser	Asp	Phe	Arg	Glu	Val	Leu	Leu
	275					280					285				
Glu	Phe	Ser	Glu	Asn	Ile	Pro	Lys	Ala	Pro	Asn	Glu	Leu	Pro	Gln	Phe
	290				295					300					
Leu	Thr	Asn	Phe	Lys	Asn	Ser	Lys	Ile	Pro	Asn	Gly	Asn	Ile	Ser	Phe
	305			310						315				320	
Ser	Pro	Pro	Lys	Asn	Ser	Pro	Ser	Ile	Ser	Ser	Tyr	Ala	Leu	Ser	Asp

325 330 335
 Lys Ile Lys Arg Glu Val Arg Asp Thr Phe Asp Arg Tyr Leu Trp His
 340 345 350
 Gly Tyr Ser Lys Ile Pro Gln Glu Lys Arg Ile Ala Lys Ile Lys Glu
 355 360 365
 Gln Val Lys Glu Glu Ile Lys Leu Asn Pro Ser Phe Arg Asn Tyr Arg
 370 375 380
 Val Asp Ser Glu Gln Asn Arg Lys Ile Asn Glu Ile Ala Glu Gly Leu
 385 390 395 400
 Lys Ser Gly Lys Ile Ile Gly Lys Lys Val Ile Ala Asn Ala Phe Asp
 405 410 415
 Leu Asn Ala Ser Leu Leu Phe Tyr Tyr Ser
 420 425

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...705
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

TTGCTAATGC GTTCGATCTA A ATG CTA GCT TAT TGT TTT ATT ACT CCT GAT	51
Met Leu Ala Tyr Cys Phe Ile Thr Pro Asp	10
1 5	
GAT TTA AAG AAT TTA AAG GAA CGA TTA TTT ATA GAT ATT ATC AAT GCT	99
Asp Leu Lys Asn Leu Lys Glu Arg Leu Phe Ile Asp Ile Ile Asn Ala	25
15 20	
ATC AAC CAA AAA AAG AGA GTC GCG CTC GAT CAT GCT CAA ATA GAT GAC	147
Ile Asn Gln Lys Lys Arg Val Ala Leu Asp His Ala Gln Ile Asp Asp	40
30 35	
ATC CAG TAT AAT GTG CTT GAT AAT GCG TTT TAT TTT ATC TTT GAT GTT	195
Ile Gln Tyr Asn Val Leu Asp Asn Ala Phe Tyr Phe Ile Phe Asp Val	55
45 50	
GGT AAC CCT TCT CAA TTA GCT ATT AAA GTG CCT AGA AAA TCT TTA GAA	243
Gly Asn Pro Ser Gln Leu Ala Ile Lys Val Pro Arg Lys Ser Leu Glu	70
60 65	
AAT GAT GAG TTG CCC AAC ACT AAA AAA AAC ATA TTC AAT GGA TTA ATA	291
Asn Asp Glu Leu Pro Asn Thr Lys Lys Asn Ile Phe Asn Gly Leu Ile	90
75 80 85	
AGA ACT ATC TAT GGG TGT ATT GAT GAT GAA AAT TCA TTT TTA TTA GAA	339
Arg Thr Ile Tyr Gly Cys Ile Asp Asp Glu Asn Ser Phe Leu Leu Glu	

	95	100	105	
AAC GAT AAA ACC ATC AAG GAT TTA AAT ATT CAG GAT TTA TTG GGG CCA				387
Asn Asp Lys Thr Ile Lys Asp Leu Asn Ile Gln Asp Leu Leu Gly Pro	110	115	120	
TTA AAA ACT CAA GCA TTT CCA TTA TCA TAC ATT ATT ACT GAC GCT ATC				435
Leu Lys Thr Gln Ala Phe Pro Leu Ser Tyr Ile Ile Thr Asp Ala Ile	125	130	135	
AAT CAA AAA GAA GGG GTG GCT CTC GAT TAC GCT CTA ATA AAC GAT ATT				483
Asn Gln Lys Glu Gly Val Ala Leu Asp Tyr Ala Leu Ile Asn Asp Ile	140	145	150	
AAG TAT AAT TTG CTT GAT AAC ACA TTC CAT TTT ATC TTT GAT GTT GGT				531
Lys Tyr Asn Leu Leu Asp Asn Thr Phe His Phe Ile Phe Asp Val Gly	155	160	165	170
AAT CCT TTG TTG AAA GAG TCA AGT CAA TTT ATT ATT GAA GTG CCT AGA				579
Asn Pro Leu Leu Lys Glu Ser Ser Gln Phe Ile Ile Glu Val Pro Arg	175	180	185	
GAG GCG TTG GAT CTA GAG AAT GTT GAT CGG CTT GTT GAA TAT ACG CTG				627
Glu Ala Leu Asp Leu Glu Asn Val Asp Arg Leu Val Glu Tyr Thr Leu	190	195	200	
TCT CCT AAT AAT CAT AGT CAA AGT TCT TTA GTG TAT CAT ATT TCT GAA				675
Ser Pro Asn Asn His Ser Gln Ser Ser Leu Val Tyr His Ile Ser Glu	205	210	215	
GGC TCT TAT ATC ATT CAC TTA ATA GAT GAC TAAACTTAAA TGAAA				720
Gly Ser Tyr Ile Ile His Leu Ile Asp Asp	220	225		

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met	Leu	Ala	Tyr	Cys	Phe	Ile	Thr	Pro	Asp	Asp	Leu	Lys	Asn	Leu	Lys
1				5				10					15		
Glu	Arg	Leu	Phe	Ile	Asp	Ile	Ile	Asn	Ala	Ile	Asn	Gln	Lys	Lys	Arg
		20						25				30			
Val	Ala	Leu	Asp	His	Ala	Gln	Ile	Asp	Asp	Ile	Gln	Tyr	Asn	Val	Leu
		35					40				45				
Asp	Asn	Ala	Phe	Tyr	Phe	Ile	Phe	Asp	Val	Gly	Asn	Pro	Ser	Gln	Leu
50						55				60					
Ala	Ile	Lys	Val	Pro	Arg	Lys	Ser	Leu	Glu	Asn	Asp	Glu	Leu	Pro	Asn
65				70						75				80	
Thr	Lys	Lys	Asn	Ile	Phe	Asn	Gly	Leu	Ile	Arg	Thr	Ile	Tyr	Gly	Cys

85 90 95
 Ile Asp Asp Glu Asn Ser Phe Leu Leu Glu Asn Asp Lys Thr Ile Lys
 100 105 110
 Asp Leu Asn Ile Gln Asp Leu Leu Gly Pro Leu Lys Thr Gln Ala Phe
 115 120 125
 Pro Leu Ser Tyr Ile Ile Thr Asp Ala Ile Asn Gln Lys Glu Gly Val
 130 135 140
 Ala Leu Asp Tyr Ala Leu Ile Asn Asp Ile Lys Tyr Asn Leu Leu Asp
 145 150 155 160
 Asn Thr Phe His Phe Ile Phe Asp Val Gly Asn Pro Leu Leu Lys Glu
 165 170 175
 Ser Ser Gln Phe Ile Ile Glu Val Pro Arg Glu Ala Leu Asp Leu Glu
 180 185 190
 Asn Val Asp Arg Leu Val Glu Tyr Thr Leu Ser Pro Asn Asn His Ser
 195 200 205
 Gln Ser Ser Leu Val Tyr His Ile Ser Glu Gly Ser Tyr Ile Ile His
 210 215 220
 Leu Ile Asp Asp
 225

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...561
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

TTTGGGCATG CTTGGTGATC TTAA ATG AGT CAA GGT GAT GGG GTG GAA GGA	51
Met Ser Gln Gly Asp Gly Val Glu Gly	
1 5	
AAT AAT ATG GAT ACT ACG AAA GAG AAC TTG AAT GGC TCA AAA GAG CGT	99
Asn Asn Met Asp Thr Thr Lys Glu Asn Leu Asn Gly Ser Lys Glu Arg	
10 15 20 25	
TTG AGC GAT TGG GAA TAT CGA TGG GCA ATG GCT CTA GTC TAT GGA GGA	147
Leu Ser Asp Trp Glu Tyr Arg Trp Ala Met Ala Leu Val Tyr Gly Gly	
30 35 40	
TGT ATC TCC ATA ACC ACT AGG ATT TTT TAT GAC ATA AAT GGT TCA GCT	195
Cys Ile Ser Ile Thr Thr Arg Ile Phe Tyr Asp Ile Asn Gly Ser Ala	
45 50 55	
AGC GAT CCG CTT TTT GAC CCT AAA TAC AGC TAT TAT GTG TGG TTA GTG	243
Ser Asp Pro Leu Phe Asp Pro Lys Tyr Ser Tyr Tyr Val Trp Leu Val	
60 65 70	

Arg	Asp	Phe	Tyr	Val	Met	Leu	Leu	Thr	Met	Pro	Phe	Ile	Ala	Ala	Ile
	130					135					140				
His	Glu	Val	Ser	Ala	Tyr	Cys	Gly	His	Pro	Ser	Asn	Leu	Leu	Val	Glu
145					150					155					160
Gly	Leu	Val	Ile	Leu	Gly	Phe	Gln	Gly	Phe	Leu	Lys	Leu	Cys	Ala	Lys
			165						170					175	
Trp	Gly	Trp													

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 72...404
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GTTGTGGTAT	AAATATTCTT	ATCAAGGTGT	GCCAAACATG	CCTTGAATCT	CAATTTTGA	60
ATCTCAATTT	T ATG AAA	GGA TTT	GTT ATG	AGT GGA	TTA AGA	110
	Met Lys	Gly Phe	Val Met	Ser Gly	Leu Arg	
	1		5		10	
TGT GTA	GTG GTT	TTA TGC	GGT GCA	ATG GCT	AAT GTG	158
Cys Val	Val Val	Leu Cys	Gly Ala	Met Ala	Asn Val	
	15		20		25	
CCT AAA	ATA GAG	GCA AGG	GGT GAA	TTA GGC	AAA TTT	206
Pro Lys	Ile Glu	Ala Arg	Gly Glu	Leu Gly	Lys Phe	
30		35		40	45	
GTT GGG	GGT TTT	GTT GGT	GAT AAA	ATG GGC	GGA TTT	254
Val Gly	Gly Phe	Val Gly	Asp Lys	Met Gly	Gly Phe	
	50			55	60	
ATA GGA	GGA TAT	ATT GGG	TCT GAA	ATA GGC	GAT AGG	302
Ile Gly	Gly Tyr	Ile Gly	Ser Glu	Ile Gly	Asp Arg	
	65			70	75	
ATC CGT	GGT GTT	GAT AGA	GAG CCA	CAA AAC	AAA GAA	350
Ile Arg	Gly Val	Asp Arg	Glu Pro	Gln Asn	Lys Glu	
	80		85		90	
AGA GAA	CCT ATC	CGT GAT	CTT TAT	GAT TAC	GGC TAT	398
Arg Glu	Pro Ile	Arg Asp	Leu Tyr	Asp Tyr	Gly Tyr	
	95		100		105	
GCT TGG	TGATCTTAAA	TGAGTCAAGA				424
Ala Trp						

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```

Met Lys Gly Phe Val Met Ser Gly Leu Arg Thr Phe Ser Cys Val Val
 1           5           10           15
Val Leu Cys Gly Ala Met Ala Asn Val Ala Ile Ala Ser Pro Lys Ile
          20           25           30
Glu Ala Arg Gly Glu Leu Gly Lys Phe Ile Gly Gly Gly Val Gly Gly
          35           40           45
Phe Val Gly Asp Lys Met Gly Gly Phe Val Gly Gly Ala Ile Gly Gly
          50           55           60
Tyr Ile Gly Ser Glu Ile Gly Asp Arg Val Glu Asp Tyr Ile Arg Gly
65           70           75           80
Val Asp Arg Glu Pro Gln Asn Lys Glu Pro Gln Ala Pro Arg Glu Pro
          85           90           95
Ile Arg Asp Leu Tyr Asp Tyr Gly Tyr Ser Phe Gly His Ala Trp
          100          105          110

```

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 132...569
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```

GATTTTAGTG ATGACGAGTT TCACCCGTTT GATCGTGGTG TTTTCTTTTT TAAGGACCGC      60
TTTGGGCACG CAACAAACCC CCCCCACTC AAATTTTAGT CTCGCTCTCT TTGATATTGA      120
CTTTTTTCAT C ATG GAA CCT AGC CTA AAA AAG GCC TAT GAT ACA GGG ATT      170
          Met Glu Pro Ser Leu Lys Lys Ala Tyr Asp Thr Gly Ile
              1           5           10

AAG CCT TAT ATG GAT AAA AAG ATT TCT TAC ACC GAA GCG TTT GAA AAA      218
Lys Pro Tyr Met Asp Lys Lys Ile Ser Tyr Thr Glu Ala Phe Glu Lys
          15           20           25

```

AGC GCT CTG CCC TTC AAG GAA TTC ATG CTT AAA AAC ACA CGA GAA AAG	266
Ser Ala Leu Pro Phe Lys Glu Phe Met Leu Lys Asn Thr Arg Glu Lys	
30 35 40 45	
GAT CTA GCC CTT TTT TTT AGG ATT AGA AAC CTC CCT AAC CCT AAA ACC	314
Asp Leu Ala Leu Phe Phe Arg Ile Arg Asn Leu Pro Asn Pro Lys Thr	
50 55 60	
CCT GAT GAG GTG AGT TTG AGC GTT TTG ATC CCG GCA TTT ATG ATA AGC	362
Pro Asp Glu Val Ser Leu Ser Val Leu Ile Pro Ala Phe Met Ile Ser	
65 70 75	
GAG TTG AAA ACA GCG TTT CAA ATC GGC TTT TTA CTC TAC TTG CCT TTT	410
Glu Leu Lys Thr Ala Phe Gln Ile Gly Phe Leu Leu Tyr Leu Pro Phe	
80 85 90	
TTG GTG ATT GAT ATG GTG ATC AGC TCT ATT TTA ATG GCG ATG GGC ATG	458
Leu Val Ile Asp Met Val Ile Ser Ser Ile Leu Met Ala Met Gly Met	
95 100 105	
ATG ATG CTC CCG CCT GTA ATG ATT TCT CTG CCT TTT AAA ATT TTA GTG	506
Met Met Leu Pro Pro Val Met Ile Ser Leu Pro Phe Lys Ile Leu Val	
110 115 120 125	
TTT ATT CTG GTA GAT GGG TTT AAT TTA TTG ACC GAA AAT TTA GTG GCG	554
Phe Ile Leu Val Asp Gly Phe Asn Leu Leu Thr Glu Asn Leu Val Ala	
130 135 140	
AGT TTT AAA ATG GTT TGATATTAAC AAGCATTCAA GCGATAAAAG CTTGAAGCTA G	610
Ser Phe Lys Met Val	
145	
TTTAAAACTC ATAATTCAAA	630

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met Glu Pro Ser Leu Lys Lys Ala Tyr Asp Thr Gly Ile Lys Pro Tyr	
1 5 10 15	
Met Asp Lys Lys Ile Ser Tyr Thr Glu Ala Phe Glu Lys Ser Ala Leu	
20 25 30	
Pro Phe Lys Glu Phe Met Leu Lys Asn Thr Arg Glu Lys Asp Leu Ala	
35 40 45	
Leu Phe Phe Arg Ile Arg Asn Leu Pro Asn Pro Lys Thr Pro Asp Glu	
50 55 60	
Val Ser Leu Ser Val Leu Ile Pro Ala Phe Met Ile Ser Glu Leu Lys	
65 70 75 80	
Thr Ala Phe Gln Ile Gly Phe Leu Leu Tyr Leu Pro Phe Leu Val Ile	
85 90 95	

Asp Met Val Ile Ser Ser Ile Leu Met Ala Met Gly Met Met Met Leu
100 105 110
Pro Pro Val Met Ile Ser Leu Pro Phe Lys Ile Leu Val Phe Ile Leu
115 120 125
Val Asp Gly Phe Asn Leu Leu Thr Glu Asn Leu Val Ala Ser Phe Lys
130 135 140
Met Val
145

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...2313
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

AAAAGGTGGT AA ATG AAA AGA ATT TTA GTC TCT TTG GCT GTT TTG AGT CAT	51
Met Lys Arg Ile Leu Val Ser Leu Ala Val Leu Ser His	
1 5 10	
AGC GCG CAT GCT GTC AAA ACT CAT AAT TTG GAA AGG GTG GAA GCT TCA	99
Ser Ala His Ala Val Lys Thr His Asn Leu Glu Arg Val Glu Ala Ser	
15 20 25	
GGG GTG GCT AAC GAT AAG GAA GCG CCT TTA AGC TGG AGG AGC AAG GAA	147
Gly Val Ala Asn Asp Lys Glu Ala Pro Leu Ser Trp Arg Ser Lys Glu	
30 35 40 45	
GTG AGA AAC TAT ATG GGA TCT CGC ACG GTG ATT TCT AAC AAG CAA CTC	195
Val Arg Asn Tyr Met Gly Ser Arg Thr Val Ile Ser Asn Lys Gln Leu	
50 55 60	
ACT AAA AGC GCC AAT CAG AGC ATT GAA GAA GCT TTG CAA AAT GTG CCA	243
Thr Lys Ser Ala Asn Gln Ser Ile Glu Glu Ala Leu Gln Asn Val Pro	
65 70 75	
GGC GTG CAT ATT AGA AAC GCT ACG GGT ATT GGA GCT GTG CCT AGC TTT	291
Gly Val His Ile Arg Asn Ala Thr Gly Ile Gly Ala Val Pro Ser Phe	
80 85 90	
TCT GTT AGG GGC TTT GGT GGG GGA AGT TCA GGG CAT TCC AAT ACG GCT	339
Ser Val Arg Gly Phe Gly Gly Gly Ser Ser Gly His Ser Asn Thr Ala	
95 100 105	
ATG GTT TTA GTC AAT GGG ATC CCT ATT TAT GTT GCG CCC TAT GTT GAT	387
Met Val Leu Val Asn Gly Ile Pro Ile Tyr Val Ala Pro Tyr Val Asp	
110 115 120 125	

350		355		360		365	
TTT GAT CAT TTA AGG CGT TAC ATA ATG AAC GCT TTT GAG CCT AAT TTG							1155
Phe Asp His Leu Arg Arg Tyr Ile Met Asn Ala Phe Glu Pro Asn Leu							
	370			375		380	
AAC TTA GTT GTC AAT ACC AAT AAA GTT AAG CAA ACT TTT AAT GTG GGC							1203
Asn Leu Val Val Asn Thr Asn Lys Val Lys Gln Thr Phe Asn Val Gly							
	385			390		395	
ATG CGT TTT ATG ACA ATG GAT ATG TAT TTC AGA TTG GAT CAA AGC ACA							1251
Met Arg Phe Met Thr Met Asp Met Tyr Phe Arg Leu Asp Gln Ser Thr							
	400			405		410	
TGC GAA AAA ACC GAT ATT TTT AAT GGG GTG TGC CGC ATG CCT CCT TTT							1299
Cys Glu Lys Thr Asp Ile Phe Asn Gly Val Cys Arg Met Pro Pro Phe							
	415			420		425	
GTT CTT TCT AAA AAA CCC AGC AAC AAT CAA AAC CTG TTT AAC AAC TAT							1347
Val Leu Ser Lys Lys Pro Ser Asn Asn Gln Asn Leu Phe Asn Asn Tyr							
	430			435		440	445
ACA GCG GTA TGG TTG AGC GAT AAA ATA GAG CTT TTT GAT TCT AAA TTG							1395
Thr Ala Val Trp Leu Ser Asp Lys Ile Glu Leu Phe Asp Ser Lys Leu							
	450			455		460	
GTG ATA ACT CCA GGG CTT AGA TAC ACT TTT TTG AAC TAT AAC AAC AAA							1443
Val Ile Thr Pro Gly Leu Arg Tyr Thr Phe Leu Asn Tyr Asn Asn Lys							
	465			470		475	
GAG CCA GAA AAG CAT GAT TTT TCT GTG TGG AAT ATT ACA AAA AAG CGT							1491
Glu Pro Glu Lys His Asp Phe Ser Val Trp Asn Ile Thr Lys Lys Arg							
	480			485		490	
CAA AAC GAA TGG AGT CCC GCC CTT AAC ATT GGC TAT AAA CCT ATG GAA							1539
Gln Asn Glu Trp Ser Pro Ala Leu Asn Ile Gly Tyr Lys Pro Met Glu							
	495			500		505	
AAT TGG ATA TGG TAT GCG AAC TAC CGC CGC AGT TTT ATC CCC CCA CAA							1587
Asn Trp Ile Trp Tyr Ala Asn Tyr Arg Arg Ser Phe Ile Pro Pro Gln							
	510			515		520	525
CAT ACA ATG CTA GGC ATT ACT AGG ACT AAT TAC AAC CAA ATT TTT AAT							1635
His Thr Met Leu Gly Ile Thr Arg Thr Asn Tyr Asn Gln Ile Phe Asn							
	530			535		540	
GAA ATT GAA GTG GGG CAA CGC TAT AGT TAT AAA AAT CTA TTG AGC TTT							1683
Glu Ile Glu Val Gly Gln Arg Tyr Ser Tyr Lys Asn Leu Leu Ser Phe							
	545			550		555	
AAC ACG AAT TAT TTT GTG ATT TTT GCC AAG CGT TAC TAT GCG GGA GGC							1731
Asn Thr Asn Tyr Phe Val Ile Phe Ala Lys Arg Tyr Tyr Ala Gly Gly							
	560			565		570	
TAT AGC CCA CAG CCT ATT AAC GCT AGG AGT CAA GGG GTA GAA TTG GAA							1779
Tyr Ser Pro Gln Pro Ile Asn Ala Arg Ser Gln Gly Val Glu Leu Glu							
	575			580		585	

TTG TAT TAC GCG CCG ATT AGG GGT TTG CAA TTC CAT GTG GCT TAC ACC	1827
Leu Tyr Tyr Ala Pro Ile Arg Gly Leu Gln Phe His Val Ala Tyr Thr	
590 595 600 605	
TAT ATT GAT GCA CGC ATC ACT TCT AAC GCT GAT GAT ATT GCT TAT TAT	1875
Tyr Ile Asp Ala Arg Ile Thr Ser Asn Ala Asp Asp Ile Ala Tyr Tyr	
610 615 620	
TTT ACA GGC ATT GTC AAT AAA CCC TTT GAC ATT AAA GGG AAG CGT TTG	1923
Phe Thr Gly Ile Val Asn Lys Pro Phe Asp Ile Lys Gly Lys Arg Leu	
625 630 635	
CCT TAT GTG AGT CCT AAC CAA TTC ATA TTT GAC ATG ATG TAT ACT TAC	1971
Pro Tyr Val Ser Pro Asn Gln Phe Ile Phe Asp Met Met Tyr Thr Tyr	
640 645 650	
AAG CAC ACG ACT TTT GGT ATT AGC AGC TAT TTT TAT AGC CGT GCT TAT	2019
Lys His Thr Thr Phe Gly Ile Ser Ser Tyr Phe Tyr Ser Arg Ala Tyr	
655 660 665	
AGT TCT ATG CTC AAT CAG GCC AAA AGC CAA ACC GTG TGC CTG CCC TTA	2067
Ser Ser Met Leu Asn Gln Ala Lys Ser Gln Thr Val Cys Leu Pro Leu	
670 675 680 685	
AAC CCA GAA TAC ACA GGG GGG CTA GAG TAT GGT TGT AAT TCA GTA GGG	2115
Asn Pro Glu Tyr Thr Gly Gly Leu Glu Tyr Gly Cys Asn Ser Val Gly	
690 695 700	
TTA TTG CCC TTG TAT TTT GTG TTG AAC GTT CAA GTA AGC TCG GTT TTA	2163
Leu Leu Pro Leu Tyr Phe Val Leu Asn Val Gln Val Ser Ser Val Leu	
705 710 715	
TGG CAA AGC GGT AGG CAT AAA ATC ACA GGG AGT TTG CAA ATC AAT AAT	2211
Trp Gln Ser Gly Arg His Lys Ile Thr Gly Ser Leu Gln Ile Asn Asn	
720 725 730	
CTT TTT AAC ATG AAG TAT TAT TTT AGG GGA ATT GGC ACA AGC CCT ACA	2259
Leu Phe Asn Met Lys Tyr Tyr Phe Arg Gly Ile Gly Thr Ser Pro Thr	
735 740 745	
GGA AGA GAG CCC GCA CCA GGG CGA TCC ATT ACA GCG TAT TTG AAT TAT	2307
Gly Arg Glu Pro Ala Pro Gly Arg Ser Ile Thr Ala Tyr Leu Asn Tyr	
750 755 760 765	
GAG TTT TAAACTAGCT TCAAGCTTTT ATCGCTTGAA TGCTTGTTA	2352
Glu Phe	

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 767 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met	Lys	Arg	Ile	Leu	Val	Ser	Leu	Ala	Val	Leu	Ser	His	Ser	Ala	His
1				5					10					15	
Ala	Val	Lys	Thr	His	Asn	Leu	Glu	Arg	Val	Glu	Ala	Ser	Gly	Val	Ala
			20					25					30		
Asn	Asp	Lys	Glu	Ala	Pro	Leu	Ser	Trp	Arg	Ser	Lys	Glu	Val	Arg	Asn
		35					40					45			
Tyr	Met	Gly	Ser	Arg	Thr	Val	Ile	Ser	Asn	Lys	Gln	Leu	Thr	Lys	Ser
	50					55					60				
Ala	Asn	Gln	Ser	Ile	Glu	Glu	Ala	Leu	Gln	Asn	Val	Pro	Gly	Val	His
65					70					75					80
Ile	Arg	Asn	Ala	Thr	Gly	Ile	Gly	Ala	Val	Pro	Ser	Phe	Ser	Val	Arg
				85					90					95	
Gly	Phe	Gly	Gly	Gly	Ser	Ser	Gly	His	Ser	Asn	Thr	Ala	Met	Val	Leu
			100					105					110		
Val	Asn	Gly	Ile	Pro	Ile	Tyr	Val	Ala	Pro	Tyr	Val	Asp	Ile	Ser	Ile
	115						120					125			
Pro	Ile	Phe	Pro	Val	Thr	Phe	Gln	Ser	Val	Asp	Arg	Ile	Ser	Val	Thr
	130					135					140				
Lys	Gly	Gly	Glu	Ser	Val	Arg	Tyr	Gly	Pro	Asn	Val	Phe	Gly	Gly	Val
145					150					155					160
Ile	Asn	Val	Ile	Thr	Lys	Gly	Ile	Pro	Thr	Lys	Trp	Glu	Ser	Gln	Val
				165					170					175	
Ser	Glu	Arg	Ala	Thr	Phe	Trp	Gly	Lys	Ser	Glu	Asn	Gly	Gly	Phe	Phe
			180					185					190		
Asn	Gln	Asn	Ser	Lys	Asn	Leu	Asp	Lys	Ser	Leu	Ala	Asn	Asn	Met	Leu
	195						200					205			
Phe	Asp	Thr	Tyr	Leu	Arg	Thr	Gly	Gly	Met	Met	Asn	Lys	His	Phe	Gly
	210					215					220				
Ile	Gln	Ala	Gln	Ala	Asn	Trp	Leu	Lys	Gly	Gln	Gly	Phe	Arg	Tyr	Asn
225					230					235					240
Ser	Pro	Thr	Asn	Ile	Gln	Asn	Tyr	Met	Leu	Asp	Ser	Leu	Tyr	Gln	Ile
			245						250					255	
Asn	Asp	Ser	Asn	Lys	Ile	Thr	Ala	Phe	Phe	Gln	Tyr	Tyr	Asn	Tyr	Phe
			260					265					270		
Met	Ala	Asp	Pro	Gly	Ser	Leu	Gly	Ile	Glu	Ala	Tyr	Asn	Gln	Asn	Arg
	275						280					285			
Phe	Gln	Asn	Asn	Arg	Pro	Asn	Asn	Asn	Lys	Ser	Gly	Arg	Ala	Lys	Xaa
	290					295					300				
Trp	Gly	Ala	Val	Tyr	Gln	Asn	Phe	Phe	Gly	Asp	Thr	Asp	Lys	Ile	Gly
305					310					315					320
Gly	Asp	Phe	Thr	Phe	Ser	Tyr	Tyr	Gly	His	Asp	Met	Ser	Arg	Asp	Phe
			325						330					335	
Gln	Phe	Asp	Ser	Asn	Phe	Leu	Asn	Val	Asn	Thr	Asn	Pro	Lys	Leu	Gly
			340					345					350		
Pro	Val	Tyr	Thr	Asp	Gln	Asn	Tyr	Pro	Gly	Phe	Phe	Ile	Phe	Asp	His
	355						360					365			
Leu	Arg	Arg	Tyr	Ile	Met	Asn	Ala	Phe	Glu	Pro	Asn	Leu	Asn	Leu	Val
	370					375					380				
Val	Asn	Thr	Asn	Lys	Val	Lys	Gln	Thr	Phe	Asn	Val	Gly	Met	Arg	Phe
385					390					395					400
Met	Thr	Met	Asp	Met	Tyr	Phe	Arg	Leu	Asp	Gln	Ser	Thr	Cys	Glu	Lys
			405						410					415	
Thr	Asp	Ile	Phe	Asn	Gly	Val	Cys	Arg	Met	Pro	Pro	Phe	Val	Leu	Ser
			420					425					430		
Lys	Lys	Pro	Ser	Asn	Asn	Gln	Asn	Leu	Phe	Asn	Asn	Tyr	Thr	Ala	Val

Trp	Leu	Ser	Asp	Lys	Ile	Glu	Leu	Phe	Asp	Ser	Lys	Leu	Val	Ile	Thr	
450						455					460					
Pro	Gly	Leu	Arg	Tyr	Thr	Phe	Leu	Asn	Tyr	Asn	Asn	Lys	Glu	Pro	Glu	
465					470					475					480	
Lys	His	Asp	Phe	Ser	Val	Trp	Asn	Ile	Thr	Lys	Lys	Arg	Gln	Asn	Glu	
				485					490					495		
Trp	Ser	Pro	Ala	Leu	Asn	Ile	Gly	Tyr	Lys	Pro	Met	Glu	Asn	Trp	Ile	
			500					505					510			
Trp	Tyr	Ala	Asn	Tyr	Arg	Arg	Ser	Phe	Ile	Pro	Pro	Gln	His	Thr	Met	
		515					520					525				
Leu	Gly	Ile	Thr	Arg	Thr	Asn	Tyr	Asn	Gln	Ile	Phe	Asn	Glu	Ile	Glu	
	530					535					540					
Val	Gly	Gln	Arg	Tyr	Ser	Tyr	Lys	Asn	Leu	Leu	Ser	Phe	Asn	Thr	Asn	
545					550					555					560	
Tyr	Phe	Val	Ile	Phe	Ala	Lys	Arg	Tyr	Tyr	Ala	Gly	Gly	Tyr	Ser	Pro	
				565					570					575		
Gln	Pro	Ile	Asn	Ala	Arg	Ser	Gln	Gly	Val	Glu	Leu	Glu	Leu	Tyr	Tyr	
			580					585					590			
Ala	Pro	Ile	Arg	Gly	Leu	Gln	Phe	His	Val	Ala	Tyr	Thr	Tyr	Ile	Asp	
		595					600					605				
Ala	Arg	Ile	Thr	Ser	Asn	Ala	Asp	Asp	Ile	Ala	Tyr	Tyr	Phe	Thr	Gly	
	610					615					620					
Ile	Val	Asn	Lys	Pro	Phe	Asp	Ile	Lys	Gly	Lys	Arg	Leu	Pro	Tyr	Val	
625					630					635					640	
Ser	Pro	Asn	Gln	Phe	Ile	Phe	Asp	Met	Met	Tyr	Thr	Tyr	Lys	His	Thr	
				645					650					655		
Thr	Phe	Gly	Ile	Ser	Ser	Tyr	Phe	Tyr	Ser	Arg	Ala	Tyr	Ser	Ser	Met	
			660					665					670			
Leu	Asn	Gln	Ala	Lys	Ser	Gln	Thr	Val	Cys	Leu	Pro	Leu	Asn	Pro	Glu	
		675					680					685				
Tyr	Thr	Gly	Gly	Leu	Glu	Tyr	Gly	Cys	Asn	Ser	Val	Gly	Leu	Leu	Pro	
	690					695					700					
Leu	Tyr	Phe	Val	Leu	Asn	Val	Gln	Val	Ser	Ser	Val	Leu	Trp	Gln	Ser	
705					710					715					720	
Gly	Arg	His	Lys	Ile	Thr	Gly	Ser	Leu	Gln	Ile	Asn	Asn	Leu	Phe	Asn	
				725						730				735		
Met	Lys	Tyr	Tyr	Phe	Arg	Gly	Ile	Gly	Thr	Ser	Pro	Thr	Gly	Arg	Glu	
			740					745					750			
Pro	Ala	Pro	Gly	Arg	Ser	Ile	Thr	Ala	Tyr	Leu	Asn	Tyr	Glu	Phe		
		755					760					765				

(i) SEQUENCE CHARACTERISTICS:

- ```
(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:
```

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

|                                                                 |                                             |    |
|-----------------------------------------------------------------|---------------------------------------------|----|
| AGATAGGAAT GTAAAGGA                                             | ATG GAA TTT ATG AAA AAG TTT GTA GCT TTA GGG | 51 |
|                                                                 | Met Glu Phe Met Lys Lys Phe Val Ala Leu Gly |    |
|                                                                 | 1 5 10                                      |    |
| CTT CTA TCC GCA GTT TTA AGC TCT TCG TTG TTA GCC GAA GGT GAT GGT | 99                                          |    |
| Leu Leu Ser Ala Val Leu Ser Ser Ser Leu Leu Ala Glu Gly Asp Gly |                                             |    |
|                                                                 | 15 20 25                                    |    |
| GTT TAT ATA GGG ACT AAT TAT CAG CTT GGA CAA GCC CGT TTG AAT AGT | 147                                         |    |
| Val Tyr Ile Gly Thr Asn Tyr Gln Leu Gly Gln Ala Arg Leu Asn Ser |                                             |    |
|                                                                 | 30 35 40                                    |    |
| AAT ATT TAT AAT ACA GGG GAT TGC ACA GGG AGT GTT GTA GGT TGC CCC | 195                                         |    |
| Asn Ile Tyr Asn Thr Gly Asp Cys Thr Gly Ser Val Val Gly Cys Pro |                                             |    |
|                                                                 | 45 50 55                                    |    |
| CCA GGT CTT ACC GCT AAT AAG CAT AAT CCA GGA GGC ACC AAT ATC AAT | 243                                         |    |
| Pro Gly Leu Thr Ala Asn Lys His Asn Pro Gly Gly Thr Asn Ile Asn |                                             |    |
|                                                                 | 60 65 70 75                                 |    |
| TGG CAT GCT AAA TAC GCT AAT GGG GCT TTG AAT GGT CTT GGG TTG AAT | 291                                         |    |
| Trp His Ala Lys Tyr Ala Asn Gly Ala Leu Asn Gly Leu Gly Leu Asn |                                             |    |
|                                                                 | 80 85 90                                    |    |
| GTG GGT TAT AAG AAG TTC TTC CAG TTC AAG TCT TTT GAT ATG ACA AGC | 339                                         |    |
| Val Gly Tyr Lys Lys Phe Phe Gln Phe Lys Ser Phe Asp Met Thr Ser |                                             |    |
|                                                                 | 95 100 105                                  |    |
| AAG TGG TTT GGT TTT AGA GTG TAT GGG CTT TTT GAT TAT GGG CAT GCC | 387                                         |    |
| Lys Trp Phe Gly Phe Arg Val Tyr Gly Leu Phe Asp Tyr Gly His Ala |                                             |    |
|                                                                 | 110 115 120                                 |    |
| ACT TTA GGC AAG CAA GTT TAT GCA CCT AAT AAA ATC CAG TTG GAT ATG | 435                                         |    |
| Thr Leu Gly Lys Gln Val Tyr Ala Pro Asn Lys Ile Gln Leu Asp Met |                                             |    |
|                                                                 | 125 130 135                                 |    |
| GTC TCT TGG GGT GTG GGG AGC GAT TTG TTA GCT GAT ATT ATT GAT AAC | 483                                         |    |
| Val Ser Trp Gly Val Gly Ser Asp Leu Leu Ala Asp Ile Ile Asp Asn |                                             |    |
|                                                                 | 140 145 150 155                             |    |
| GAT AAC GCT TCT TTT GGT ATT TTT GGT GGG GTC GCT ATC GGC GGT AAC | 531                                         |    |
| Asp Asn Ala Ser Phe Gly Ile Phe Gly Gly Val Ala Ile Gly Gly Asn |                                             |    |
|                                                                 | 160 165 170                                 |    |
| ACT TGG AAA AGC TCA GCG GCA AAC TAT TGG AAA GAG CAA ATC ATT GAA | 579                                         |    |
| Thr Trp Lys Ser Ser Ala Ala Asn Tyr Trp Lys Glu Gln Ile Ile Glu |                                             |    |
|                                                                 | 175 180 185                                 |    |
| GCT AAG GGT CCT GAT GTT TGT ACC CCT ACT TAT TGT AAC CCT AAC GCT | 627                                         |    |
| Ala Lys Gly Pro Asp Val Cys Thr Pro Thr Tyr Cys Asn Pro Asn Ala |                                             |    |
|                                                                 | 190 195 200                                 |    |
| CCT TAT AGC ACC AAA ACT TCA ACC GTC GCT TTT CAG GTA TGG TTG AAT | 675                                         |    |
| Pro Tyr Ser Thr Lys Thr Ser Thr Val Ala Phe Gln Val Trp Leu Asn |                                             |    |
|                                                                 | 205 210 215                                 |    |

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TTT GGG GTG AGA GCC AAT ATT TAC AAG CAT AAT GGC GTA GAG TTT GGC    | 723 |
| Phe Gly Val Arg Ala Asn Ile Tyr Lys His Asn Gly Val Glu Phe Gly    |     |
| 220 225 230 235                                                    |     |
|                                                                    |     |
| GTG AGA GTG CCG CTA CTC ATC AAC AAG TTT TTG AGT GCG GGT CCT AAC    | 771 |
| Val Arg Val Pro Leu Leu Ile Asn Lys Phe Leu Ser Ala Gly Pro Asn    |     |
| 240 245 250                                                        |     |
|                                                                    |     |
| GCT ACT AAT CTT TAT TAC CAT TTG AAA CGG GAT TAT TCG CTT TAT TTA    | 819 |
| Ala Thr Asn Leu Tyr Tyr His Leu Lys Arg Asp Tyr Ser Leu Tyr Leu    |     |
| 255 260 265                                                        |     |
|                                                                    |     |
| GGG TAT AAC TAC ACT TTT TAAACCCTTT AAAAGGGTGT CTTTAAGCCC TTTTGTAGT | 875 |
| Gly Tyr Asn Tyr Thr Phe                                            |     |
| 270                                                                |     |
|                                                                    |     |
| CCTTATAAAA AGG                                                     | 888 |

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Phe | Met | Lys | Lys | Phe | Val | Ala | Leu | Gly | Leu | Leu | Ser | Ala | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ser | Ser | Ser | Leu | Leu | Ala | Glu | Gly | Asp | Gly | Val | Tyr | Ile | Gly | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Tyr | Gln | Leu | Gly | Gln | Ala | Arg | Leu | Asn | Ser | Asn | Ile | Tyr | Asn | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Asp | Cys | Thr | Gly | Ser | Val | Val | Gly | Cys | Pro | Pro | Gly | Leu | Thr | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Asn | Lys | His | Asn | Pro | Gly | Gly | Thr | Asn | Ile | Asn | Trp | His | Ala | Lys | Tyr |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Asn | Gly | Ala | Leu | Asn | Gly | Leu | Gly | Leu | Asn | Val | Gly | Tyr | Lys | Lys |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Phe | Phe | Gln | Phe | Lys | Ser | Phe | Asp | Met | Thr | Ser | Lys | Trp | Phe | Gly | Phe |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Arg | Val | Tyr | Gly | Leu | Phe | Asp | Tyr | Gly | His | Ala | Thr | Leu | Gly | Lys | Gln |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Val | Tyr | Ala | Pro | Asn | Lys | Ile | Gln | Leu | Asp | Met | Val | Ser | Trp | Gly | Val |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Gly | Ser | Asp | Leu | Leu | Ala | Asp | Ile | Ile | Asp | Asn | Asp | Asn | Ala | Ser | Phe |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Gly | Ile | Phe | Gly | Gly | Val | Ala | Ile | Gly | Gly | Asn | Thr | Trp | Lys | Ser | Ser |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ala | Ala | Asn | Tyr | Trp | Lys | Glu | Gln | Ile | Ile | Glu | Ala | Lys | Gly | Pro | Asp |
|     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |     |
| Val | Cys | Thr | Pro | Thr | Tyr | Cys | Asn | Pro | Asn | Ala | Pro | Tyr | Ser | Thr | Lys |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Thr | Ser | Thr | Val | Ala | Phe | Gln | Val | Trp | Leu | Asn | Phe | Gly | Val | Arg | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ile | Tyr | Lys | His | Asn | Gly | Val | Glu | Phe | Gly | Val | Arg | Val | Pro | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Leu | Ile | Asn | Lys | Phe | Leu | Ser | Ala | Gly | Pro | Asn | Ala | Thr | Asn | Leu | Tyr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Tyr | His | Leu | Lys | Arg | Asp | Tyr | Ser | Leu | Tyr | Leu | Gly | Tyr | Asn | Tyr | Thr |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Phe |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 37...522
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CACGGTCATT TTGCTGTGT TTTTAGTCGC GTATTC ATG CAA CTG CTT ATG GAA  | 54  |
| Met Gln Leu Leu Met Glu                                         |     |
| 1 5                                                             |     |
| CGC CTT TCT CTT GTC TTC AGG CAT CTT TTC CAT GCG CTT TTT CAA CTC | 102 |
| Arg Leu Ser Leu Val Phe Arg His Leu Phe His Ala Leu Phe Gln Leu |     |
| 10 15 20                                                        |     |
| TTT TGT GTA ATC CAC AAT ATC CTG CGG AGK ACA ACG CCA GCC ATT TTA | 150 |
| Phe Cys Val Ile His Asn Ile Leu Arg Xaa Thr Thr Pro Ala Ile Leu |     |
| 25 30 35                                                        |     |
| GCC AAA TCT TCA TCG CTT GTT TTG CTG AAA TCT TTG GCG TTC AAA GCC | 198 |
| Ala Lys Ser Ser Ser Leu Val Leu Leu Lys Ser Leu Ala Phe Lys Ala |     |
| 40 45 50                                                        |     |
| ACA AAT AGC AAC GCG CTA ACA GAA AGT ATT TTC AAC GCT TTT TTC ATT | 246 |
| Thr Asn Ser Asn Ala Leu Thr Glu Ser Ile Phe Asn Ala Phe Phe Ile |     |
| 55 60 65 70                                                     |     |
| TTT TAT CCT TTT AAA TTA AAT TTA TCT CAC TTA GGA GAG CAA TGC TCG | 294 |
| Phe Tyr Pro Phe Lys Leu Asn Leu Ser His Leu Gly Glu Gln Cys Ser |     |
| 75 80 85                                                        |     |
| TCT TTT TTC TTA ACA GCC CTA CAC CAA ACT TTT CTC GTA TCG CCG CTG | 342 |
| Ser Phe Phe Leu Thr Ala Leu His Gln Thr Phe Leu Val Ser Pro Leu |     |
| 90 95 100                                                       |     |
| CAA ACG CTC ACA TTA AGT CCT TTT GCC TTG ATT TCT TCA TCG CTC AAA | 390 |
| Gln Thr Leu Thr Leu Ser Pro Phe Ala Leu Ile Ser Ser Ser Leu Lys |     |
| 105 110 115                                                     |     |

CCT TTG GTT TTT TCT TCT AAT TCT TTA CGC ACT TCT TCA CGC ATT TTT 438  
 Pro Leu Val Phe Ser Ser Asn Ser Leu Arg Thr Ser Ser Arg Ile Phe  
 120 125 130  
  
 TTG AAA TCC TTC GCT CAT TTT GGA AAG ATT CTT CCT AGC GAT CCG GCT 486  
 Leu Lys Ser Phe Ala His Phe Gly Lys Ile Leu Pro Ser Asp Pro Ala  
 135 140 145 150  
  
 GAA ATT CGC GCG GAA TTT CTT AGC GTC CTC AGC GTT TAAAGTTTTA AGGCGT 538  
 Glu Ile Arg Ala Glu Phe Leu Ser Val Leu Ser Val  
 155 160  
  
 TTAGACACTT CCATGCGATA AT 560

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met Gln Leu Leu Met Glu Arg Leu Ser Leu Val Phe Arg His Leu Phe  
 1 5 10 15  
 His Ala Leu Phe Gln Leu Phe Cys Val Ile His Asn Ile Leu Arg Xaa  
 20 25 30  
 Thr Thr Pro Ala Ile Leu Ala Lys Ser Ser Ser Leu Val Leu Leu Lys  
 35 40 45  
 Ser Leu Ala Phe Lys Ala Thr Asn Ser Asn Ala Leu Thr Glu Ser Ile  
 50 55 60  
 Phe Asn Ala Phe Phe Ile Phe Tyr Pro Phe Lys Leu Asn Leu Ser His  
 65 70 75 80  
 Leu Gly Glu Gln Cys Ser Ser Phe Phe Leu Thr Ala Leu His Gln Thr  
 85 90 95  
 Phe Leu Val Ser Pro Leu Gln Thr Leu Thr Leu Ser Pro Phe Ala Leu  
 100 105 110  
 Ile Ser Ser Ser Leu Lys Pro Leu Val Phe Ser Ser Asn Ser Leu Arg  
 115 120 125  
 Thr Ser Ser Arg Ile Phe Leu Lys Ser Phe Ala His Phe Gly Lys Ile  
 130 135 140  
 Leu Pro Ser Asp Pro Ala Glu Ile Arg Ala Glu Phe Leu Ser Val Leu  
 145 150 155 160  
 Ser Val

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 41...1132
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

|                                                                 |                     |     |
|-----------------------------------------------------------------|---------------------|-----|
| AAGGCATCCA CCATTAAACCC TTTTAAATT TATTTTAACG                     | ATG TTT TAC TAT ACT | 55  |
|                                                                 | Met Phe Tyr Tyr Thr |     |
|                                                                 | 1 5                 |     |
| ATA AAA TCT TTT AAT TTC AAA AGG TGG TCC ATA ATG AGA ATA TTT TTG |                     | 103 |
| Ile Lys Ser Phe Asn Phe Lys Arg Trp Ser Ile Met Arg Ile Phe Leu |                     |     |
|                                                                 | 10 15 20            |     |
| AAA TTG TTG ATT CTT TTA TTT TGT TTG AAG GGG CAG GTT ATG GCT CAA |                     | 151 |
| Lys Leu Leu Ile Leu Leu Phe Cys Leu Lys Gly Gln Val Met Ala Gln |                     |     |
|                                                                 | 25 30 35            |     |
| AAT TTA CCC ACC ATT GCT TTA CTG GCG ACA GGG GGG ACG ATT GCA GGG |                     | 199 |
| Asn Leu Pro Thr Ile Ala Leu Ala Thr Gly Gly Thr Ile Ala Gly     |                     |     |
|                                                                 | 40 45 50            |     |
| AGT GGT GCG AGC GCG AGT TTG GGT AGT TAT AAG AGT GGT GAG TTG GGC |                     | 247 |
| Ser Gly Ala Ser Ala Ser Leu Gly Ser Tyr Lys Ser Gly Glu Leu Gly |                     |     |
|                                                                 | 55 60 65            |     |
| ATC AAA GAG CTT TTG AAG GCT ATC CCT AGT CTT AAC AGA CTC GCT CGC |                     | 295 |
| Ile Lys Glu Leu Leu Lys Ala Ile Pro Ser Leu Asn Arg Leu Ala Arg |                     |     |
|                                                                 | 70 75 80 85         |     |
| ATT CAA GGG GAG CAG ATT TCT AAC ATC GGC TCA CAA GAC ATG AAT GAA |                     | 343 |
| Ile Gln Gly Glu Gln Ile Ser Asn Ile Gly Ser Gln Asp Met Asn Glu |                     |     |
|                                                                 | 90 95 100           |     |
| GAG GTA TGG TTC AAG CTC GCC AAA CGT GCC CAA GAA TTG CTA GAT GAT |                     | 391 |
| Glu Val Trp Phe Lys Leu Ala Lys Arg Ala Gln Glu Leu Leu Asp Asp |                     |     |
|                                                                 | 105 110 115         |     |
| AGC CGT ATT CAA GGC GTG GTC ATC ACG CAT GGC ACG GAC ACT TTA GAA |                     | 439 |
| Ser Arg Ile Gln Gly Val Val Ile Thr His Gly Thr Asp Thr Leu Glu |                     |     |
|                                                                 | 120 125 130         |     |
| GAG AGC GCG TAT TTT TTA AAC TTA GTT TTA CGC TCC ACA AAA CCG GTC |                     | 487 |
| Glu Ser Ala Tyr Phe Leu Asn Leu Val Leu Arg Ser Thr Lys Pro Val |                     |     |
|                                                                 | 135 140 145         |     |
| GTG CTG GTG GGA GCG ATG CGT AAT GCT GCT TCT TTG AGC GCG GAT GGG |                     | 535 |
| Val Leu Val Gly Ala Met Arg Asn Ala Ala Ser Leu Ser Ala Asp Gly |                     |     |
|                                                                 | 150 155 160 165     |     |
| GCT TTG AAT TTA TAT AAT GCT GTG AGC GTA GCG CTC AAT GAA AAA AGT |                     | 583 |
| Ala Leu Asn Leu Tyr Asn Ala Val Ser Val Ala Leu Asn Glu Lys Ser |                     |     |
|                                                                 | 170 175 180         |     |
| GCG AAT AAA GGC GTG TTA GTG GTG ATG GAC GAT AAT ATT TTT AGC GCT |                     | 631 |





(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Tyr | Tyr | Thr | Ile | Lys | Ser | Phe | Asn | Phe | Lys | Arg | Trp | Ser | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Arg | Ile | Phe | Leu | Lys | Leu | Leu | Ile | Leu | Leu | Phe | Cys | Leu | Lys | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Gln | Val | Met | Ala | Gln | Asn | Leu | Pro | Thr | Ile | Ala | Leu | Leu | Ala | Thr | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Thr | Ile | Ala | Gly | Ser | Gly | Ala | Ser | Ala | Ser | Leu | Gly | Ser | Tyr | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Gly | Glu | Leu | Gly | Ile | Lys | Glu | Leu | Leu | Lys | Ala | Ile | Pro | Ser | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asn | Arg | Leu | Ala | Arg | Ile | Gln | Gly | Glu | Gln | Ile | Ser | Asn | Ile | Gly | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Asp | Met | Asn | Glu | Glu | Val | Trp | Phe | Lys | Leu | Ala | Lys | Arg | Ala | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Leu | Leu | Asp | Asp | Ser | Arg | Ile | Gln | Gly | Val | Val | Ile | Thr | His | Gly |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Asp | Thr | Leu | Glu | Glu | Ser | Ala | Tyr | Phe | Leu | Asn | Leu | Val | Leu | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Thr | Lys | Pro | Val | Val | Leu | Val | Gly | Ala | Met | Arg | Asn | Ala | Ala | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Ser | Ala | Asp | Gly | Ala | Leu | Asn | Leu | Tyr | Asn | Ala | Val | Ser | Val | Ala |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Asn | Glu | Lys | Ser | Ala | Asn | Lys | Gly | Val | Leu | Val | Val | Met | Asp | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asn | Ile | Phe | Ser | Ala | Arg | Glu | Val | Ile | Lys | Thr | His | Thr | Thr | His | Thr |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Ser | Thr | Phe | Lys | Ala | Leu | Asn | Ser | Gly | Ala | Ile | Gly | Ser | Val | Tyr | Tyr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Lys | Thr | Arg | Tyr | Tyr | Met | Gln | Pro | Leu | Arg | Lys | His | Thr | Thr | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ser | Glu | Phe | Ser | Leu | Ser | Gln | Leu | Lys | Thr | Pro | Leu | Pro | Lys | Val | Asp |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ile | Ile | Tyr | Thr | His | Ala | Gly | Met | Thr | Pro | Asp | Leu | Phe | Gln | Ala | Ser |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Leu | Asn | Ser | His | Ala | Lys | Gly | Val | Val | Ile | Ala | Gly | Val | Gly | Asn | Gly |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asn | Val | Ser | Ala | Gly | Phe | Leu | Lys | Ala | Met | Gln | Glu | Ala | Ser | Gln | Met |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gly | Val | Val | Ile | Val | Arg | Ser | Ser | Arg | Val | Asn | Ser | Gly | Glu | Ile | Thr |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ser | Gly | Glu | Ile | Asp | Asp | Lys | Ala | Phe | Ile | Thr | Ser | Asp | Asn | Leu | Asn |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Pro | Gln | Lys | Ala | Arg | Val | Leu | Leu | Gln | Leu | Ala | Leu | Thr | Lys | Thr | Asn |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Asn | Lys | Glu | Lys | Ile | Gln | Glu | Met | Phe | Glu | Glu | Tyr |     |     |     |     |
|     | 355 |     |     |     |     | 360 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 37...612  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

|                                                                 |                         |     |
|-----------------------------------------------------------------|-------------------------|-----|
| AGTAAACAT CGTTAAATA AATTTAAAA GGGTTA                            | ATG GTG GAT GCC TTT TTC | 54  |
|                                                                 | Met Val Asp Ala Phe Phe |     |
|                                                                 | 1 5                     |     |
| CAA ATT GCA GTG TTA CTT TTT TCG CTT TTT TTA GGG GCA AGG CTA GGG |                         | 102 |
| Gln Ile Ala Val Leu Leu Phe Ser Leu Phe Leu Gly Ala Arg Leu Gly |                         |     |
|                                                                 | 10 15 20                |     |
| GGC TTG GGA GTG GGC TAT GCG GGG GGC TTG GGC GTG CTT ATT TTA TGC |                         | 150 |
| Gly Leu Gly Val Gly Tyr Ala Gly Gly Leu Gly Val Leu Ile Leu Cys |                         |     |
|                                                                 | 25 30 35                |     |
| TTA TTT TTG GGG CTA AAT CCG GGC AAA ATC CCT TTT GAT GTG ATT TTA |                         | 198 |
| Leu Phe Leu Gly Leu Asn Pro Gly Lys Ile Pro Phe Asp Val Ile Leu |                         |     |
|                                                                 | 40 45 50                |     |
| ATC ATC ATG GCA GTC ATT AGC GCT ATT AGC GCG ATG CAA AAA GCG GGG |                         | 246 |
| Ile Ile Met Ala Val Ile Ser Ala Ile Ser Ala Met Gln Lys Ala Gly |                         |     |
|                                                                 | 55 60 65 70             |     |
| GGC TTG GAT TAC TTA GTC AAA ATC GCT GAA AAA ATT TTA AGG AAA CAC |                         | 294 |
| Gly Leu Asp Tyr Leu Val Lys Ile Ala Glu Lys Ile Leu Arg Lys His |                         |     |
|                                                                 | 75 80 85                |     |
| CCC AAG CAA ATC AAT TAC CTT GCG CCA AGC GTG GCG TAT TGT TTA ACG |                         | 342 |
| Pro Lys Gln Ile Asn Tyr Leu Ala Pro Ser Val Ala Tyr Cys Leu Thr |                         |     |
|                                                                 | 90 95 100               |     |
| ATA CTA GCC GGC ACC GGG CAT ACG GTT TTT TCC TTG ATC CCG GTG ATT |                         | 390 |
| Ile Leu Ala Gly Thr Gly His Thr Val Phe Ser Leu Ile Pro Val Ile |                         |     |
|                                                                 | 105 110 115             |     |
| GTG GAA GTG AGC CAG AGC CAA AAC ATC AAG CCT AAA GCG CCT TTA AGC |                         | 438 |
| Val Glu Val Ser Gln Ser Gln Asn Ile Lys Pro Lys Ala Pro Leu Ser |                         |     |
|                                                                 | 120 125 130             |     |
| TTA GCG GTA GTC TCT AGT CAA GTC GCT ATT ACT GCA AGC CCG GTG AGC |                         | 486 |
| Leu Ala Val Val Ser Ser Gln Val Ala Ile Thr Ala Ser Pro Val Ser |                         |     |
|                                                                 | 135 140 145 150         |     |
| GCA GCG GTN GGT GTT TAT GAG CGG CAT TTT AGA GCC TTT AGG AGC AAA |                         | 534 |
| Ala Ala Xaa Gly Val Tyr Glu Arg His Phe Arg Ala Phe Arg Ser Lys |                         |     |
|                                                                 | 155 160 165             |     |
| TTA CTT GAC CCT TTT AAT GGT TTG GAT CCC TAC GAC TTT TTT AGC ATG |                         | 582 |
| Leu Leu Asp Pro Phe Asn Gly Leu Asp Pro Tyr Asp Phe Phe Ser Met |                         |     |
|                                                                 | 170 175 180             |     |



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

|     |     |     |     |     |      |      |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AAA | ACT | TTT | GTA | TAT | GAGA | AATA | A   | ATG | GAC | TTT | AAA | AAT | AAA | AAA | TGG | CTT | TTT | 51  |
|     |     |     |     |     |      |      |     | Met | Asp | Phe | Lys | Asn | Lys | Lys | Trp | Leu | Phe |     |
|     |     |     |     |     |      |      |     | 1   |     |     |     | 5   |     |     |     |     | 10  |     |
| CTA | GCC | CCT | TTA | GCA | GGC  | TAT  | ACG | GAT | TTG | CCT | TTC | AGG | AGC | GTG | GTG |     |     | 99  |
| Leu | Ala | Pro | Leu | Ala | Gly  | Tyr  | Thr | Asp | Leu | Pro | Phe | Arg | Ser | Val | Val |     |     |     |
|     |     |     |     |     | 15   |      |     |     | 20  |     |     |     |     | 25  |     |     |     |     |
| AAA | AAA | TTT | GGC | GTG | GAT  | GTT  | ACC | ACG | AGC | GAA | ATG | GTG | AGC | TCG | CAT |     |     | 147 |
| Lys | Lys | Phe | Gly | Val | Asp  | Val  | Thr | Thr | Ser | Glu | Met | Val | Ser | Ser | His |     |     |     |
|     |     |     | 30  |     |      |      |     | 35  |     |     |     |     | 40  |     |     |     |     |     |
| TCG | TTG | GTG | TAT | GCG | TTT  | GAT  | AAA | ACT | TCT | AAA | ATG | TTG | GAA | AAA | TCC |     |     | 195 |
| Ser | Leu | Val | Tyr | Ala | Phe  | Asp  | Lys | Thr | Ser | Lys | Met | Leu | Glu | Lys | Ser |     |     |     |
|     |     |     | 45  |     |      |      | 50  |     |     |     |     | 55  |     |     |     |     |     |     |
| CCT | TTA | GAA | GAT | CAT | TTC  | ATG  | GCG | CAA | ATT | TCA | GGC | TCT | AAA | GAA | AGC |     |     | 243 |
| Pro | Leu | Glu | Asp | His | Phe  | Met  | Ala | Gln | Ile | Ser | Gly | Ser | Lys | Glu | Ser |     |     |     |
|     |     |     | 60  |     |      |      | 65  |     |     |     | 70  |     |     |     |     |     |     |     |
| GTA | GTC | AAA | GAA | GCG | GTG  | GAG  | AAA | ATC | AAC | GCT | TTA | GAG | CAT | GTG | AAT |     |     | 291 |
| Val | Val | Lys | Glu | Ala | Val  | Glu  | Lys | Ile | Asn | Ala | Leu | Glu | His | Val | Asn |     |     |     |
|     |     |     | 75  |     |      | 80   |     |     |     | 85  |     |     |     |     | 90  |     |     |     |
| GGG | ATT | GAT | TTT | AAT | TGC  | GGT  | TGT | CCC | GCT | CCT | AAA | GTG | GCT | AAT | CAT |     |     | 339 |
| Gly | Ile | Asp | Phe | Asn | Cys  | Gly  | Cys | Pro | Ala | Pro | Lys | Val | Ala | Asn | His |     |     |     |
|     |     |     |     | 95  |      |      |     | 100 |     |     |     |     |     | 105 |     |     |     |     |
| GGT | AAT | GGT | AGT | GGG | TTA  | TTG  | AAG | GAT | TTA | AAC | CAC | TTA | GTG | AAG | CTT |     |     | 387 |
| Gly | Asn | Gly | Ser | Gly | Leu  | Leu  | Lys | Asp | Leu | Asn | His | Leu | Val | Lys | Leu |     |     |     |
|     |     |     | 110 |     |      |      |     | 115 |     |     |     |     | 120 |     |     |     |     |     |
| TTA | AAA | ACC | ATC | AGA | GAA  | AAC  | ACT | AGT | AAA | AAA | ATC | ACA | AGC | GTG | AAA |     |     | 435 |
| Leu | Lys | Thr | Ile | Arg | Glu  | Asn  | Thr | Ser | Lys | Lys | Ile | Thr | Ser | Val | Lys |     |     |     |
|     |     |     | 125 |     |      |      | 130 |     |     |     |     | 135 |     |     |     |     |     |     |
| GTG | CGT | TTA | GGC | TTT | GAA  | AAG  | AAA | ATC | CCT | AAA | GAA | ATC | GCT | CAT | GCC |     |     | 483 |
| Val | Arg | Leu | Gly | Phe | Glu  | Lys  | Lys | Ile | Pro | Lys | Glu | Ile | Ala | His | Ala |     |     |     |
|     |     |     | 140 |     |      | 145  |     |     |     | 150 |     |     |     |     |     |     |     |     |
| CTA | AAT | GAC | GCA | CCG | GTG  | GAT  | TAT | GTG | GTG | GTG | CAT | GGG | AGG | ACA | CGA |     |     | 531 |
| Leu | Asn | Asp | Ala | Pro | Val  | Asp  | Tyr | Val | Val | Val | His | Gly | Arg | Thr | Arg |     |     |     |
|     |     |     |     |     | 160  |      |     |     |     | 165 |     |     |     |     | 170 |     |     |     |
| AGC | GAT | AAA | TAC | CAA | AAA  | GAC  | AAA | ATA | GAT | TAC | GAA | AGC | ATC | GCT | TTA |     |     | 579 |
| Ser | Asp | Lys | Tyr | Gln | Lys  | Asp  | Lys | Ile | Asp | Tyr | Glu | Ser | Ile | Ala | Leu |     |     |     |
|     |     |     |     | 175 |      |      |     | 180 |     |     |     |     |     | 185 |     |     |     |     |
| ATG | AAA | AAG | ATT | TTA | AAA  | AAG  | CCG | GTG | ATA | GCC | AAT | GGC | GAA | ATT | GAC |     |     | 627 |
| Met | Lys | Lys | Ile | Leu | Lys  | Lys  | Pro | Val | Ile | Ala | Asn | Gly | Glu | Ile | Asp |     |     |     |
|     |     |     |     | 190 |      |      |     | 195 |     |     |     |     | 200 |     |     |     |     |     |
| AGC | GTG | AAA | AAG | GCT | TTT  | GAA  | GTT | TTA | CAA | ATC | ACT | CAA | GCG | GAT | GGG |     |     | 675 |
| Ser | Val | Lys | Lys | Ala | Phe  | Glu  | Val | Leu | Gln | Ile | Thr | Gln | Ala | Asp | Gly |     |     |     |
|     |     |     |     | 205 |      |      |     | 210 |     |     |     | 215 |     |     |     |     |     |     |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| CTA ATG ATA GGG CGA GCG GCC TTA AGA GCC CCA TGG ATA TTT TGG CAA   | 723  |
| Leu Met Ile Gly Arg Ala Ala Leu Arg Ala Pro Trp Ile Phe Trp Gln   |      |
| 220 225 230                                                       |      |
| ATC AGA AAC AAC ACC ACA AAA TTA CCC GCA GTC GTG AAA AAA GAC CTG   | 771  |
| Ile Arg Asn Asn Thr Thr Lys Leu Pro Ala Val Val Lys Lys Asp Leu   |      |
| 235 240 245 250                                                   |      |
| GTT TTA GAA CAT TTT GAT AAA ATG GTG GAG TTT TAT GGG GAT ATG GGG   | 819  |
| Val Leu Glu His Phe Asp Lys Met Val Glu Phe Tyr Gly Asp Met Gly   |      |
| 255 260 265                                                       |      |
| GTA ATC ATG TTT AGG AAA AAT TTG CAT GCT TAC GCT AAG GGC GAA ATG   | 867  |
| Val Ile Met Phe Arg Lys Asn Leu His Ala Tyr Ala Lys Gly Glu Met   |      |
| 270 275 280                                                       |      |
| CAA GCG AGC GCG TTT CGT AAC TGC GTC AAT ACC CTT ACA GAA ATA AAG   | 915  |
| Gln Ala Ser Ala Phe Arg Asn Cys Val Asn Thr Leu Thr Glu Ile Lys   |      |
| 285 290 295                                                       |      |
| AGC ATG CGA GAG AGC ATA GAG GAA TTT TTT AAT CAA GAA ATG TTG CAA   | 963  |
| Ser Met Arg Glu Ser Ile Glu Glu Phe Phe Asn Gln Glu Met Leu Gln   |      |
| 300 305 310                                                       |      |
| AGT GAA GTG CCG TTA TGG GTA GAA TTG AAT CAA AAA AGC GTT TGAAAGCGC | 1014 |
| Ser Glu Val Pro Leu Trp Val Glu Leu Asn Gln Lys Ser Val           |      |
| 315 320 325                                                       |      |
| TTGTTTTTTTT AGCCAGCTTG GGGG                                       | 1038 |

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 328 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Asp Phe Lys Asn Lys Lys Trp Leu Phe Leu Ala Pro Leu Ala Gly |  |
| 1 5 10 15                                                       |  |
| Tyr Thr Asp Leu Pro Phe Arg Ser Val Val Lys Lys Phe Gly Val Asp |  |
| 20 25 30                                                        |  |
| Val Thr Thr Ser Glu Met Val Ser Ser His Ser Leu Val Tyr Ala Phe |  |
| 35 40 45                                                        |  |
| Asp Lys Thr Ser Lys Met Leu Glu Lys Ser Pro Leu Glu Asp His Phe |  |
| 50 55 60                                                        |  |
| Met Ala Gln Ile Ser Gly Ser Lys Glu Ser Val Val Lys Glu Ala Val |  |
| 65 70 75 80                                                     |  |
| Glu Lys Ile Asn Ala Leu Glu His Val Asn Gly Ile Asp Phe Asn Cys |  |
| 85 90 95                                                        |  |
| Gly Cys Pro Ala Pro Lys Val Ala Asn His Gly Asn Gly Ser Gly Leu |  |
| 100 105 110                                                     |  |
| Leu Lys Asp Leu Asn His Leu Val Lys Leu Leu Lys Thr Ile Arg Glu |  |
| 115 120 125                                                     |  |







|                                                                   |      |
|-------------------------------------------------------------------|------|
| CCA AGC TTG AGC ATG ACA ACG ATT GTT AAT GAG CAT GCC AAA GAA TTG   | 917  |
| Pro Ser Leu Ser Met Thr Thr Ile Val Asn Glu His Ala Lys Glu Leu   |      |
| 285 290 295                                                       |      |
| AGA AAC CTT TTA AAA GAA AAA TAC CAG GTG CAA TTT GCG GGC GGT CAA   | 965  |
| Arg Asn Leu Leu Lys Glu Lys Tyr Gln Val Gln Phe Ala Gly Gly Gln   |      |
| 300 305 310                                                       |      |
| GAG CCT TAT AAA GAT GCG CTC ATT CGT ATC AAC CAC ATG GGG ATC ATT   | 1013 |
| Glu Pro Tyr Lys Asp Ala Leu Ile Arg Ile Asn His Met Gly Ile Ile   |      |
| 315 320 325 330                                                   |      |
| CCT GTT TAT AAA AGC GCT TAC GCT TTA AAC GCC CTA GAG TTA GCC CTA   | 1061 |
| Pro Val Tyr Lys Ser Ala Tyr Ala Leu Asn Ala Leu Glu Leu Ala Leu   |      |
| 335 340 345                                                       |      |
| AAC GAC TTG GAT TTA AGG GAA TTT GAT GGC GTG GCG AAC GCA ACT TTT   | 1109 |
| Asn Asp Leu Asp Leu Arg Glu Phe Asp Gly Val Ala Asn Ala Thr Phe   |      |
| 350 355 360                                                       |      |
| TTA AAG CAA TAT TAT GGA ATT TAAGGATCAC AATGCATTAT TCTTATGAAA CCTT | 1164 |
| Leu Lys Gln Tyr Tyr Gly Ile                                       |      |
| 365                                                               |      |
| TTTAAA                                                            | 1170 |

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Leu Leu Phe Thr Pro Gly Pro Val Ala Ile Asn Glu Glu Met Arg |  |
| 1 5 10 15                                                       |  |
| Thr Ser Phe Ser Gln Pro Met Pro His His Arg Thr Lys Asp Phe Glu |  |
| 20 25 30                                                        |  |
| Lys Ile Phe Gln Ser Val Arg Glu Asn Leu Lys Lys Met Thr Gly Leu |  |
| 35 40 45                                                        |  |
| Glu Glu Val Leu Leu Leu Ser Ser Ser Gly Thr Gly Ala Met Glu Ala |  |
| 50 55 60                                                        |  |
| Ser Val Ile Ser Leu Cys Gln Lys Glu Leu Leu Phe Val Asn Ala Gly |  |
| 65 70 75 80                                                     |  |
| Lys Phe Gly Glu Arg Phe Gly Lys Ile Ala Lys Ala His Ser Ile Lys |  |
| 85 90 95                                                        |  |
| Ala His Glu Leu Val Tyr Glu Trp Asp Thr Pro Ala Gln Val Asp Glu |  |
| 100 105 110                                                     |  |
| Ile Leu Ser Val Leu Lys Ala Asn Pro Asn Ile Asp Ala Phe Cys Ile |  |
| 115 120 125                                                     |  |
| Gln Ala Cys Glu Ser Ser Gly Gly Leu Arg His Pro Val Glu Lys Ile |  |
| 130 135 140                                                     |  |
| Ala Gln Ala Ile Lys Glu Thr Asn Pro Asn Val Phe Val Ile Val Asp |  |
| 145 150 155 160                                                 |  |



GAT AAA GAA GTT AAA GGG GGC TTA GGG GTT GTG GCT GAT GAC GCT TTA 201  
 Asp Lys Glu Val Lys Gly Gly Leu Gly Val Val Ala Asp Asp Ala Leu  
 40 45 50

GCG GGT GTT TTA GCC GGA TTG AGC GCG TTA TTA GTC ATC CAT ATT TTA 249  
 Ala Gly Val Leu Ala Gly Leu Ser Ala Leu Leu Val Ile His Ile Leu  
 55 60 65

GGA TTT TTT AAC ATT AAA CTT TAATTTTAAG AAAAT 285  
 Gly Phe Phe Asn Ile Lys Leu  
 70 75

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Met Trp Leu Ala Met Ala Ile Ser Gly Leu Ser Leu Ala Gly Val Ile  
 1 5 10 15  
 Leu Ser Phe Ile Phe Phe Arg Ile Tyr Asp Ile Thr Lys Pro Ser Leu  
 20 25 30  
 Ile Gly Lys Ile Asp Lys Glu Val Lys Gly Gly Leu Gly Val Val Ala  
 35 40 45  
 Asp Asp Ala Leu Ala Gly Val Leu Ala Gly Leu Ser Ala Leu Leu Val  
 50 55 60  
 Ile His Ile Leu Gly Phe Phe Asn Ile Lys Leu  
 65 70 75

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 70...957
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

AAAGATAGGA TTAAATATTT TATTTTTTTTA GATGAAAACC ATCATTTTTA TTTGATTGAA 60  
 GAATCCAAC ATG CAT TCA AAA TAC TTC GCT CAA ATC AAA GAA AAA AAA TTA 111  
 Met His Ser Lys Tyr Phe Ala Gln Ile Lys Glu Lys Lys Leu  
 1 5 10



|                                                                   |      |     |  |     |     |
|-------------------------------------------------------------------|------|-----|--|-----|-----|
| 240                                                               |      | 245 |  | 250 |     |
| GGC AGT TTG GCC AAT TAT TTG TTT GAT GAT TTT AAA ACA ACG CTA GAA   | 879  |     |  |     |     |
| Gly Ser Leu Ala Asn Tyr Leu Phe Asp Asp Phe Lys Thr Thr Leu Glu   |      |     |  |     |     |
| 255                                                               |      | 260 |  | 265 | 270 |
| AAT TTA GCG CAA TCA TTA CCC AAA ACC CCT AAG ATC CAA ATC AAA AAC   | 927  |     |  |     |     |
| Asn Leu Ala Gln Ser Leu Pro Lys Thr Pro Lys Ile Gln Ile Lys Asn   |      |     |  |     |     |
|                                                                   |      | 275 |  | 280 | 285 |
| TCT TAT TTG TTG CAA ATC CAA AAG AAT AAG TAATGGCCAA ACGCAGTATC GCT | 980  |     |  |     |     |
| Ser Tyr Leu Leu Gln Ile Gln Lys Asn Lys                           |      |     |  |     |     |
|                                                                   |      | 290 |  | 295 |     |
| TATTTGGATA GCGTTTTTGA CATTTCCTAC ACTTTTATAG A                     | 1021 |     |  |     |     |

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Ser | Lys | Tyr | Phe | Ala | Gln | Ile | Lys | Glu | Lys | Lys | Leu | Pro | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ile | Leu | Thr | His | Asn | Gly | Leu | Leu | Lys | Asn | Ser | Phe | Leu | Gly | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Ile | Ile | Glu | Leu | Pro | Leu | Val | Ile | Asn | Leu | Val | His | Gly | Gly | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Glu | Asp | Gly | Lys | Leu | Ala | Ser | Leu | Leu | Glu | Phe | Tyr | Arg | Ile | Ala |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Ile | Gly | Pro | Arg | Ile | Glu | Ala | Ser | Val | Leu | Ser | Tyr | Asn | Lys | Tyr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Thr | Lys | Leu | Tyr | Ala | Lys | Asp | Leu | Gly | Val | Lys | Thr | Leu | Asp | His |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Leu | Leu | Asn | Glu | Lys | Asn | Arg | Ala | Asn | Ala | Leu | Asp | Leu | Met | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Asn | Phe | Pro | Phe | Ile | Ile | Lys | Pro | Asn | Asn | Ala | Gly | Ser | Ser | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Val | Asn | Val | Val | Lys | Glu | Glu | Lys | Glu | Leu | Val | Tyr | Ala | Leu | Asp |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Ala | Phe | Glu | Tyr | Ser | Lys | Glu | Val | Leu | Ile | Glu | Pro | Phe | Ile | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Val | Lys | Glu | Tyr | Asn | Leu | Ala | Gly | Cys | Lys | Ile | Lys | Lys | Asp | Phe |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Cys | Phe | Ser | Tyr | Val | Glu | Glu | Pro | Asn | Lys | Gln | Glu | Phe | Leu | Asp | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Gln | Lys | Tyr | Leu | Asp | Phe | Ser | Arg | Asn | Lys | Ala | Pro | Lys | Ala | Asn |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Ser | Asn | Ala | Leu | Glu | Glu | Gln | Leu | Lys | Glu | Asn | Phe | Lys | Lys | Leu |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Tyr | Asn | Asp | Leu | Phe | Asp | Gly | Ala | Ile | Ile | Arg | Cys | Asp | Phe | Phe | Val |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ile | Lys | Asn | Glu | Val | Tyr | Leu | Asn | Glu | Ile | Asn | Pro | Ile | Pro | Gly | Ser |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |  |
| Leu | Ala | Asn | Tyr | Leu | Phe | Asp | Asp | Phe | Lys | Thr | Thr | Leu | Glu | Asn | Leu |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |  |
| Ala | Gln | Ser | Leu | Pro | Lys | Thr | Pro | Lys | Ile | Gln | Ile | Lys | Asn | Ser | Tyr |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |  |
| Leu | Leu | Gln | Ile | Gln | Lys | Asn | Lys |     |     |     |     |     |     |     |     |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 47...628
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CAAAGCCTAT GCGAGAGTCA ATTCCGTTGC ATTTTCATTT AGAGGC ATG GAA GTC  | 55  |
| Met Glu Val                                                     |     |
| 1                                                               |     |
| CCC ATT GAA GGT TTA GAA GAA TTG GTA GAT GAA ACG AAA AAA TGC TTG | 103 |
| Pro Ile Glu Gly Leu Glu Glu Leu Val Asp Glu Thr Lys Lys Cys Leu |     |
| 5 10 15                                                         |     |
| ATA GAA GCT AAG AAA AAC AAA CAA AAC CAT TTC TTG CTG ATT CAA AAA | 151 |
| Ile Glu Ala Lys Lys Asn Lys Gln Asn His Phe Leu Leu Ile Gln Lys |     |
| 20 25 30 35                                                     |     |
| GCT AAC ATC CAA GCA AGA AAA CAA GCC ATG ATA GAT GAA AGT AAA ACC | 199 |
| Ala Asn Ile Gln Ala Arg Lys Gln Ala Met Ile Asp Glu Ser Lys Thr |     |
| 40 45 50                                                        |     |
| ATT ATC CAT GTT GCA TCA GGA GCG GCT GGA GCG GCC GGG CTT ATC CCC | 247 |
| Ile Ile His Val Ala Ser Gly Ala Ala Gly Ala Ala Gly Leu Ile Pro |     |
| 55 60 65                                                        |     |
| ATA CCC TTT AGC GAT GCA CTC GCT ATC GCG CCC ATT CAA GCA GGA ATG | 295 |
| Ile Pro Phe Ser Asp Ala Leu Ala Ile Ala Pro Ile Gln Ala Gly Met |     |
| 70 75 80                                                        |     |
| ATC TAC AAA ATG AAT GAC GCT TTT GGA ATG GAT TTG GAT AAA TCT GTA | 343 |
| Ile Tyr Lys Met Asn Asp Ala Phe Gly Met Asp Leu Asp Lys Ser Val |     |
| 85 90 95                                                        |     |
| GCC GCA TCA TTA ATC ACC GGA TTG TTA GGC GTA ACC GCT GTC GCG CAA | 391 |
| Ala Ala Ser Leu Ile Thr Gly Leu Leu Gly Val Thr Ala Val Ala Gln |     |
| 100 105 110 115                                                 |     |



Thr Gln

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 6...821
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AGAAG ATG GGG AAG TTT ATG AAT ACT CTT AAA AAG CAT TTA GCC TTT ATC | 50  |
| Met Gly Lys Phe Met Asn Thr Leu Lys Lys His Leu Ala Phe Ile       |     |
| 1 5 10 15                                                         |     |
| ATT CCC CTA GTA GCG TTA TTG TTT AGC TTG GAG TGC GTG TTA TTT ATC   | 98  |
| Ile Pro Leu Val Ala Leu Leu Phe Ser Leu Glu Cys Val Leu Phe Ile   |     |
| 20 25 30                                                          |     |
| AAT CAA GCG ATC GAA CAG AAA GAA AAA AAA TTG ATT GAA GAT TAT TCG   | 146 |
| Asn Gln Ala Ile Glu Gln Lys Glu Lys Lys Leu Ile Glu Asp Tyr Ser   |     |
| 35 40 45                                                          |     |
| GTC GTG TTG GCC AGC ACG CAA AAA TTA AAC TTG GAA TTG TTG CGT CAA   | 194 |
| Val Val Leu Ala Ser Thr Gln Lys Leu Asn Leu Glu Leu Leu Arg Gln   |     |
| 50 55 60                                                          |     |
| AAT TTT AGC GAA ATC ATA GCG TTA AAA GAA ATT GAT CCT AAT TAT TCT   | 242 |
| Asn Phe Ser Glu Ile Ile Ala Leu Lys Glu Ile Asp Pro Asn Tyr Ser   |     |
| 65 70 75                                                          |     |
| TTA GAA CCT CTT CAA AAA ACC TTA GGC ATA GAT GGG CTT AAG GAA TTA   | 290 |
| Leu Glu Pro Leu Gln Lys Thr Leu Gly Ile Asp Gly Leu Lys Glu Leu   |     |
| 80 85 90 95                                                       |     |
| AGA AAA AAT TTG CCC TTT TTT TAT TCT TTA CAA CTT TCC ACA TTC CCC   | 338 |
| Arg Lys Asn Leu Pro Phe Phe Tyr Ser Leu Gln Leu Ser Thr Phe Pro   |     |
| 100 105 110                                                       |     |
| ACT CAA GAG CGT TTA GAA AAC ATT AAA GAA AAA TTG CTC AAA ATC CCT   | 386 |
| Thr Gln Glu Arg Leu Glu Asn Ile Lys Glu Lys Leu Leu Lys Ile Pro   |     |
| 115 120 125                                                       |     |
| GGC GTT CAA AAA GTT GAA GTC TTT GCC AAA ACT TAC ATG CAA GTG TAT   | 434 |
| Gly Val Gln Lys Val Glu Val Phe Ala Lys Thr Tyr Met Gln Val Tyr   |     |
| 130 135 140                                                       |     |
| GAT CTC TTG AGT TTT ATT AAA ACA GCG GTC TAT ATC TTT GCG TTA GTG   | 482 |



|            |            |             |            |            |            |        |     |     |     |     |     |     |     |     |     |     |  |
|------------|------------|-------------|------------|------------|------------|--------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asp        | Leu        | Leu         | Ser        | Phe        | Ile        | Lys    | Thr | Ala | Val | Tyr | Ile | Phe | Ala | Leu | Val |     |  |
| 145        |            |             |            |            |            | 150    |     |     |     |     | 155 |     |     |     |     |     |  |
| GTC        | TTT        | GTT         | TTA        | TCG        | GTT        | TTA    | TTG | ATG | TTT | AAA | CAA | GTC | CGC | ATC | TGG | 530 |  |
| Val        | Phe        | Val         | Leu        | Ser        | Val        | Leu    | Leu | Met | Phe | Lys | Gln | Val | Arg | Ile | Trp |     |  |
| 160        |            |             |            |            | 165        |        |     |     |     | 170 |     |     |     |     | 175 |     |  |
| ATC        | TAT        | CAA         | TAC        | CAT        | GAG        | AGA    | TTA | GAG | ATC | ATG | GAT | TTA | TTA | GGG | GCT | 578 |  |
| Ile        | Tyr        | Gln         | Tyr        | His        | Glu        | Arg    | Leu | Glu | Ile | Met | Asp | Leu | Leu | Gly | Ala |     |  |
|            |            |             |            | 180        |            |        |     |     | 185 |     |     |     |     | 190 |     |     |  |
| TCG        | GTG        | TCT         | TTT        | AAA        | AAC        | GGG    | TTT | TTG | TAT | AAA | ATA | GCT | TTA | ATG | GAT | 626 |  |
| Ser        | Val        | Ser         | Phe        | Lys        | Asn        | Gly    | Phe | Leu | Tyr | Lys | Ile | Ala | Leu | Met | Asp |     |  |
|            |            |             | 195        |            |            |        |     | 200 |     |     |     |     | 205 |     |     |     |  |
| TCT        | GTA        | ATC         | GCT        | AGT        | TTT        | TTA    | GCC | CCC | ATG | CTC | ATG | CTC | TAT | ACC | ACT | 674 |  |
| Ser        | Val        | Ile         | Ala        | Ser        | Phe        | Leu    | Ala | Pro | Met | Leu | Met | Leu | Tyr | Thr | Thr |     |  |
|            |            | 210         |            |            |            |        | 215 |     |     |     |     |     | 220 |     |     |     |  |
| TCG        | CAA        | AAA         | GGT        | TTT        | GAA        | AAA    | ACG | ATG | GAT | ACT | TTG | GGT | ATT | ATA | GGA | 722 |  |
| Ser        | Gln        | Lys         | Gly        | Phe        | Glu        | Lys    | Thr | Met | Asp | Thr | Leu | Gly | Ile | Ile | Gly |     |  |
|            | 225        |             |            |            |            | 230    |     |     |     |     | 235 |     |     |     |     |     |  |
| GGC        | GCG        | TTT         | GTT        | TTA        | AAC        | CAT    | TTT | TTA | TGG | GGA | CTG | CTT | TTT | AGC | CTT | 770 |  |
| Gly        | Ala        | Phe         | Val        | Leu        | Asn        | His    | Phe | Leu | Trp | Gly | Leu | Leu | Phe | Ser | Leu |     |  |
| 240        |            |             |            |            | 245        |        |     |     |     | 250 |     |     |     |     | 255 |     |  |
| GTG        | GTC        | TCA         | TTT        | GTT        | TCT        | GTT    | TTA | CTT | GTA | GCT | TGG | AGG | ACT | AGG | CAT | 818 |  |
| Val        | Val        | Ser         | Phe        | Val        | Ser        | Val    | Leu | Leu | Val | Ala | Trp | Arg | Thr | Arg | His |     |  |
|            |            |             |            | 260        |            |        |     |     | 265 |     |     |     |     | 270 |     |     |  |
| GTA        | TAAATTAGGG | GTGTTTTTTGT | TAGCCACCTT | ACTATCAGCT | AACACGCAAA | AAGTGA | 877 |     |     |     |     |     |     |     |     |     |  |
| Val        |            |             |            |            |            |        |     |     |     |     |     |     |     |     |     |     |  |
| GCGATATTGC | TAAAGATATC | CAA         | 900        |            |            |        |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Gly | Lys | Phe | Met | Asn | Thr | Leu | Lys | Lys | His | Leu | Ala | Phe | Ile | Ile |  |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |  |
| Pro | Leu | Val | Ala | Leu | Leu | Phe | Ser | Leu | Glu | Cys | Val | Leu | Phe | Ile | Asn |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Gln | Ala | Ile | Glu | Gln | Lys | Glu | Lys | Lys | Leu | Ile | Glu | Asp | Tyr | Ser | Val |  |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |
| Val | Leu | Ala | Ser | Thr | Gln | Lys | Leu | Asn | Leu | Glu | Leu | Arg | Gln | Asn |     |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |  |
| Phe | Ser | Glu | Ile | Ile | Ala | Leu | Lys | Glu | Ile | Asp | Pro | Asn | Tyr | Ser | Leu |  |  |









|                                                                 |     |     |  |     |  |     |      |
|-----------------------------------------------------------------|-----|-----|--|-----|--|-----|------|
| 270                                                             |     | 275 |  | 280 |  | 285 |      |
| TCT CAA GAT GAA GAA GTC TTG GAA GTG GCG CGA TCT TAT TTG ATC GCT |     |     |  |     |  |     | 975  |
| Ser Gln Asp Glu Glu Val Leu Glu Val Ala Arg Ser Tyr Leu Ile Ala |     |     |  |     |  |     |      |
|                                                                 | 290 |     |  | 295 |  | 300 |      |
| GTG GGC CTC TCT CAA GCC CCC TTA ATT GGG TAT TTT GTG CTA GAT GGA |     |     |  |     |  |     | 1023 |
| Val Gly Leu Ser Gln Ala Pro Leu Ile Gly Tyr Phe Val Leu Asp Gly |     |     |  |     |  |     |      |
|                                                                 | 305 |     |  | 310 |  | 315 |      |
| GTT TTT AGA GGG GCT GGC ATT TCT AAA GTC TCA CTG TAT ATT AAC ACC |     |     |  |     |  |     | 1071 |
| Val Phe Arg Gly Ala Gly Ile Ser Lys Val Ser Leu Tyr Ile Asn Thr |     |     |  |     |  |     |      |
|                                                                 | 320 |     |  | 325 |  | 330 |      |
| CTA AGC TTA TGG GGG TTA AGG ATC ATG CCC ATT TAC TTG CTT TTA ATT |     |     |  |     |  |     | 1119 |
| Leu Ser Leu Trp Gly Leu Arg Ile Met Pro Ile Tyr Leu Leu Leu Ile |     |     |  |     |  |     |      |
|                                                                 | 335 |     |  | 340 |  | 345 |      |
| CAT CAT TTT AAG GTG GAA TTT ATT TTT GTA GTG ATC GCA TCA GAA ACT |     |     |  |     |  |     | 1167 |
| His His Phe Lys Val Glu Phe Ile Phe Val Val Ile Ala Ser Glu Thr |     |     |  |     |  |     |      |
|                                                                 | 350 |     |  | 355 |  | 360 | 365  |
| TTT TTG CGC TCA TTC ATC TAT TAT AAA GTT TTT TCT AAA GGC ATT TGG |     |     |  |     |  |     | 1215 |
| Phe Leu Arg Ser Phe Ile Tyr Tyr Lys Val Phe Ser Lys Gly Ile Trp |     |     |  |     |  |     |      |
|                                                                 | 370 |     |  | 375 |  | 380 |      |
| AAA AGG TGC GGG AAA AAG GCT TGATTATTGC TTGAGCGTAG CGGT          |     |     |  |     |  |     | 1260 |
| Lys Arg Cys Gly Lys Lys Ala                                     |     |     |  |     |  |     |      |
|                                                                 | 385 |     |  |     |  |     |      |

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Phe | Tyr | Gly | Ile | Asn | Thr | Ile | Leu | Tyr | Thr | Gly | Thr | Asn | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Leu | Ser | Arg | Leu | Val | Gly | Ala | Arg | Asp | Phe | Thr | Gln | Ile | Asn | His |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Phe | Ser | Ser | Ile | Phe | Ile | Gly | Ala | Phe | Met | Ile | Cys | Leu | Gly | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Phe | Val | Ser | Tyr | Phe | Leu | Ile | Glu | Pro | Phe | Leu | Asn | Trp | Met | Gln |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Gln | Asp | Pro | Ser | Arg | Gln | Leu | Thr | Gln | Asp | Tyr | Leu | Glu | Val | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Val | Ala | Leu | Pro | Ser | Ile | Phe | Leu | Lys | Asn | Ile | Leu | Val | Ser | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Ala | Ser | Phe | Ser | Asp | Thr | Leu | Thr | Pro | Phe | Ile | Val | Lys | Ile | Ile |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Met | Val | Ile | Ala | Cys | Ile | Phe | Leu | Asn | Gln | Ala | Leu | Ile | Phe | Gly | Asp |









(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met Pro Leu Pro Phe Ile Ile Ala Ala Gly Val Ala Leu Val Ala Ala  
1 5 10 15  
Xaa Tyr Gly Val Lys Lys Lys Val Asp Ala Asp Ile Leu Ser Glu Glu  
20 25 30  
Thr Asn Glu Tyr Ile Lys Tyr Ile Asn Glu Gly Asn Asp Leu Leu Glu  
35 40 45  
Glu Ala Glu Glu Val Ile Lys Ala Val Ala Ser Asp Cys Glu Phe Ala  
50 55 60  
Leu Ala Arg Phe Glu Glu Lys Arg Cys Tyr Ile Arg Asn His Val Ile  
65 70 75 80  
Ser Glu Phe Leu His His Phe Asn Gln Leu Glu Gly Phe Glu Leu Thr  
85 90 95  
Asn Lys Lys Asp Ser Met Glu Asn Ile Gln Leu Asp Val Ser Asn Thr  
100 105 110  
Leu Lys Ile Ile Asp Lys Asn Leu Lys Met Ser Ser Phe Asp Thr Leu  
115 120 125  
Gly Ala Val Gly Asn Val Val Gly Gly Phe Ser Met Gly Phe Gly Leu  
130 135 140  
Ala Ala Gly Gly Ile Val Gly Ser Val Gly Leu Ala Gly Pro Thr  
145 150 155 160  
Leu Ala Ile Phe Gly Ala Leu Arg Ala Ala Glu Met Glu Lys Lys Leu  
165 170 175  
Glu Asp Ala Lys Ala Tyr Cys Ser Gln Val Glu Ala Ala Val Lys Lys  
180 185 190  
Ala Asp Ala Met Ile Asp Asn Leu Gln Ala Val Arg Lys Met Ala Asp  
195 200 205  
Leu Phe Thr Arg Gln Ile Thr Lys Phe Asp Ala Leu Phe Phe Ser Leu  
210 215 220  
Ala Gln Glu Ala Ile Ala Thr Met Lys Lys His Asn Tyr Asp Phe Ser  
225 230 235 240  
His Tyr Asn Gln Lys Glu Gln Asp Gln Leu Ala Thr Ala Ser Ser Thr  
245 250 255  
Leu Lys Thr Leu Gly Ala Phe Leu Lys Val Pro Ile Met Asp Lys His  
260 265 270  
Gln Lys Leu Asn Glu Ala Thr Gln Ser Lys Leu Glu Phe Met Gln Arg  
275 280 285  
Glu Met Ser Ser Leu Glu Ala Lys His Tyr Asp Ser Val Lys Ile Lys  
290 295 300  
Phe Gly Leu Val Arg Arg Leu Phe Glu Phe Phe Arg Ser Leu Trp Gly  
305 310 315 320  
Lys Asn Gly Arg Ile Gln Arg Ala Lys Thr Thr Pro Asp Arg Phe Pro  
325 330 335  
Cys Thr Ser Cys Gly Leu Cys Cys Lys Asn Ile Ala Gly Ile Ile Glu  
340 345 350  
Leu Ile Gly Phe Asp Ala Gly Asn Gly Val Cys Lys Phe Leu Asp Leu  
355 360 365  
Glu Thr Asn Leu Cys Lys Ile Tyr Glu Ser Arg Pro Leu Ile Cys Arg  
370 375 380  
Ile Asp Glu Ala His Lys Lys Leu Tyr Pro His Ile Pro Leu Lys Glu  
385 390 395 400  
Phe Tyr Ala Lys Asn Ala Glu Val Cys Asn Ala Leu Gln Glu Ala Asn  
405 410 415  
His Met Asp Lys Ser Phe Arg Val Ile Leu Lys Lys  
420 425

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 30...851
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TATTAACACC GTTAAAGAGG GGGTAATTC ATG TTA GAA AAC ATG CAA GAT ATT | 53  |
| Met Leu Glu Asn Met Gln Asp Ile                                 |     |
| 1 5                                                             |     |
| TCA TTG CAA AGC TCT CAT GAA GTA GGA GTG GAT ATT ACA GAG AGC AAA | 101 |
| Ser Leu Gln Ser Ser His Glu Val Gly Val Asp Ile Thr Glu Ser Lys |     |
| 10 15 20                                                        |     |
| ATG CTT ACA AAA TTT GCA TCC TCG TTA TTA ATG AAT TTA TAT GAA TAT | 149 |
| Met Leu Thr Lys Phe Ala Ser Ser Leu Leu Met Asn Leu Tyr Glu Tyr |     |
| 25 30 35 40                                                     |     |
| ATT GGA AAT GGC AAG GAT CCC AAA GAA GCG TCC GAT CAT GCC ATG AGG | 197 |
| Ile Gly Asn Gly Lys Asp Pro Lys Glu Ala Ser Asp His Ala Met Arg |     |
| 45 50 55                                                        |     |
| GAT GCA AAG GAT GTG GTG CTT AGT TGT GGT AGA GTA GCC TTT CTT AAA | 245 |
| Asp Ala Lys Asp Val Val Leu Ser Cys Gly Arg Val Ala Phe Leu Lys |     |
| 60 65 70                                                        |     |
| GAC ATA GTT TCA AAT AGT CCA AAC GAA ACA ATC CAA AGT TTT GAT GGA | 293 |
| Asp Ile Val Ser Asn Ser Pro Asn Glu Thr Ile Gln Ser Phe Asp Gly |     |
| 75 80 85                                                        |     |
| GAC TTA GAA GTT GCG ATG CAT TTA GAA AAA ATT GGC ATA GAA TGT TAT | 341 |
| Asp Leu Glu Val Ala Met His Leu Glu Lys Ile Gly Ile Glu Cys Tyr |     |
| 90 95 100                                                       |     |
| AAG ATA TTT ATT GAC TAT GGT TCT CAA AAG ATC GAT GAT AAT GAG CTT | 389 |
| Lys Ile Phe Ile Asp Tyr Gly Ser Gln Lys Ile Asp Asp Asn Glu Leu |     |
| 105 110 115 120                                                 |     |
| TCT TGT CGT TTG TTA CAC ACT GGC ACG AAA ATT TTA GGC ACA AAA GCT | 437 |
| Ser Cys Arg Leu Leu His Thr Gly Thr Lys Ile Leu Gly Thr Lys Ala |     |
| 125 130 135                                                     |     |
| ATG GCA GTT GTT GGT CAA ACA TTC ATC CCC ATT CCT GGA GTT GGA GCG | 485 |
| Met Ala Val Val Gly Gln Thr Phe Ile Pro Ile Pro Gly Val Gly Ala |     |
| 140 145 150                                                     |     |

|                                                                                                                                                       |     |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| ATA ATT GGA AAT TTT GTG GGT GCA TTA CTG AGC AAA ACT CTC TGT GAA<br>Ile Ile Gly Asn Phe Val Gly Ala Leu Leu Ser Lys Thr Leu Cys Glu<br>155 160 165     | 533 |
| AAT TTG CGA GAT GTT TTA AAA GAG GCT AAA TTG GCG CGC CAA AGG CGT<br>Asn Leu Arg Asp Val Leu Lys Glu Ala Lys Leu Ala Arg Gln Arg Arg<br>170 175 180     | 581 |
| ATA GAG ATT GAA AAA GAA TGC CGT GAA AGT ATT AGG CTG TTA GAG ATC<br>Ile Glu Ile Glu Lys Glu Cys Arg Glu Ser Ile Arg Leu Leu Glu Ile<br>185 190 195 200 | 629 |
| TAT CGC AAT CAA TTT AAG GAA GTG TTT GAG CGG TAT TTT CAT GGG AAT<br>Tyr Arg Asn Gln Phe Lys Glu Val Phe Glu Arg Tyr Phe His Gly Asn<br>205 210 215     | 677 |
| GTA AAA TTC TTT AAT GAG AAT TTT AAT AAT CTT GAG AGG GCG CTT TAT<br>Val Lys Phe Phe Asn Glu Asn Phe Asn Asn Leu Glu Arg Ala Leu Tyr<br>220 225 230     | 725 |
| GCA GGA GAT GCG GAT TTG GCC ATA GGA GTC AAT AAT GAG ATT CAA GAA<br>Ala Gly Asp Ala Asp Leu Ala Ile Gly Val Asn Asn Glu Ile Gln Glu<br>235 240 245     | 773 |
| AGA CTA GGT CAA AAA CCC TTG TTT AAT AAT ACC CAA GAA TTT TTG GAA<br>Arg Leu Gly Gln Lys Pro Leu Phe Asn Asn Thr Gln Glu Phe Leu Glu<br>250 255 260     | 821 |
| CTC ATG AAT AAT GGT GGA AAA ATA GAA ATT TAAAGGAGAA ATCATGGAAG AAC<br>Leu Met Asn Asn Gly Gly Lys Ile Glu Ile<br>265 270                               | 874 |
| AAAAGGATAT GGGTCAAAGT                                                                                                                                 | 894 |

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

|                                                                                |
|--------------------------------------------------------------------------------|
| Met Leu Glu Asn Met Gln Asp Ile Ser Leu Gln Ser Ser His Glu Val<br>1 5 10 15   |
| Gly Val Asp Ile Thr Glu Ser Lys Met Leu Thr Lys Phe Ala Ser Ser<br>20 25 30    |
| Leu Leu Met Asn Leu Tyr Glu Tyr Ile Gly Asn Gly Lys Asp Pro Lys<br>35 40 45    |
| Glu Ala Ser Asp His Ala Met Arg Asp Ala Lys Asp Val Val Leu Ser<br>50 55 60    |
| Cys Gly Arg Val Ala Phe Leu Lys Asp Ile Val Ser Asn Ser Pro Asn<br>65 70 75 80 |
| Glu Thr Ile Gln Ser Phe Asp Gly Asp Leu Glu Val Ala Met His Leu<br>85 90 95    |



| 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | ACT | TAT | GAA | GTT | AAA | ATC | CTT | AAA | GAC | AAG | CTT | TAT | GTT | TCT | ATC | 303 |
| Met | Thr | Tyr | Glu | Val | Lys | Ile | Leu | Lys | Asp | Lys | Leu | Tyr | Val | Ser | Ile |     |
|     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |
| GTG | GAG | AAA | AAG | CCC | TTA | ATT | AGG | CAT | CAA | ATG | GCG | TTA | AAA | CCA | CCC | 351 |
| Val | Glu | Lys | Lys | Pro | Leu | Ile | Arg | His | Gln | Met | Ala | Leu | Lys | Pro | Pro |     |
|     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |
| AAA | CAC | CAT | GCA | CTC | AAA | CAC | ACA | ACG | CCA | AAA | CCC | GCC | CAT | AAG | CCC | 399 |
| Lys | His | His | Ala | Leu | Lys | His | Thr | Thr | Pro | Lys | Pro | Ala | His | Lys | Pro |     |
| 95  |     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |
| ATT | AAA | AAA | GAG | GCT | AAA | AAG | GTT | AAA | GAA | AAA | ACG | CCA | ACT | AAA | CAT | 447 |
| Ile | Lys | Lys | Glu | Ala | Lys | Lys | Val | Lys | Glu | Lys | Thr | Pro | Thr | Lys | His |     |
|     |     |     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| GCG | CAT | TCA | AAA | CAC | ACG | CAT | TCC | CCA | TTG | AAC | GAA | AGG | AGC | ACT | AAA | 495 |
| Ala | His | Ser | Lys | His | Thr | His | Ser | Pro | Leu | Asn | Glu | Arg | Ser | Thr | Lys |     |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| AAA | GAA | ATT | CCT | AAA | AAA | GAA | ATT | CCT | AAA | AAA | GAA | GCG | GAA | AAT | GAG | 543 |
| Lys | Glu | Ile | Pro | Lys | Lys | Glu | Ile | Pro | Lys | Lys | Glu | Ala | Glu | Asn | Glu |     |
|     |     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |
| AGC | AAG | AAC | CAA | GTC | TTT | ATA | GCA | GAA | AAA | AAT | GAT | ACT | TTC | ATC | AAA | 591 |
| Ser | Lys | Asn | Gln | Val | Phe | Ile | Ala | Glu | Lys | Asn | Asp | Thr | Phe | Ile | Lys |     |
|     | 160 |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |
| ACC | AAA | CGC | AAA | AAA | CAC | AAA | AAG | ATC | GTT | TTA | GAC | GCT | GGG | CAT | GGG | 639 |
| Thr | Lys | Arg | Lys | Lys | His | Lys | Lys | Ile | Val | Leu | Asp | Ala | Gly | His | Gly |     |
| 175 |     |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |
| GGG | AAA | GAT | TGC | GGG | GCG | ATG | AGC | GCG | AAT | TTG | GTG | TGT | GAA | AAA | GAC | 687 |
| Gly | Lys | Asp | Cys | Gly | Ala | Met | Ser | Ala | Asn | Leu | Val | Cys | Glu | Lys | Asp |     |
|     |     |     | 195 |     |     |     |     |     | 200 |     |     |     | 205 |     |     |     |
| ATT | GTT | TTA | GAA | GTG | GTG | AAG | TTT | TTA | CAC | AAA | GAG | CTT | AAA | AAA | AGA | 735 |
| Ile | Val | Leu | Glu | Val | Val | Lys | Phe | Leu | His | Lys | Glu | Leu | Lys | Lys | Arg |     |
|     |     | 210 |     |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| GAT | TAT | AGC | GTT | TTA | TTG | ACA | AGG | GAT | AAG | GAT | ATT | TAT | ATT | GAT | TTA | 783 |
| Asp | Tyr | Ser | Val | Leu | Leu | Thr | Arg | Asp | Lys | Asp | Ile | Tyr | Ile | Asp | Leu |     |
|     |     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |
| GTG | GCT | CGC | ACG | GAA | TTA | GCC | AAT | AAA | AAA | AGC | GCG | GAT | TTA | TTC | ATC | 831 |
| Val | Ala | Arg | Thr | Glu | Leu | Ala | Asn | Lys | Lys | Ser | Ala | Asp | Leu | Phe | Ile |     |
|     | 240 |     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     |
| TCA | GTG | CAT | GCC | AAT | TCC | ATC | CCC | AAA | CAT | TCC | ACT | TCT | AAC | GCT | CAT | 879 |
| Ser | Val | His | Ala | Asn | Ser | Ile | Pro | Lys | His | Ser | Thr | Ser | Asn | Ala | His |     |
| 255 |     |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |
| GGT | ATA | GAG | ACT | TAT | TTT | TTA | TCC | ACC | GCA | AGG | AGC | GAA | AGG | GCT | AGG | 927 |
| Gly | Ile | Glu | Thr | Tyr | Phe | Leu | Ser | Thr | Ala | Arg | Ser | Glu | Arg | Ala | Arg |     |
|     |     |     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |











|                         |                         |                     |  |     |
|-------------------------|-------------------------|---------------------|--|-----|
| 50                      |                         | 55                  |  | 60  |
| Ala Lys Lys Pro Phe Glu | Ala Leu Asn Phe Tyr Ser | Lys Lys Ala Leu     |  |     |
| 65                      |                         | 70                  |  | 80  |
| Asn Glu Ile Phe Ala Asn | Ala Arg Lys Ile Cys Gly | Asn Asn Pro Leu     |  |     |
|                         | 85                      | 90                  |  | 95  |
| Gly Ala Asn Ile Leu Tyr | Ala Ile Asn Asp Tyr Gly | Arg Val Leu Arg     |  |     |
|                         | 100                     | 105                 |  | 110 |
| Asp Ser Cys Glu Ala Gly | Ala Asn Ile Ile Ile Thr | Gly Ala Gly Leu     |  |     |
|                         | 115                     | 120                 |  | 125 |
| Pro Thr Asn Met Pro Glu | Phe Ala Lys Asp Phe Ser | Asp Val Ala Leu     |  |     |
|                         | 130                     | 135                 |  | 140 |
| Ile Pro Ile Ile Ser Ser | Ala Lys Ala Leu Lys     | Ile Leu Cys Lys Arg |  |     |
| 145                     |                         | 150                 |  | 160 |
| Trp Ser Asp Arg Tyr Lys | Arg Ile Pro Asp Ala Phe | Ile Val Glu Gly     |  |     |
|                         | 165                     | 170                 |  | 175 |
| Pro Leu Ser Gly Gly His | Gln Gly Phe Lys Tyr     | Glu Asp Cys Phe Lys |  |     |
|                         | 180                     | 185                 |  | 190 |
| Glu Glu Phe Arg Leu Glu | Asn Leu Val Pro Lys     | Val Val Glu Ala Ser |  |     |
|                         | 195                     | 200                 |  | 205 |
| Lys Glu Trp Gly Asn Ile | Pro Ile Ile Ala Ala     | Gly Gly Ile Trp Asp |  |     |
|                         | 210                     | 215                 |  | 220 |
| Arg Lys Asp Ile Asp Thr | Met Leu Ser Leu Gly     | Ala Ser Gly Val Gln |  |     |
| 225                     |                         | 230                 |  | 235 |
| Met Ala Thr Arg Phe Leu | Gly Thr Lys Glu Cys     | Asp Ala Lys Val Tyr |  |     |
|                         | 245                     | 250                 |  | 255 |
| Ala Asp Leu Leu Pro Thr | Leu Lys Lys Glu Asp     | Ile Leu Leu Ile Lys |  |     |
|                         | 260                     | 265                 |  | 270 |
| Ser Pro Val Gly Tyr Pro | Ala Arg Ala Ile Asn     | Thr Gly Val Ile Lys |  |     |
|                         | 275                     | 280                 |  | 285 |
| Arg Ile Glu Glu Gly Asn | Ala Pro Lys Ile Ala     | Cys Val Ser Asn Cys |  |     |
|                         | 290                     | 295                 |  | 300 |
| Val Ala Pro Cys Asn Arg | Gly Glu Glu Ala Lys     | Lys Val Gly Tyr Cys |  |     |
| 305                     |                         | 310                 |  | 315 |
| Ile Ala Asp Gly Leu Gly | Arg Ser Tyr Leu Gly     | Asn Arg Glu Glu Gly |  |     |
|                         | 325                     | 330                 |  | 335 |
| Leu Tyr Phe Thr Gly Ala | Asn Gly Tyr Arg Val     | Asp Lys Ile Ile Ser |  |     |
|                         | 340                     | 345                 |  | 350 |
| Val His Glu Leu Ile Lys | Glu Leu Thr Glu Gly     |                     |  |     |
|                         | 355                     | 360                 |  |     |

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...2337
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:





|                                                                 |      |
|-----------------------------------------------------------------|------|
| TTA CTC AAT CAG GAA TTA AGA AGT GGG GAT GTG GTT AAA ATC ATT AAA | 1443 |
| Leu Leu Asn Gln Glu Leu Arg Ser Gly Asp Val Val Lys Ile Ile Lys |      |
| 465 470 475                                                     |      |
| GGC GAT AAA ATA ATA CCT CGT TTC ATT TGG ATG GAT CAG CTT AAA ACT | 1491 |
| Gly Asp Lys Ile Ile Pro Arg Phe Ile Trp Met Asp Gln Leu Lys Thr |      |
| 480 485 490                                                     |      |
| TCT AAG GCT AAA AAC CAT TTG CGC ATC CAA AGA AGA AAC CGC TTG AAA | 1539 |
| Ser Lys Ala Lys Asn His Leu Arg Ile Gln Arg Arg Asn Arg Leu Lys |      |
| 495 500 505                                                     |      |
| GAG GTT GAC ACT AAG AGC ATG ATC AAT ATC TTA GCG ACT TTT TTT GGG | 1587 |
| Glu Val Asp Thr Lys Ser Met Ile Asn Ile Leu Ala Thr Phe Phe Gly |      |
| 510 515 520 525                                                 |      |
| CGC TCT GTT TTT GAA GAC ATG GAT TTA AAG GAT TAT AAA AAC TTT GAA | 1635 |
| Arg Ser Val Phe Glu Asp Met Asp Leu Lys Asp Tyr Lys Asn Phe Glu |      |
| 530 535 540                                                     |      |
| GAA AGA TTA ACA GAT TGC GGG GTG GAG ACC ACC TTA ACA GAA GCG ATG | 1683 |
| Glu Arg Leu Thr Asp Cys Gly Val Glu Thr Thr Leu Thr Glu Ala Met |      |
| 545 550 555                                                     |      |
| AAA AGT TTT GAA AAT TTA GCC AAA CTC ACT GAA GAA ATT GAA AAT AAG | 1731 |
| Lys Ser Phe Glu Asn Leu Ala Lys Leu Thr Glu Glu Ile Glu Asn Lys |      |
| 560 565 570                                                     |      |
| GTG TTT TCT TTA AAA GAA GAT GCG ATT TTA GAA TAC CAA GAG ATG AGT | 1779 |
| Val Phe Ser Leu Lys Glu Asp Ala Ile Leu Glu Tyr Gln Glu Met Ser |      |
| 575 580 585                                                     |      |
| TTA TGG ACT CGA GGT TTA AGG TAT TTG GGC TTT AAA ACC AAT GTC TTG | 1827 |
| Leu Trp Thr Arg Gly Leu Arg Tyr Leu Gly Phe Lys Thr Asn Val Leu |      |
| 590 595 600 605                                                 |      |
| AAT TTT TTA GCC CCC AAT CGG CAG TGG CAG TGT AAG GAA TTA GAA CAT | 1875 |
| Asn Phe Leu Ala Pro Asn Arg Gln Trp Gln Cys Lys Glu Leu Glu His |      |
| 610 615 620                                                     |      |
| TTT AGC GTT TGT TCA AGC AAC GCT TTA GAA ATC AAA CAG GTG TTG TTG | 1923 |
| Phe Ser Val Cys Ser Ser Asn Ala Leu Glu Ile Lys Gln Val Leu Leu |      |
| 625 630 635                                                     |      |
| AAT GAT TGT TGT TAC CCT AAA TAT GGC GAT GAA ATC ATT GCG ATT GTA | 1971 |
| Asn Asp Cys Cys Tyr Pro Lys Tyr Gly Asp Glu Ile Ile Ala Ile Val |      |
| 640 645 650                                                     |      |
| ACG GAT TTA AAA GAT CCA AAA GCG ATT GCG CAC CAT AAA TTT TGC AAA | 2019 |
| Thr Asp Leu Lys Asp Pro Lys Ala Ile Ala His His Lys Phe Cys Lys |      |
| 655 660 665                                                     |      |
| AAA GCG ATG GCG GAA GTA GAT GCT AAA GTG CCT ATG GTT TAT ATA GAA | 2067 |
| Lys Ala Met Ala Glu Val Asp Ala Lys Val Pro Met Val Tyr Ile Glu |      |
| 670 675 680 685                                                 |      |
| TGG CAC AAG CGG GAT CGA ACG ATT TAT AAA ATG ATG TTT TAT TTG GGC | 2115 |
| Trp His Lys Arg Asp Arg Thr Ile Tyr Lys Met Met Phe Tyr Leu Gly |      |









Cys Ile Ser Leu Arg Pro Tyr Ile Tyr Asn Trp Arg  
80 85 90

AAATGAAAGC ATGCG

310

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ala | Val | Lys | Lys | Ile | Val | Val | Ser | Trp | Cys | Val | Ala | Leu | Ala | Phe |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Leu | Ser | Ala | Asp | Ser | Ala | Gln | Ala | Asn | Lys | Ala | Ile | Ser | Asn | Ala | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ile | Lys | Glu | Ile | Arg | Asp | Leu | Lys | Lys | Ile | Ile | Ser | Ala | Gln | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Thr | Glu | Ile | Asn | Asn | Leu | Arg | Lys | Val | Gln | Glu | Val | Leu | Ser | Gly | Gln |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Gly | Asp | Met | Arg | Lys | Asp | Ile | Leu | Ser | Thr | Arg | Asp | Tyr | Cys | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Leu | Arg | Pro | Tyr | Ile | Tyr | Asn | Trp | Arg |     |     |     |     |     |     |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...1569
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

|            |            |            |            |            |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| TGAAAAAGAA | CTCAAAGAGC | TGCAAAAAAA | ACAAAAACAC | GAGTAACAAC | C   | ATG | ATT | 57  |     |     |     |     |     |     |     |     |
|            |            |            |            |            |     | Met | Ile |     |     |     |     |     |     |     |     |     |
|            |            |            |            |            |     | 1   |     |     |     |     |     |     |     |     |     |     |
| AAC        | ACG        | ATG        | TTT        | TGC        | GCG | ACC | ATG | CAA | AGG | GGA | GTG | GCG | GAA | ATC | GTG | 105 |
| Asn        | Thr        | Met        | Phe        | Cys        | Ala | Thr | Met | Gln | Arg | Gly | Val | Ala | Glu | Ile | Val |     |
|            |            | 5          |            |            |     |     |     | 10  |     |     |     | 15  |     |     |     |     |
| GCT        | GTG        | GAA        | GCG        | ACT        | TTC | ACA | AGG | GCT | TTG | CCG | GCG | TTT | GTG | ATT | TCA | 153 |
| Ala        | Val        | Glu        | Ala        | Thr        | Phe | Thr | Arg | Ala | Leu | Pro | Ala | Phe | Val | Ile | Ser |     |





485

490

495

GCG CTG AGT TTT AGA AAG ATT TCT TAAAAGGATT TTTATAAGGG AGAAAAAATG 1599  
 Ala Leu Ser Phe Arg Lys Ile Ser  
 500 505

CAAGAATACC ACATTCATAA TTTGGATTGC CC 1631

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 506 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Asn | Thr | Met | Phe | Cys | Ala | Thr | Met | Gln | Arg | Gly | Val | Ala | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Val | Ala | Val | Glu | Ala | Thr | Phe | Thr | Arg | Ala | Leu | Pro | Ala | Phe | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Ser | Gly | Leu | Ala | Asn | Ser | Ser | Ile | Gln | Glu | Ala | Lys | Gln | Arg | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Ser | Ala | Leu | Gln | Asn | Asn | Asp | Phe | Thr | Phe | Pro | Pro | Leu | Lys | Ile |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Ile | Asn | Leu | Ser | Pro | Ser | Asp | Leu | Pro | Lys | Ser | Gly | Ser | His | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asp | Leu | Pro | Ile | Ala | Leu | Leu | Ile | Ala | Leu | Gln | Lys | Gln | Glu | Leu | Ala |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Lys | Glu | Trp | Phe | Ala | Phe | Gly | Glu | Leu | Gly | Leu | Asp | Gly | Lys | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Pro | Asn | Pro | Asn | Ile | Phe | Pro | Met | Leu | Leu | Asp | Ile | Ala | Ile | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| His | Pro | His | Ala | Lys | Ile | Ile | Ala | Pro | Lys | Ala | Asn | Glu | Glu | Leu | Phe |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Leu | Ile | Pro | Asn | Leu | Gln | Cys | Phe | Phe | Val | Gly | His | Phe | Lys | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ala | Leu | Glu | Ile | Leu | Gln | Asn | Pro | Glu | Thr | Lys | Ala | Asp | Thr | His | Thr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Lys | Leu | Pro | Phe | Lys | Thr | Ile | Glu | Leu | Asn | Asp | Lys | Glu | Tyr | Tyr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Phe | Ser | Asp | Ala | Tyr | Ala | Leu | Asp | Phe | Lys | Glu | Val | Lys | Gly | Gln | Ala |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Ala | Lys | Glu | Ala | Ala | Leu | Ile | Ala | Ser | Ala | Gly | Phe | His | Asn | Leu |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Leu | Glu | Gly | Ser | Pro | Gly | Cys | Gly | Lys | Ser | Met | Ile | Ile | Asn | Arg |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Met | Arg | Tyr | Ile | Leu | Pro | Pro | Leu | Ser | Leu | Asn | Glu | Ile | Leu | Glu | Ala |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Thr | Lys | Leu | Arg | Ile | Leu | Ser | Glu | Gln | Asp | Ser | Ala | Tyr | Tyr | Pro | Leu |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Arg | Ser | Phe | Arg | Asn | Pro | His | Gln | Ser | Ala | Ser | Lys | Ser | Ser | Ile | Leu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Ser | Ser | Ser | Leu | Arg | Glu | Pro | Lys | Pro | Gly | Glu | Ile | Ala | Leu | Ala |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |



|            |         |     |     |     |            |            |            |            |     |     |     |     |     |     |     |     |  |
|------------|---------|-----|-----|-----|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser        | Glu     | Gly | Ile | Gly | Leu        | Ala        | Ala        | Ile        | Gln | Val | Gly | Leu | Pro | Leu | Arg |     |  |
|            |         |     | 45  |     |            |            |            | 50         |     |     |     |     | 55  |     |     |     |  |
| ATG        | CTC     | ATC | ATC | AAC | CTC        | CCG        | CAA        | GAA        | GAC | GGC | GTG | CAA | CAC | AAA | GAA | 244 |  |
| Met        | Leu     | Ile | Ile | Asn | Leu        | Pro        | Gln        | Glu        | Asp | Gly | Val | Gln | His | Lys | Glu |     |  |
|            |         |     | 60  |     |            |            | 65         |            |     |     |     | 70  |     |     |     |     |  |
| GAC        | TGC     | TTG | GAA | ATC | ATT        | AAC        | CCT        | AAG        | TTT | ATA | GAA | ACT | GGG | GGA | TCA | 292 |  |
| Asp        | Cys     | Leu | Glu | Ile | Ile        | Asn        | Pro        | Lys        | Phe | Ile | Glu | Thr | Gly | Gly | Ser |     |  |
|            |         |     | 75  |     |            | 80         |            |            |     |     | 85  |     |     |     |     |     |  |
| ATG        | ATG     | TAT | AGA | GAA | GGG        | TGC        | TTG        | TCT        | GTG | CCG | GGA | TTT | TAC | GAA | GAA | 340 |  |
| Met        | Met     | Tyr | Arg | Glu | Gly        | Cys        | Leu        | Ser        | Val | Pro | Gly | Phe | Tyr | Glu | Glu |     |  |
|            |         |     |     |     | 95         |            |            |            |     | 100 |     |     |     |     | 105 |     |  |
| GTG        | GAG     | CGT | TTT | GAA | AAG        | GTT        | AAG        | ATA        | GAG | TAT | CAA | AAC | CGC | TTC | GCT | 388 |  |
| Val        | Glu     | Arg | Phe | Glu | Lys        | Val        | Lys        | Ile        | Glu | Tyr | Gln | Asn | Arg | Phe | Ala |     |  |
|            |         |     |     | 110 |            |            |            |            | 115 |     |     |     |     | 120 |     |     |  |
| GAA        | GTG     | AAA | GTT | TTA | GAA        | GCG        | AGC        | GAG        | CTT | TTA | GCG | GTA | GCC | ATT | CAG | 436 |  |
| Glu        | Val     | Lys | Val | Leu | Glu        | Ala        | Ser        | Glu        | Leu | Leu | Ala | Val | Ala | Ile | Gln |     |  |
|            |         |     |     | 125 |            |            |            | 130        |     |     |     |     | 135 |     |     |     |  |
| CAT        | GAG     | ATC | GAT | CAC | CTC        | AAT        | GGC        | GTG        | TTA | TTC | GTG | GAT | AAA | TTA | TCC | 484 |  |
| His        | Glu     | Ile | Asp | His | Leu        | Asn        | Gly        | Val        | Leu | Phe | Val | Asp | Lys | Leu | Ser |     |  |
|            |         |     | 140 |     |            |            | 145        |            |     |     |     | 150 |     |     |     |     |  |
| ATT        | TTG     | AAG | CGT | AAG | AAA        | TTT        | GAA        | AAA        | GAA | CTC | AAA | GAG | CTG | CAA | AAA | 532 |  |
| Ile        | Leu     | Lys | Arg | Lys | Lys        | Phe        | Glu        | Lys        | Glu | Leu | Lys | Glu | Leu | Gln | Lys |     |  |
|            |         |     | 155 |     |            | 160        |            |            |     |     | 165 |     |     |     |     |     |  |
| AAA        | CAA     | AAA | CAC | GAG | TAACAACCAT | GATTAACACG | ATGTTTTGCG | CGACCATGCA | A   |     |     |     |     |     |     | 588 |  |
| Lys        | Gln     | Lys | His | Glu |            |            |            |            |     |     |     |     |     |     |     |     |  |
|            |         |     |     |     |            |            |            |            |     |     |     |     |     |     |     | 170 |  |
| AGGGGAGTGG | CGGAAAT |     |     |     |            |            |            |            |     |     |     |     |     |     |     | 605 |  |

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Ala | Leu | Leu | Glu | Ile | Ile | His | Tyr | Pro | Ser | Lys | Ile | Leu | Arg | Thr |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Ile | Ser | Lys | Glu | Val | Val | Ser | Phe | Asp | Ser | Lys | Leu | His | Gln | Gln | Leu |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Asp | Asp | Met | His | Glu | Thr | Met | Ile | Ala | Ser | Glu | Gly | Ile | Gly | Leu | Ala |  |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |  |
| Ala | Ile | Gln | Val | Gly | Leu | Pro | Leu | Arg | Met | Leu | Ile | Ile | Asn | Leu | Pro |  |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Gln | Glu | Asp | Gly | Val | Gln | His | Lys | Glu | Asp | Cys | Leu | Glu | Ile | Ile | Asn |  |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Lys | Phe | Ile | Glu | Thr | Gly | Gly | Ser | Met | Met | Tyr | Arg | Glu | Gly | Cys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Ser | Val | Pro | Gly | Phe | Tyr | Glu | Glu | Val | Glu | Arg | Phe | Glu | Lys | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Ile | Glu | Tyr | Gln | Asn | Arg | Phe | Ala | Glu | Val | Lys | Val | Leu | Glu | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Glu | Leu | Leu | Ala | Val | Ala | Ile | Gln | His | Glu | Ile | Asp | His | Leu | Asn |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Val | Leu | Phe | Val | Asp | Lys | Leu | Ser | Ile | Leu | Lys | Arg | Lys | Lys | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Glu | Lys | Glu | Leu | Lys | Glu | Leu | Gln | Lys | Lys | Gln | Lys | His | Glu |     |     |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...495
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CCCCAAACAA TAGGATAAAA A ATG CCG CTC ACT CAT TTG AAT GAA GAA AAT | 51  |
| Met Pro Leu Thr His Leu Asn Glu Glu Asn                         |     |
| 1 5 10                                                          |     |
| CAG CCT AAA ATG GTG GAT ATA GGG GAT AAA GAA ACC ACT GAA AGA ATC | 99  |
| Gln Pro Lys Met Val Asp Ile Gly Asp Lys Glu Thr Thr Glu Arg Ile |     |
| 15 20 25                                                        |     |
| GCT TTA GCA AGC GGT CGT ATC AGC ATG AAT AAA GAG GCT TAT GAC GCT | 147 |
| Ala Leu Ala Ser Gly Arg Ile Ser Met Asn Lys Glu Ala Tyr Asp Ala |     |
| 30 35 40                                                        |     |
| ATT ATC AAT CAT TGC GTC AAA AAG GGT CCG GTG TTA CAG ACT GCT ATT | 195 |
| Ile Ile Asn His Cys Val Lys Lys Gly Pro Val Leu Gln Thr Ala Ile |     |
| 45 50 55                                                        |     |
| ATT GCT GGA ATT ATG GGG GCT AAA AAG ACA AGC GAG CTC ATT CCC ATG | 243 |
| Ile Ala Gly Ile Met Gly Ala Lys Lys Thr Ser Glu Leu Ile Pro Met |     |
| 60 65 70                                                        |     |
| TGC CAT CCA ATC ATG CTC AAT GGG GTG GAT ATT GAT ATT TTA GAA GAA | 291 |
| Cys His Pro Ile Met Leu Asn Gly Val Asp Ile Asp Ile Leu Glu Glu |     |
| 75 80 85 90                                                     |     |
| AAA GAG ACT TGT AGT TTT AAA CTC TAT GCG AGA GTC AAA ACT CAA GCT | 339 |
| Lys Glu Thr Cys Ser Phe Lys Leu Tyr Ala Arg Val Lys Thr Gln Ala |     |



| 95  |     |      |     |     |      |     |     |     |     | 100 |     |     |     |     | 105 |     |  |  |  |  |
|-----|-----|------|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| AAA | ACG | GGC  | GTA | GAA | ATG  | GAA | GCG | CTA | ATG | AGT | GTG | AGC | ATA | GGG | CTT | 387 |  |  |  |  |
| Lys | Thr | Gly  | Val | Glu | Met  | Glu | Ala | Leu | Met | Ser | Val | Ser | Ile | Gly | Leu |     |  |  |  |  |
|     |     |      | 110 |     |      |     |     | 115 |     |     |     |     | 120 |     |     |     |  |  |  |  |
| TTA | ACC | ATT  | TAT | GAC | ATG  | GTG | AAA | GCC | ATT | GAC | AAG | AGC | ATG | ACA | ATT | 435 |  |  |  |  |
| Leu | Thr | Ile  | Tyr | Asp | Met  | Val | Lys | Ala | Ile | Asp | Lys | Ser | Met | Thr | Ile |     |  |  |  |  |
|     |     | 125  |     |     |      |     | 130 |     |     |     |     | 135 |     |     |     |     |  |  |  |  |
| AGC | GGT | GTG  | ATG | TTG | GAG  | CAT | AAA | AGT | GGA | GGC | AAA | AGT | GGG | GAT | TAT | 483 |  |  |  |  |
| Ser | Gly | Val  | Met | Leu | Glu  | His | Lys | Ser | Gly | Gly | Lys | Ser | Gly | Asp | Tyr |     |  |  |  |  |
|     | 140 |      |     |     |      | 145 |     |     |     |     | 150 |     |     |     |     |     |  |  |  |  |
| AAC | GCT | AAA  | AAA | TAG | AAAA | AGA | CCA | ATA | AAT | CT  | AA  | GAT | GT  | T   | A   | 540 |  |  |  |  |
| Asn | Ala | Lys  | Lys |     |      |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
| 155 |     |      |     |     |      |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
| TTG | ACA | ACAA | AAG | CGT | GTT  | G   | TTG |     |     |     |     |     |     |     |     | 564 |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Leu | Thr | His | Leu | Asn | Glu | Glu | Asn | Gln | Pro | Lys | Met | Val | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Gly | Asp | Lys | Glu | Thr | Thr | Glu | Arg | Ile | Ala | Leu | Ala | Ser | Gly | Arg |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ile | Ser | Met | Asn | Lys | Glu | Ala | Tyr | Asp | Ala | Ile | Ile | Asn | His | Cys | Val |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Lys | Gly | Pro | Val | Leu | Gln | Thr | Ala | Ile | Ile | Ala | Gly | Ile | Met | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Lys | Lys | Thr | Ser | Glu | Leu | Ile | Pro | Met | Cys | His | Pro | Ile | Met | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asn | Gly | Val | Asp | Ile | Asp | Ile | Leu | Glu | Glu | Lys | Glu | Thr | Cys | Ser | Phe |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Lys | Leu | Tyr | Ala | Arg | Val | Lys | Thr | Gln | Ala | Lys | Thr | Gly | Val | Glu | Met |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Ala | Leu | Met | Ser | Val | Ser | Ile | Gly | Leu | Leu | Thr | Ile | Tyr | Asp | Met |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Lys | Ala | Ile | Asp | Lys | Ser | Met | Thr | Ile | Ser | Gly | Val | Met | Leu | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| His | Lys | Ser | Gly | Gly | Lys | Ser | Gly | Asp | Tyr | Asn | Ala | Lys | Lys |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...552
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

|            |            |      |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|------------|------------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| CTTTTAGCTT | AAAAAGGAGT | TCAA | ATG | CAA | ACG | ATT | CAT | ATA | GGC | GTT | TTG | 51  |     |     |     |    |
|            |            |      | Met | Gln | Thr | Ile | His | Ile | Gly | Val | Leu |     |     |     |     |    |
|            |            |      | 1   |     |     |     | 5   |     |     |     |     |     |     |     |     |    |
| AGC        | GCG        | AGC  | GAT | AGA | GCG | TCA | AAA | GGG | ATT | TAT | GAA | GAT | TTA | AGC | GGT | 99 |
| Ser        | Ala        | Ser  | Asp | Arg | Ala | Ser | Lys | Gly | Ile | Tyr | Glu | Asp | Leu | Ser | Gly |    |
| 10         |            |      |     |     | 15  |     |     |     | 20  |     |     |     | 25  |     |     |    |











|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ala | Val | Met | Gly | Leu | Met | Leu | Ala | Leu | Gln | Lys | Leu | Asp | Asn | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Glu | Met | Ala | Ala | Gly | Ile | Ala | Gly | Ala | Phe | Thr | Ala | Thr | Val | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Ile | Met | Cys | Ser | Tyr | Ala | Ile | Phe | Gly | Pro | Phe | Gly | His | Lys | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Ala | Lys | Ser | Lys | Asp | Ile | Ile | Lys | Glu | Lys | Thr | Val | Leu | Leu | Glu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Ile | Leu | Gly | Ile | Ala | Asn | Gly | Glu | Asn | Pro | Arg | Asp | Leu | Glu | Asn |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 |     |     |     |
| Lys | Leu | Leu | Asn | Tyr | Ile | Ala | Pro | Gly | Glu | Pro | Lys | Lys | Ser | Gln | Phe |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     | 210 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...783
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

|            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| TGAGGGCTAA | AG  | ATG | GCT | AAG | AAA | AAC | AMA | CCC | ACC | GAA | TGC | CCC | GCC | GGT | 51  |     |
|            | Met | Ala | Lys | Lys | Asn | Xaa | Pro | Thr | Glu | Cys | Pro | Ala | Gly |     |     |     |
|            | 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     |     |
| GAA        | AAA | TGG | GCG | GTT | CCT | TAT | GCG | GAC | TTT | TTG | TCG | TTG | TTG | CTC | GCG | 99  |
| Glu        | Lys | Trp | Ala | Val | Pro | Tyr | Ala | Asp | Phe | Leu | Ser | Leu | Leu | Leu | Ala |     |
|            | 15  |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |     |
| CTT        | TTT | ATC | GCT | CTT | TAT | GCC | ATT | TCA | GCG | GTC | AAC | AAA | TCC | AAA | GTG | 147 |
| Leu        | Phe | Ile | Ala | Leu | Tyr | Ala | Ile | Ser | Ala | Val | Asn | Lys | Ser | Lys | Val |     |
|            | 30  |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| GAA        | GCC | TTA | AAA | ACC | GAA | TTT | ATT | AAG | ATT | TTT | AAT | TAC | GCT | CCC | AAG | 195 |
| Glu        | Ala | Leu | Lys | Thr | Glu | Phe | Ile | Lys | Ile | Phe | Asn | Tyr | Ala | Pro | Lys |     |
|            |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| CCA        | GAG | GCG | ATG | CAG | CCG | GTT | GTA | GTG | ATC | CCG | CCT | GAT | TCA | GGG | AAA | 243 |
| Pro        | Glu | Ala | Met | Gln | Pro | Val | Val | Val | Ile | Pro | Pro | Asp | Ser | Gly | Lys |     |
|            |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |
| GAA        | GAA | GAA | CAA | ATG | GCG | AGC | GAA | AGC | TCC | AAA | CCG | GCT | TCG | CAA | AAT | 291 |
| Glu        | Glu | Glu | Gln | Met | Ala | Ser | Glu | Ser | Ser | Lys | Pro | Ala | Ser | Gln | Asn |     |
|            |     | 80  |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |
| ACC        | GAA | ACA | AAA | GCC | ACT | ATC | GCT | CGC | AAA | GGC | GAA | GGC | AGT | GTT | TTA | 339 |











(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Lys Cys Tyr Phe Phe Ile Thr Phe Ser Tyr Ser Tyr Gly Tyr Val Val  
1 5 10 15  
Ile Phe Leu Pro Glu Asn Phe Ile Leu Arg Asn Ile Tyr Val Gly Asn  
20 25 30  
Leu Val Tyr Ser Ala Thr Ser Glu Gln Val Lys Glu Leu Phe Ser Gln  
35 40 45  
Phe Gly Lys Val Phe Asn Val Lys Leu Ile Tyr Asp Arg Glu Thr Lys  
50 55 60  
Lys Pro Lys Gly Phe Gly Phe Val Glu Met Gln Glu Glu Ser Val Ser  
65 70 75 80  
Glu Ala Ile Ala Lys Leu Asp Asn Thr Asp Phe Met Gly Arg Thr Ile  
85 90 95  
Arg Val Thr Glu Ala Asn Pro Lys Lys Ser  
100 105

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...1473
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

TTAGATTTAA AATTAGATTA AGGATAGAAA ATG AGA ATT TTA CAA AGG GCT TTG 54  
Met Arg Ile Leu Gln Arg Ala Leu  
1 5  
ACT TTT GAA GAT GTG TTG ATG GTG CCT AGA AAG TCT AGC GTT TTA CCT 102  
Thr Phe Glu Asp Val Leu Met Val Pro Arg Lys Ser Ser Val Leu Pro  
10 15 20  
AAA GAT GTG AGC TTA AAG TCT CGC TTA ACT AAA AAC ATT CGT TTG AAT 150  
Lys Asp Val Ser Leu Lys Ser Arg Leu Thr Lys Asn Ile Arg Leu Asn  
25 30 35 40  
ATC CCC TTT ATC AGT GCG GCT ATG GAT ACG GTT ACA GAG CAT AAA ACC 198

|                   |                   |                   |                   |                   |            |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |     |
|-------------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| Ile               | Pro               | Phe               | Ile               | Ser<br>45         | Ala        | Ala               | Met               | Asp               | Thr<br>50         | Val               | Thr               | Glu               | His               | Lys<br>55         | Thr               |     |
| GCT<br>Ala        | ATC<br>Ile        | GCT<br>Ala        | ATG<br>Met<br>60  | CGC<br>Ala        | CGC<br>Arg | CTT<br>Leu        | GGG<br>Gly        | GGT<br>Gly<br>65  | ATT<br>Ile        | GGC<br>Gly        | ATC<br>Ile        | GTG<br>Val<br>70  | CAT<br>His        | AAA<br>Lys        | AAC<br>Asn        | 246 |
| ATG<br>Met        | GAT<br>Asp        | ATT<br>Ile<br>75  | CAA<br>Gln        | ACG<br>Thr        | CAA<br>Gln | GTT<br>Val        | AAA<br>Lys<br>80  | GAA<br>Glu        | ATC<br>Ile        | ACT<br>Thr        | AAG<br>Lys        | GTT<br>Val<br>85  | AAA<br>Lys        | AAA<br>Lys        | AGC<br>Ser        | 294 |
| GAG<br>Glu        | AGC<br>Ser<br>90  | GGG<br>Gly        | GTG<br>Val        | ATT<br>Ile        | AAT<br>Asn | GAT<br>Asp<br>95  | CCT<br>Pro        | ATT<br>Ile        | TTT<br>Phe        | ATC<br>Ile        | CAT<br>His<br>100 | CGC<br>Ala        | CAC<br>His        | AGG<br>Arg        | ACG<br>Thr        | 342 |
| CTA<br>Leu<br>105 | CGC<br>Ala        | GAC<br>Asp        | GCT<br>Ala        | AAA<br>Lys<br>110 | GTC<br>Val | ATA<br>Ile        | ACG<br>Thr        | GAT<br>Asp        | AAT<br>Asn        | TAC<br>Tyr<br>115 | AAG<br>Lys        | ATT<br>Ile        | TCA<br>Ser        | GGC<br>Gly        | GTG<br>Val<br>120 | 390 |
| CCT<br>Pro        | GTG<br>Val        | GTA<br>Val        | GAT<br>Asp<br>125 | GAT<br>Asp        | AAG<br>Lys | GGG<br>Gly        | TTG<br>Leu        | TTG<br>Leu        | ATT<br>Ile<br>130 | GGG<br>Gly        | ATT<br>Ile        | TTA<br>Leu        | ACC<br>Thr        | AAC<br>Asn<br>135 | AGA<br>Arg        | 438 |
| GAT<br>Asp        | GTG<br>Val        | CGC<br>Arg        | TTT<br>Phe<br>140 | GAA<br>Glu        | ACC<br>Thr | GAT<br>Asp        | TTG<br>Leu        | AGT<br>Ser<br>145 | AAA<br>Lys        | AAA<br>Lys        | GTG<br>Val        | GGC<br>Gly        | GAT<br>Asp<br>150 | GTG<br>Val        | ATG<br>Met        | 486 |
| ACT<br>Thr        | AAA<br>Lys        | ATG<br>Met<br>155 | CCT<br>Pro        | TTA<br>Leu        | GTT<br>Val | ACC<br>Thr        | GCT<br>Ala<br>160 | CAT<br>His        | GTG<br>Val        | GGT<br>Gly        | ATC<br>Ile        | AGT<br>Ser<br>165 | TTG<br>Leu        | GAT<br>Asp        | GAA<br>Glu        | 534 |
| GCG<br>Ala        | AGC<br>Ser<br>170 | GAT<br>Asp        | TTG<br>Leu        | ATG<br>Met        | CAC<br>His | AAG<br>Lys<br>175 | CAT<br>His        | AAG<br>Lys        | ATT<br>Ile        | GAA<br>Glu        | AAA<br>Lys<br>180 | TTG<br>Leu        | CCC<br>Pro        | ATT<br>Ile        | GTG<br>Val        | 582 |
| GAT<br>Asp<br>185 | AAA<br>Lys        | GAT<br>Asp        | AAT<br>Asn        | GTC<br>Val<br>190 | TTA<br>Leu | AAA<br>Lys        | GGC<br>Gly        | TTG<br>Leu        | ATC<br>Ile        | ACG<br>Thr<br>195 | ATC<br>Ile        | AAA<br>Lys        | GAT<br>Asp        | ATT<br>Ile        | CAA<br>Gln<br>200 | 630 |
| AAA<br>Lys        | CGC<br>Arg        | ATT<br>Ile        | GAA<br>Glu<br>205 | TAC<br>Tyr        | CCT<br>Pro | GAG<br>Glu        | GCC<br>Ala        | AAT<br>Asn        | AAA<br>Lys<br>210 | GAT<br>Asp        | GAT<br>Asp        | TTT<br>Phe        | GGG<br>Gly        | AGG<br>Arg<br>215 | TTG<br>Leu        | 678 |
| AGA<br>Arg        | GTG<br>Val        | GGG<br>Gly        | GCG<br>Ala<br>220 | GCT<br>Ala        | ATT<br>Ile | GGA<br>Gly        | GTG<br>Val        | GGG<br>Gly<br>225 | CAG<br>Gln        | TTG<br>Leu        | GAT<br>Asp        | AGG<br>Arg        | GCT<br>Ala<br>230 | GAG<br>Glu        | ATG<br>Met        | 726 |
| TTA<br>Leu        | GTT<br>Val        | AAA<br>Lys<br>235 | GCG<br>Ala        | GGG<br>Gly        | GTG<br>Val | GAT<br>Asp        | GCA<br>Ala<br>240 | CTG<br>Leu        | GTG<br>Val        | CTA<br>Leu        | GAC<br>Asp        | AGC<br>Ser<br>245 | GCA<br>Ala        | CAT<br>His        | GGG<br>Gly        | 774 |
| CAT<br>His        | TCA<br>Ser<br>250 | GCC<br>Ala        | AAT<br>Asn        | ATC<br>Ile        | TTA<br>Leu | CAC<br>His<br>255 | ACT<br>Thr        | TTA<br>Leu        | GAA<br>Glu        | GAG<br>Glu        | ATT<br>Ile<br>260 | AAA<br>Lys        | AAA<br>Lys        | AGC<br>Ser        | TTG<br>Leu        | 822 |
| GTA<br>Val<br>265 | GTG<br>Val        | GAT<br>Asp        | GTG<br>Val        | ATT<br>Ile<br>270 | GTG<br>Val | GGG<br>Gly        | AAT<br>Asn        | GTG<br>Val        | GTT<br>Val        | ACT<br>Thr<br>275 | AAA<br>Lys        | GAA<br>Glu        | GCC<br>Ala        | ACA<br>Thr        | AGC<br>Ser<br>280 | 870 |

|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |            |                   |                   |                   |                   |                   |      |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|------|
| GAT<br>Asp        | TTG<br>Leu        | ATT<br>Ile        | AGC<br>Ser        | GCG<br>Ala<br>285 | GGA<br>Gly        | GCA<br>Ala        | GAC<br>Asp        | GCT<br>Ala<br>290 | ATT<br>Ile        | AAA<br>Lys | GTG<br>Val        | GGT<br>Gly        | ATT<br>Ile        | GGG<br>Gly<br>295 | CCA<br>Pro        | 918  |      |
| GGA<br>Gly        | AGC<br>Ser        | ATT<br>Ile        | TGC<br>Cys<br>300 | ACC<br>Thr        | ACT<br>Thr        | AGG<br>Arg        | ATT<br>Ile        | GTG<br>Val<br>305 | GCT<br>Ala        | GGG<br>Gly | GTG<br>Val        | GGA<br>Gly        | ATG<br>Met<br>310 | CCC<br>Pro        | CAA<br>Gln        | 966  |      |
| GTG<br>Val        | AGC<br>Ser        | GCG<br>Ala<br>315 | ATT<br>Ile        | GAT<br>Asp        | AAT<br>Asn        | TGC<br>Cys        | GTA<br>Val<br>320 | GAA<br>Glu        | GTG<br>Val        | GCG<br>Ala | TCT<br>Ser        | AAA<br>Lys<br>325 | TTT<br>Phe        | GAT<br>Asp        | ATT<br>Ile        | 1014 |      |
| CCT<br>Pro        | GTG<br>Val<br>330 | ATT<br>Ile        | GCA<br>Ala        | GAT<br>Asp        | GGA<br>Gly        | GGG<br>Gly<br>335 | ATC<br>Ile        | CGC<br>Arg        | TAT<br>Tyr        | TCA<br>Ser | GGC<br>Gly<br>340 | GAT<br>Asp        | GTG<br>Val        | GCT<br>Ala        | AAG<br>Lys        | 1062 |      |
| GCT<br>Ala<br>345 | TTG<br>Leu        | GCT<br>Ala        | TTG<br>Leu        | GGG<br>Gly<br>350 | GCA<br>Ala        | TCA<br>Ser        | AGC<br>Ser        | GTG<br>Val        | ATG<br>Met<br>355 | ATA<br>Ile | GGC<br>Gly        | TCT<br>Ser        | TTA<br>Leu        | CTC<br>Leu        | GCT<br>Ala<br>360 | 1110 |      |
| GGC<br>Gly        | ACA<br>Thr        | GAA<br>Glu        | GAA<br>Glu<br>365 | TCT<br>Ser        | CCT<br>Pro        | GGG<br>Gly        | GAT<br>Asp        | TTT<br>Phe<br>370 | ATG<br>Met        | ATC<br>Ile | TAT<br>Tyr        | CAA<br>Gln        | GGG<br>Gly<br>375 | AGG<br>Arg        | CAA<br>Gln        | 1158 |      |
| TAT<br>Tyr        | AAA<br>Lys        | AGC<br>Ser        | TAT<br>Tyr<br>380 | AGG<br>Arg        | GGC<br>Gly        | ATG<br>Met        | GGC<br>Gly<br>385 | AGC<br>Ser        | ATT<br>Ile        | GGG<br>Gly | GCT<br>Ala        | ATG<br>Met<br>390 | ACT<br>Thr        | AAA<br>Lys        | GGG<br>Gly        | 1206 |      |
| AGC<br>Ser        | TCT<br>Ser        | GAT<br>Asp<br>395 | AGG<br>Arg        | TAT<br>Tyr        | TTT<br>Phe        | CAA<br>Gln        | GAG<br>Glu<br>400 | GGC<br>Gly        | GTA<br>Val        | GCG<br>Ala | AGT<br>Ser        | GAA<br>Glu<br>405 | AAG<br>Lys        | TTA<br>Leu        | GTC<br>Val        | 1254 |      |
| CCA<br>Pro        | GAA<br>Glu<br>410 | GGC<br>Gly        | ATT<br>Ile        | GAA<br>Glu        | GGG<br>Gly        | CGT<br>Arg<br>415 | GTG<br>Val        | CCT<br>Pro        | TAT<br>Tyr        | CGT<br>Arg | GGT<br>Gly<br>420 | AAG<br>Lys        | GTT<br>Val        | TCG<br>Ser        | GAT<br>Asp        | 1302 |      |
| ATG<br>Met<br>425 | ATT<br>Ile        | TTC<br>Phe        | CAA<br>Gln        | TTA<br>Leu        | GTA<br>Val<br>430 | GGG<br>Gly        | GGC<br>Gly        | GTG<br>Val        | CGC<br>Arg        | TCT<br>Ser | TCT<br>Ser        | ATG<br>Met        | GGG<br>Gly        | TAT<br>Tyr        | CAG<br>Gln<br>440 | 1350 |      |
| GGG<br>Gly        | GCG<br>Ala        | AAA<br>Lys        | AAT<br>Asn<br>445 | ATT<br>Ile        | TTG<br>Leu        | GAA<br>Glu        | TTG<br>Leu        | TAT<br>Tyr<br>450 | CAA<br>Gln        | AAC<br>Asn | GCT<br>Ala        | GAA<br>Glu        | TTT<br>Phe        | GTA<br>Val<br>455 | GAA<br>Glu        | 1398 |      |
| ATC<br>Ile        | ACT<br>Thr        | AGC<br>Ser        | GCG<br>Ala<br>460 | GGG<br>Gly        | TTA<br>Leu        | AAA<br>Lys        | GAA<br>Glu        | AGC<br>Ser<br>465 | CAT<br>His        | GTG<br>Val | CAT<br>His        | GGC<br>Gly        | GTG<br>Val        | GAT<br>Asp<br>470 | ATT<br>Ile        | 1446 |      |
| ACT<br>Thr        | AAA<br>Lys        | GAA<br>Glu<br>475 | GCC<br>Ala        | CCT<br>Pro        | AAT<br>Asn        | TAT<br>Tyr        | TAT<br>Tyr<br>480 | GGG<br>Gly        | TGAATTGTAA        |            |                   | AAGAAAACAA        |                   |                   | GACAAAT           |      | 1500 |
| CGTTAAAAAA        |                   |                   | CTCGTTAAAA        |                   |                   | AGCTTGTTTT        |                   |                   | AATGAGTTTT        |            |                   | TAAAACTTAA        |                   |                   | TTGCTACA          |      | 1558 |

(i) SEQUENCE CHARACTERISTICS:

-193-

(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Ile | Leu | Gln | Arg | Ala | Leu | Thr | Phe | Glu | Asp | Val | Leu | Met | Val | 1   | 5   | 10  | 15  |
| Pro | Arg | Lys | Ser | Ser | Val | Leu | Pro | Lys | Asp | Val | Ser | Leu | Lys | Ser | Arg | 20  | 25  | 30  |     |
| Leu | Thr | Lys | Asn | Ile | Arg | Leu | Asn | Ile | Pro | Phe | Ile | Ser | Ala | Ala | Met | 35  | 40  | 45  |     |
| Asp | Thr | Val | Thr | Glu | His | Lys | Thr | Ala | Ile | Ala | Met | Ala | Arg | Leu | Gly | 50  | 55  | 60  |     |
| Gly | Ile | Gly | Ile | Val | His | Lys | Asn | Met | Asp | Ile | Gln | Thr | Gln | Val | Lys | 65  | 70  | 75  | 80  |
| Glu | Ile | Thr | Lys | Val | Lys | Lys | Ser | Glu | Ser | Gly | Val | Ile | Asn | Asp | Pro | 85  | 90  | 95  |     |
| Ile | Phe | Ile | His | Ala | His | Arg | Thr | Leu | Ala | Asp | Ala | Lys | Val | Ile | Thr | 100 | 105 | 110 |     |
| Asp | Asn | Tyr | Lys | Ile | Ser | Gly | Val | Pro | Val | Val | Asp | Asp | Lys | Gly | Leu | 115 | 120 | 125 |     |
| Leu | Ile | Gly | Ile | Leu | Thr | Asn | Arg | Asp | Val | Arg | Phe | Glu | Thr | Asp | Leu | 130 | 135 | 140 |     |
| Ser | Lys | Lys | Val | Gly | Asp | Val | Met | Thr | Lys | Met | Pro | Leu | Val | Thr | Ala | 145 | 150 | 155 | 160 |
| His | Val | Gly | Ile | Ser | Leu | Asp | Glu | Ala | Ser | Asp | Leu | Met | His | Lys | His | 165 | 170 | 175 |     |
| Lys | Ile | Glu | Lys | Leu | Pro | Ile | Val | Asp | Lys | Asp | Asn | Val | Leu | Lys | Gly | 180 | 185 | 190 |     |
| Leu | Ile | Thr | Ile | Lys | Asp | Ile | Gln | Lys | Arg | Ile | Glu | Tyr | Pro | Glu | Ala | 195 | 200 | 205 |     |
| Asn | Lys | Asp | Asp | Phe | Gly | Arg | Leu | Arg | Val | Gly | Ala | Ala | Ile | Gly | Val | 210 | 215 | 220 |     |
| Gly | Gln | Leu | Asp | Arg | Ala | Glu | Met | Leu | Val | Lys | Ala | Gly | Val | Asp | Ala | 225 | 230 | 235 | 240 |
| Leu | Val | Leu | Asp | Ser | Ala | His | Gly | His | Ser | Ala | Asn | Ile | Leu | His | Thr | 245 | 250 | 255 |     |
| Leu | Glu | Glu | Ile | Lys | Lys | Ser | Leu | Val | Val | Asp | Val | Ile | Val | Gly | Asn | 260 | 265 | 270 |     |
| Val | Val | Thr | Lys | Glu | Ala | Thr | Ser | Asp | Leu | Ile | Ser | Ala | Gly | Ala | Asp | 275 | 280 | 285 |     |
| Ala | Ile | Lys | Val | Gly | Ile | Gly | Pro | Gly | Ser | Ile | Cys | Thr | Thr | Arg | Ile | 290 | 295 | 300 |     |
| Val | Ala | Gly | Val | Gly | Met | Pro | Gln | Val | Ser | Ala | Ile | Asp | Asn | Cys | Val | 305 | 310 | 315 | 320 |
| Glu | Val | Ala | Ser | Lys | Phe | Asp | Ile | Pro | Val | Ile | Ala | Asp | Gly | Gly | Ile | 325 | 330 | 335 |     |
| Arg | Tyr | Ser | Gly | Asp | Val | Ala | Lys | Ala | Leu | Ala | Leu | Gly | Ala | Ser | Ser | 340 | 345 | 350 |     |
| Val | Met | Ile | Gly | Ser | Leu | Leu | Ala | Gly | Thr | Glu | Glu | Ser | Pro | Gly | Asp | 355 | 360 | 365 |     |
| Phe | Met | Ile | Tyr | Gln | Gly | Arg | Gln | Tyr | Lys | Ser | Tyr | Arg | Gly | Met | Gly | 370 | 375 | 380 |     |
| Ser | Ile | Gly | Ala | Met | Thr | Lys | Gly | Ser | Ser | Asp | Arg | Tyr | Phe | Gln | Glu | 385 | 390 | 395 | 400 |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Val | Ala | Ser | Glu | Lys | Leu | Val | Pro | Glu | Gly | Ile | Glu | Gly | Arg | Val |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Pro | Tyr | Arg | Gly | Lys | Val | Ser | Asp | Met | Ile | Phe | Gln | Leu | Val | Gly | Gly |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Val | Arg | Ser | Ser | Met | Gly | Tyr | Gln | Gly | Ala | Lys | Asn | Ile | Leu | Glu | Leu |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Tyr | Gln | Asn | Ala | Glu | Phe | Val | Glu | Ile | Thr | Ser | Ala | Gly | Leu | Lys | Glu |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Ser | His | Val | His | Gly | Val | Asp | Ile | Thr | Lys | Glu | Ala | Pro | Asn | Tyr | Tyr |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 919 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 58...876
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

|                                                                 |            |            |            |            |          |     |    |
|-----------------------------------------------------------------|------------|------------|------------|------------|----------|-----|----|
| TAATGAAAAA                                                      | TAGTTCATGA | ACGCTTTTGC | ATTAAGGCTC | AAAAAAAGCG | CCGTTTAA | ATG | 60 |
|                                                                 |            |            |            |            |          | Met |    |
|                                                                 |            |            |            |            |          | 1   |    |
| GAT TTT TGT AAA ATA AAA GAA ATT TTA AGG AGG CTT GTG GTG TTG AAA | 108        |            |            |            |          |     |    |
| Asp Phe Cys Lys Ile Lys Glu Ile Leu Arg Arg Leu Val Val Leu Lys |            |            |            |            |          |     |    |
| 5 10 15                                                         |            |            |            |            |          |     |    |
| GAA TTA CGC CAA AAA CGC CCT TTA GTG CAT AAT ATC ACC AAT TAT GTG | 156        |            |            |            |          |     |    |
| Glu Leu Arg Gln Lys Arg Pro Leu Val His Asn Ile Thr Asn Tyr Val |            |            |            |            |          |     |    |
| 20 25 30                                                        |            |            |            |            |          |     |    |
| GCG GCG CAA TTT GTG GCT AAT GGT TTG TTA GCT TTA GGG GCA TCG CCT | 204        |            |            |            |          |     |    |
| Ala Ala Gln Phe Val Ala Asn Gly Leu Leu Ala Leu Gly Ala Ser Pro |            |            |            |            |          |     |    |
| 35 40 45                                                        |            |            |            |            |          |     |    |
| TTA ATG AGC GAT GCG ATT GAT GAA ATG CGA GAT TTA GCG AAA ATT TCT | 252        |            |            |            |          |     |    |
| Leu Met Ser Asp Ala Ile Asp Glu Met Arg Asp Leu Ala Lys Ile Ser |            |            |            |            |          |     |    |
| 50 55 60 65                                                     |            |            |            |            |          |     |    |
| GAC GCG CTC GCT ATC AAT ATT GGC ACC CTT AAT GAT CGC GCT ATT TTA | 300        |            |            |            |          |     |    |
| Asp Ala Leu Ala Ile Asn Ile Gly Thr Leu Asn Asp Arg Ala Ile Leu |            |            |            |            |          |     |    |
| 70 75 80                                                        |            |            |            |            |          |     |    |
| TGC GCT AAA GAG GCT ATC AAG CAT TAC AAG GCT TTG AAC AAA CCC ATT | 348        |            |            |            |          |     |    |
| Cys Ala Lys Glu Ala Ile Lys His Tyr Lys Ala Leu Asn Lys Pro Ile |            |            |            |            |          |     |    |
| 85 90 95                                                        |            |            |            |            |          |     |    |

[illegible]

- (2) INFORMATION FOR SEQ ID NO:136:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Phe | Cys | Lys | Ile | Lys | Glu | Ile | Leu | Arg | Arg | Leu | Val | Val | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Glu | Leu | Arg | Gln | Lys | Arg | Pro | Leu | Val | His | Asn | Ile | Thr | Asn | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Val | Ala | Ala | Gln | Phe | Val | Ala | Asn | Gly | Leu | Leu | Ala | Leu | Gly | Ala | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Pro | Leu | Met | Ser | Asp | Ala | Ile | Asp | Glu | Met | Arg | Asp | Leu | Ala | Lys | Ile |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ser | Asp | Ala | Leu | Ala | Ile | Asn | Ile | Gly | Thr | Leu | Asn | Asp | Arg | Ala | Ile |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Cys | Ala | Lys | Glu | Ala | Ile | Lys | His | Tyr | Lys | Ala | Leu | Asn | Lys | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ile | Val | Leu | Asp | Pro | Val | Gly | Cys | Ser | Ala | Ser | Ala | Leu | Arg | His | Asp |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Thr | Ser | Leu | Glu | Leu | Leu | Lys | Ser | Gly | Gly | Ile | Ser | Ala | Leu | Arg | Gly |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Asn | Ala | Ala | Glu | Leu | Gly | Ser | Leu | Val | Gly | Ile | Ser | Cys | Glu | Ser | Lys |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Leu | Asp | Ser | Asn | Asp | Ala | Ala | Thr | Pro | Val | Glu | Ile | Ile | Lys | Leu |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Ala | Ala | Gln | Lys | Tyr | Ser | Val | Ile | Ala | Val | Met | Thr | Gly | Lys | Thr | Asp |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Tyr | Val | Ser | Asp | Gly | Lys | Lys | Val | Leu | Ser | Ile | Thr | Gly | Gly | Ser | Glu |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Tyr | Leu | Ala | Leu | Ile | Thr | Gly | Ala | Gly | Cys | Leu | His | Ala | Ala | Ala | Cys |
|     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Ala | Ser | Phe | Leu | Ser | Leu | Lys | Lys | Asp | Pro | Leu | Asp | Ser | Met | Ala | Gln |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Cys | Ala | Leu | Tyr | Lys | Gln | Ala | Ala | Phe | Asn | Ala | Gln | Lys | Lys | Val |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Leu | Glu | Asn | Asn | Gly | Ser | Asn | Gly | Ser | Phe | Leu | Phe | Tyr | Phe | Leu | Asp |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Ala | Leu | Ser | Leu | Pro | Ile | Glu | Leu | Glu | Asn | Ser | Leu | Ile | Lys | Glu | Glu |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Trp |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 78...971
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

|            |            |                 |             |             |            |     |
|------------|------------|-----------------|-------------|-------------|------------|-----|
| ATCCAAATAA | TTGGGCGATT | AAAGAGGGAA      | TTTATTCAAT  | CAAACCAAAT  | AAAAAAATAG | 60  |
| TATTTCCAAG | ATTTTATA   | ATG TTT TGC TTT | GAA AAT TTG | AAT ATT CAA | AAT        | 110 |
|            |            | Met Phe Cys Phe | Glu Asn Leu | Asn Ile Gln | Asn        |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|-----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|-----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|-----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 1   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 5   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 10  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| GMT | ATA | AAA | AGT | AAA | AGT | TTT | GGA | GGA | ATA | GTT | AAA | AGT | ATA | TCA | ATG | 158 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Xaa | Ile | Lys | Ser | Lys | Ser | Phe | Gly | Gly | Ile | Val | Lys | Ser | Ile | Ser | Met |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 15  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 20  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 25  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| AAC | GAT | TTA | CAA | CAA | ATA | ACC | ATC | CCC | ATC | CCA | CCC | CTA | GAG | ATC | CAA | 206 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Asn | Asp | Leu | Gln | Gln | Ile | Thr | Ile | Pro | Ile | Pro | Pro | Leu | Glu | Ile | Gln |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 30  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 35  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 40  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| CAA | GAG | ATC | GTT | AAG | ATT | TTG | GAC | GCT | TTC | ACA | GAA | TTA | AAC | ACA | GAA | 254 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Gln | Glu | Ile | Val | Lys | Ile | Leu | Asp | Ala | Phe | Thr | Glu | Leu | Asn | Thr | Glu |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 45  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 50  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 55  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| TTA | AAC | ACA | GAA | TTA | AAA | GCG | CGC | AAA | AAG | CAA | TAT | GAG | TAT | TAC | CAA | 302 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Leu | Asn | Thr | Glu | Leu | Lys | Ala | Arg | Lys | Lys | Gln | Tyr | Glu | Tyr | Tyr | Gln |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 60  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 65  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 70  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 75  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| AAC | ATG | CTT | TTA | GAC | TTT | AAC | GAT | ATT | AAT | CAA | AAC | CAC | AAA | GAC | GCC | 350 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Asn | Met | Leu | Leu | Asp | Phe | Asn | Asp | Ile | Asn | Gln | Asn | His | Lys | Asp | Ala |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 80  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 85  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 90  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| AAA | ATA | AAA | ACC | TAC | CCT | AAA | CGC | TTG | AAA | ACC | TTA | CTC | CAC | ACT | TTA | 398 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Lys | Ile | Lys | Thr | Tyr | Pro | Lys | Arg | Leu | Lys | Thr | Leu | Leu | His | Thr | Leu |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 95  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 100 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 105 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| GCG | CCT | AAG | GGG | GTG | GAG | TTT | AGG | AAA | TTG | GGG | GAG | GTG | TGT | GAA | AGC | 446 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Ala | Pro | Lys | Gly | Val | Glu | Phe | Arg | Lys | Leu | Gly | Glu | Val | Cys | Glu | Ser |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 110 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 115 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 120 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ACA | AAT | AAA | AAA | ACA | CTC | AAA | ATA | AGC | GAA | GTA | AGT | GAA | GTA | AAA | AAT | 494 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Thr | Asn | Lys | Lys | Thr | Leu | Lys | Ile | Ser | Glu | Val | Ser | Glu | Val | Lys | Asn |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 125 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 130 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 135 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| AAG | GGA | ATG | TAT | CCA | GTG | ATA | AAT | TCA | GGG | AGG | GAT | TTG | TAT | GGT | TAT | 542 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Lys | Gly | Met | Tyr | Pro | Val | Ile | Asn | Ser | Gly | Arg | Asp | Leu | Tyr | Gly | Tyr |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 140 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 145 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 150 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 155 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| TAC | CAT | GAT | TTT | AAC | AAT | GAT | GGA | GAA | AAT | ATA | ACT | ATT | GCA | TCT | AGG | 590 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Tyr | His | Asp | Phe | Asn | Asn | Asp | Gly | Glu | Asn | Ile | Thr | Ile | Ala | Ser | Arg |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 160 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 165 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 170 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| GGA | GAA | TAT | GCA | GGA | TTT | ATA | AAC | TAT | TTC | AAT | GAA | AAA | TTT | TTT | GCA | 638 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Gly | Glu | Tyr | Ala | Gly | Phe | Ile | Asn | Tyr | Phe | Asn | Glu | Lys | Phe | Phe | Ala |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 175 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 180 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 185 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| GGG | GGT | CTA | TGT | TAT | CCC | TAT | AAA | GTT | AAA | GAC | ACT | AAC | GAG | CTT | TTA | 686 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Gly | Gly | Leu | Cys | Tyr | Pro | Tyr | Lys | Val | Lys | Asp | Thr | Asn | Glu | Leu | Leu |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 190 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 195 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 200 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ACA | AAA | TTT | TTA | TAC | TTT | TAT | CTC | AAA | ACT | AAT | GAA | ATC | CAA | ATT | ATG | 734 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Thr | Lys | Phe | Leu | Tyr | Phe | Tyr | Leu | Lys | Thr | Asn | Glu | Ile | Gln | Ile | Met |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 205 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 210 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 215 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| GAG | AAC | CTT | GTT | TTT | CGT | GGC | AGT | ATC | CCC | GCA | CTC | AAT | AAA | GCA | GAT | 782 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Glu | Asn | Leu | Val | Phe | Arg | Gly | Ser | Ile | Pro | Ala | Leu | Asn | Lys | Ala | Asp |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 220 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 225 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 230 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | 235 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |





|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| Ser               | Val               | Arg               | Glu<br>105        | Phe               | Ser               | Gly               | Asn               | Tyr<br>110        | Asp               | Asp               | Trp               | Tyr               | Ile<br>115        | Ala               | Ser               |      |
| ACT<br>Thr        | CTG<br>Leu        | ATC<br>Ile<br>120 | GCT<br>Ala        | AAA<br>Lys        | CAG<br>Gln        | CAA<br>Gln        | GAG<br>Glu<br>125 | GCC<br>Ala        | GAA<br>Glu        | CGC<br>Arg        | AAT<br>Asn        | AAA<br>Lys<br>130 | AAA<br>Lys        | CTC<br>Leu        | AAA<br>Lys        | 440  |
| GAA<br>Glu        | AAA<br>Lys<br>135 | GAA<br>Glu        | GAG<br>Glu        | CTA<br>Leu        | GAA<br>Glu        | AAA<br>Lys<br>140 | TTC<br>Phe<br>140 | ATC<br>Ile        | GCG<br>Ala        | CGC<br>Arg        | TTT<br>Phe<br>145 | ARN<br>Xaa        | NNN<br>Xaa        | NAC<br>Xaa        | GCT<br>Ala        | 488  |
| TCT<br>Ser<br>150 | AAA<br>Lys        | GCC<br>Ala        | AAG<br>Lys        | CAA<br>Gln<br>155 | GCC<br>Ala        | ACC<br>Thr        | AGC<br>Ser        | CGC<br>Arg        | CAA<br>Gln<br>160 | AAA<br>Lys        | CAA<br>Gln        | CTG<br>Leu        | GAT<br>Asp        | AAA<br>Lys        | TTA<br>Leu<br>165 | 536  |
| GAC<br>Asp        | ATT<br>Ile        | CAA<br>Gln        | AGT<br>Ser<br>170 | TTA<br>Leu        | GCG<br>Ala        | GTA<br>Val        | TCT<br>Ser        | AGC<br>Ser        | AGG<br>Arg<br>175 | AGG<br>Arg        | GAT<br>Asp        | CCT<br>Pro        | AGC<br>Ser        | ATT<br>Ile<br>180 | ATT<br>Ile        | 584  |
| TTT<br>Phe        | AAA<br>Lys        | CCC<br>Pro<br>185 | AAA<br>Lys        | CGC<br>Arg        | ACC<br>Thr        | ATT<br>Ile        | GGT<br>Gly<br>190 | AAT<br>Asn<br>190 | GAA<br>Glu        | GCC<br>Ala        | TTA<br>Leu        | GAG<br>Glu<br>195 | TGC<br>Cys<br>195 | GAA<br>Glu        | AAC<br>Asn        | 632  |
| ATC<br>Ile        | TCT<br>Ser<br>200 | AAA<br>Lys        | AGT<br>Ser        | TAT<br>Tyr        | GAC<br>Asp        | GAC<br>Asp        | CAA<br>Gln<br>205 | ATC<br>Ile        | GTT<br>Val        | TTA<br>Leu        | AAT<br>Asn<br>210 | CAA<br>Gln<br>210 | GTG<br>Val        | AGC<br>Ser        | TTG<br>Leu        | 680  |
| AAA<br>Lys<br>215 | GTG<br>Val        | ATG<br>Met        | CCT<br>Pro        | AAA<br>Lys        | GAC<br>Asp        | AAG<br>Lys<br>220 | ATC<br>Ile        | GCC<br>Ala        | CTC<br>Leu        | ATA<br>Ile        | GGG<br>Gly<br>225 | CCA<br>Pro        | AAC<br>Asn        | GGC<br>Gly        | GTG<br>Val        | 728  |
| GGT<br>Gly<br>230 | AAA<br>Lys        | TCC<br>Ser        | ACG<br>Thr        | CTT<br>Leu        | TGT<br>Cys<br>235 | AAA<br>Lys        | ATT<br>Ile        | CTA<br>Leu        | GTA<br>Val        | GAA<br>Glu<br>240 | GAA<br>Glu        | TTA<br>Leu        | AAG<br>Lys        | CCG<br>Pro        | GAT<br>Asp<br>245 | 776  |
| AAG<br>Lys        | GGC<br>Gly        | GTG<br>Val        | GTG<br>Val        | AAA<br>Lys<br>250 | TGG<br>Trp        | GGG<br>Gly        | GCG<br>Ala        | ACG<br>Thr        | GTT<br>Val<br>255 | TCA<br>Ser        | AAA<br>Lys        | GGC<br>Gly        | TAT<br>Tyr        | TTC<br>Phe<br>260 | CCT<br>Pro        | 824  |
| CAA<br>Gln        | AAC<br>Asn        | GTG<br>Val        | AGC<br>Ser<br>265 | GAA<br>Glu        | GAA<br>Glu        | ATT<br>Ile        | AGC<br>Ser        | GGG<br>Gly<br>270 | GAA<br>Glu        | GAG<br>Glu        | ACC<br>Thr        | TTG<br>Leu<br>275 | TAT<br>Tyr        | CAA<br>Gln        | TGG<br>Trp        | 872  |
| CTC<br>Leu        | TTT<br>Phe<br>280 | AAC<br>Asn        | TTC<br>Phe        | AAT<br>Asn        | AAA<br>Lys        | AAG<br>Lys        | ATT<br>Ile<br>285 | GAA<br>Glu        | AGC<br>Ser        | GCT<br>Ala        | GAG<br>Glu<br>290 | GTT<br>Val        | AGG<br>Arg        | AAC<br>Asn        | GCT<br>Ala        | 920  |
| TTA<br>Leu        | GGG<br>Gly<br>295 | AGG<br>Arg        | ATG<br>Met        | CTG<br>Leu        | TTT<br>Phe        | AAT<br>Asn<br>300 | GGC<br>Gly        | GAA<br>Glu        | GAG<br>Glu        | CAA<br>Gln<br>305 | GAA<br>Glu        | AAA<br>Lys        | TGC<br>Cys        | GTG<br>Val        | AAC<br>Asn        | 968  |
| GCT<br>Ala<br>310 | TTA<br>Leu        | AGT<br>Ser        | GGG<br>Gly        | GGC<br>Gly        | GAA<br>Glu<br>315 | AAA<br>Lys        | CAC<br>His        | CGA<br>Arg        | ATG<br>Met        | GTT<br>Val<br>320 | TTA<br>Leu        | TCC<br>Ser        | AAG<br>Lys        | CTC<br>Leu        | ATG<br>Met<br>325 | 1016 |
| CTA<br>Leu        | GAG<br>Glu        | GGG<br>Gly        | GGG<br>Gly        | AAT<br>Asn<br>330 | TTT<br>Phe        | TTA<br>Leu        | GTC<br>Val        | TTA<br>Leu<br>335 | GAT<br>Asp        | GAG<br>Glu        | CCA<br>Pro        | ACC<br>Thr        | AAC<br>Asn        | CAT<br>His<br>340 | TTG<br>Leu        | 1064 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| GAT TTA GAA GCG ATT ATC GCT TTA GGC GAA GCG CTC TTT AAA TTT GAT   | 1112 |
| Asp Leu Glu Ala Ile Ile Ala Leu Gly Glu Ala Leu Phe Lys Phe Asp   |      |
| 345 350 355                                                       |      |
|                                                                   |      |
| GGG GCG CTG ATT TGC GTA AGC CAT GAC AGA GAG CTC ATT GAT GCG TAT   | 1160 |
| Gly Ala Leu Ile Cys Val Ser His Asp Arg Glu Leu Ile Asp Ala Tyr   |      |
| 360 365 370                                                       |      |
|                                                                   |      |
| GCT AAT AGG ATC ATT GAA TTA GTC CCA AGC CCT AAA GGC GCT TCA ATC   | 1208 |
| Ala Asn Arg Ile Ile Glu Leu Val Pro Ser Pro Lys Gly Ala Ser Ile   |      |
| 375 380 385                                                       |      |
|                                                                   |      |
| ATT GAT TTT AAA GGC AGT TAT GAA GAG TAT TTG GCG AGC AAA AAA TGAAA | 1258 |
| Ile Asp Phe Lys Gly Ser Tyr Glu Glu Tyr Leu Ala Ser Lys Lys       |      |
| 390 395 400                                                       |      |
|                                                                   |      |
| CCGCAAGACA TTGAAATCGT TCAAAGCGTT TTAGAGATTA CAGGACC               | 1305 |

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Tyr Glu Cys Glu Val Ala Ile Glu Lys Ile Leu Glu Asp Leu Gly |  |
| 1 5 10 15                                                       |  |
| Ile Pro Ser Ser Lys His Asn Asp Leu Met Lys Thr Leu Pro Ser Ser |  |
| 20 25 30                                                        |  |
| Asp Lys Phe Lys Ile Leu Leu Ala Gln Val Leu Phe Pro Lys Pro Asp |  |
| 35 40 45                                                        |  |
| Ile Leu Leu Leu Asp Glu Pro Thr Asn Asn Leu Asp Leu Asn Ala Ile |  |
| 50 55 60                                                        |  |
| Glu Trp Leu Glu Asn Asn Leu Lys Arg His Glu Gly Thr Met Val Val |  |
| 65 70 75 80                                                     |  |
| Ile Ser His Asp Arg His Phe Leu Asn Ala Val Cys Thr His Ile Leu |  |
| 85 90 95                                                        |  |
| Asp Leu Asp Phe His Ser Val Arg Glu Phe Ser Gly Asn Tyr Asp Asp |  |
| 100 105 110                                                     |  |
| Trp Tyr Ile Ala Ser Thr Leu Ile Ala Lys Gln Gln Glu Ala Glu Arg |  |
| 115 120 125                                                     |  |
| Asn Lys Lys Leu Lys Glu Lys Glu Glu Leu Glu Lys Phe Ile Ala Arg |  |
| 130 135 140                                                     |  |
| Phe Xaa Xaa Xaa Ala Ser Lys Ala Lys Gln Ala Thr Ser Arg Gln Lys |  |
| 145 150 155 160                                                 |  |
| Gln Leu Asp Lys Leu Asp Ile Gln Ser Leu Ala Val Ser Ser Arg Arg |  |
| 165 170 175                                                     |  |
| Asp Pro Ser Ile Ile Phe Lys Pro Lys Arg Thr Ile Gly Asn Glu Ala |  |
| 180 185 190                                                     |  |
| Leu Glu Cys Glu Asn Ile Ser Lys Ser Tyr Asp Asp Gln Ile Val Leu |  |
| 195 200 205                                                     |  |
| Asn Gln Val Ser Leu Lys Val Met Pro Lys Asp Lys Ile Ala Leu Ile |  |
| 210 215 220                                                     |  |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Pro | Asn | Gly | Val | Gly | Lys | Ser | Thr | Leu | Cys | Lys | Ile | Leu | Val | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Leu | Lys | Pro | Asp | Lys | Gly | Val | Val | Lys | Trp | Gly | Ala | Thr | Val | Ser |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Lys | Gly | Tyr | Phe | Pro | Gln | Asn | Val | Ser | Glu | Glu | Ile | Ser | Gly | Glu | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Thr | Leu | Tyr | Gln | Trp | Leu | Phe | Asn | Phe | Asn | Lys | Lys | Ile | Glu | Ser | Ala |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Glu | Val | Arg | Asn | Ala | Leu | Gly | Arg | Met | Leu | Phe | Asn | Gly | Glu | Glu | Gln |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Glu | Lys | Cys | Val | Asn | Ala | Leu | Ser | Gly | Gly | Glu | Lys | His | Arg | Met | Val |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Leu | Ser | Lys | Leu | Met | Leu | Glu | Gly | Gly | Asn | Phe | Leu | Val | Leu | Asp | Glu |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Pro | Thr | Asn | His | Leu | Asp | Leu | Glu | Ala | Ile | Ile | Ala | Leu | Gly | Glu | Ala |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Leu | Phe | Lys | Phe | Asp | Gly | Ala | Leu | Ile | Cys | Val | Ser | His | Asp | Arg | Glu |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Leu | Ile | Asp | Ala | Tyr | Ala | Asn | Arg | Ile | Ile | Glu | Leu | Val | Pro | Ser | Pro |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Lys | Gly | Ala | Ser | Ile | Ile | Asp | Phe | Lys | Gly | Ser | Tyr | Glu | Glu | Tyr | Leu |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Ala | Ser | Lys | Lys |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...756
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

|            |          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AAAAGCAGGG | ATACTAGA | ATG | CAA | ATG | ATG | CAC | AAT | TTG | AGT | TTT | TTG | GGC |     |     |     |     |
|            |          | Met | Gln | Met | Met | His | Asn | Leu | Ser | Phe | Leu | Gly | 51  |     |     |     |
|            |          | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     |
| ATG        | TTT      | TTA | GCC | GCT | TTG | AGC | ATG | TCT | TTA | GGG | CAT | TGT | GTG | GGC | ATG | 99  |
| Met        | Phe      | Leu | Ala | Ala | Leu | Ser | Met | Ser | Leu | Gly | His | Cys | Val | Gly | Met |     |
|            |          |     | 15  |     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |
| TGT        | GGG      | GGG | ATT | GTG | AGC | GCG | TTC | AGT | CAA | ATA | AGA | TTT | TCT | AAA | GTT | 147 |
| Cys        | Gly      | Gly | Ile | Val | Ser | Ala | Phe | Ser | Gln | Ile | Arg | Phe | Ser | Lys | Val |     |
|            |          | 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |
| ACA        | AGC      | TTT | TCT | TAC | CAG | CTC | ACT | TGC | CAT | GCC | CTT | TAT | AAT | GTA | GGG | 195 |
| Thr        | Ser      | Phe | Ser | Tyr | Gln | Leu | Thr | Cys | His | Ala | Leu | Tyr | Asn | Val | Gly |     |
|            | 45       |     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |     |

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AGG ATC AGC ACT TAC ATG CTT TTA GGG GCT ATA GCG GCA AGT TTG GGG   | 243 |
| Arg Ile Ser Thr Tyr Met Leu Leu Gly Ala Ile Ala Ala Ser Leu Gly   |     |
| 60 65 70 75                                                       |     |
| CAT AGT CTT AGC GTG AGC ATG GGT TTT AGG GGT GTT TTA TTC ATT AGC   | 291 |
| His Ser Leu Ser Val Ser Met Gly Phe Arg Gly Val Leu Phe Ile Ser   |     |
| 80 85 90                                                          |     |
| ATG GGG ATT ATT TTG ATC TGT TTA GCG TTG CTA GGG GCA AGA ATG GAA   | 339 |
| Met Gly Ile Ile Leu Ile Cys Leu Ala Leu Leu Gly Ala Arg Met Glu   |     |
| 95 100 105                                                        |     |
| AAA TTA AGC TTT CAA ATC CCT TTT ATT TCT TTT TTG ATG AAA AAA ACC   | 387 |
| Lys Leu Ser Phe Gln Ile Pro Phe Ile Ser Phe Leu Met Lys Lys Thr   |     |
| 110 115 120                                                       |     |
| TTG CAA TCT CAA AAC ATT CTA GGG CTG TAT TTC TTA GGC GTG TTG AAC   | 435 |
| Leu Gln Ser Gln Asn Ile Leu Gly Leu Tyr Phe Leu Gly Val Leu Asn   |     |
| 125 130 135                                                       |     |
| GGG TTT TTA CCT TGC ATG ATG GTG TAT TCG TTT TTA GCG AGC GTG ATT   | 483 |
| Gly Phe Leu Pro Cys Met Met Val Tyr Ser Phe Leu Ala Ser Val Ile   |     |
| 140 145 150 155                                                   |     |
| CTC AGT CAT AGC GCG TTT ATG GGA GCG ATG CTA GGC CTT TCT TTT GGG   | 531 |
| Leu Ser His Ser Ala Phe Met Gly Ala Met Leu Gly Leu Ser Phe Gly   |     |
| 160 165 170                                                       |     |
| CTT GGC ACC AGC ATG CCG TTG TTT TTA ATG GGG ATT TTT TTA AGC AAA   | 579 |
| Leu Gly Thr Ser Met Pro Leu Phe Leu Met Gly Ile Phe Leu Ser Lys   |     |
| 175 180 185                                                       |     |
| ATT TCC GTT TCT TAC AGG AAA TTT TTC AAT CTT TTG TCT AAA ATT TTA   | 627 |
| Ile Ser Val Ser Tyr Arg Lys Phe Phe Asn Leu Leu Ser Lys Ile Leu   |     |
| 190 195 200                                                       |     |
| ATG GGG GTT TTT GGG CTT TAT ATC CTT TAT ATG GGG ATC ATG CTC ATT   | 675 |
| Met Gly Val Phe Gly Leu Tyr Ile Leu Tyr Met Gly Ile Met Leu Ile   |     |
| 205 210 215                                                       |     |
| AAC CAC AAA ATG CCT CAT GCC ATG CAT CAT CAA AAC AAC ACC ACT CAG   | 723 |
| Asn His Lys Met Pro His Ala Met His His Gln Asn Asn Thr Thr Gln   |     |
| 220 225 230 235                                                   |     |
| CAT GAT CAT AAA GGA GTG CAT TCG CAT GAA CAC TAACAAAGCC CTTTTTTTGG | 776 |
| His Asp His Lys Gly Val His Ser His Glu His                       |     |
| 240 245                                                           |     |
| ACAGAGACGG CATTATCAAT ATTGA                                       | 801 |

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 246 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met Gln Met Met His Asn Leu Ser Phe Leu Gly Met Phe Leu Ala Ala  
1 5 10 15  
Leu Ser Met Ser Leu Gly His Cys Val Gly Met Cys Gly Gly Ile Val  
20 25 30  
Ser Ala Phe Ser Gln Ile Arg Phe Ser Lys Val Thr Ser Phe Ser Tyr  
35 40 45  
Gln Leu Thr Cys His Ala Leu Tyr Asn Val Gly Arg Ile Ser Thr Tyr  
50 55 60  
Met Leu Leu Gly Ala Ile Ala Ala Ser Leu Gly His Ser Leu Ser Val  
65 70 75 80  
Ser Met Gly Phe Arg Gly Val Leu Phe Ile Ser Met Gly Ile Ile Leu  
85 90 95  
Ile Cys Leu Ala Leu Leu Gly Ala Arg Met Glu Lys Leu Ser Phe Gln  
100 105 110  
Ile Pro Phe Ile Ser Phe Leu Met Lys Lys Thr Leu Gln Ser Gln Asn  
115 120 125  
Ile Leu Gly Leu Tyr Phe Leu Gly Val Leu Asn Gly Phe Leu Pro Cys  
130 135 140  
Met Met Val Tyr Ser Phe Leu Ala Ser Val Ile Leu Ser His Ser Ala  
145 150 155 160  
Phe Met Gly Ala Met Leu Gly Leu Ser Phe Gly Leu Gly Thr Ser Met  
165 170 175  
Pro Leu Phe Leu Met Gly Ile Phe Leu Ser Lys Ile Ser Val Ser Tyr  
180 185 190  
Arg Lys Phe Phe Asn Leu Leu Ser Lys Ile Leu Met Gly Val Phe Gly  
195 200 205  
Leu Tyr Ile Leu Tyr Met Gly Ile Met Leu Ile Asn His Lys Met Pro  
210 215 220  
His Ala Met His His Gln Asn Asn Thr Thr Gln His Asp His Lys Gly  
225 230 235 240  
Val His Ser His Glu His  
245

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 735 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...693
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

AAC TGC CTN TCN TCG CTC AAC ACG ATT GTA TTA AAC CAT AAT AAA TTG  
Asn Cys Xaa Xaa Ser Leu Asn Thr Ile Val Leu Asn His Asn Lys Leu  
1 5 10 15

48

|          |     |     |     |     |     |     |            |            |            |      |     |     |     |     |     |     |
|----------|-----|-----|-----|-----|-----|-----|------------|------------|------------|------|-----|-----|-----|-----|-----|-----|
| TAT      | TCT | TTA | GAA | AAA | CGA | GGG | TAT        | GTG        | ATA        | GAG  | GTG | GAT | TTA | AAT | GAT | 96  |
| Tyr      | Ser | Leu | Glu | Lys | Arg | Gly | Tyr        | Val        | Ile        | Glu  | Val | Asp | Leu | Asn | Asp |     |
|          |     | 20  |     |     |     |     |            | 25         |            |      |     |     | 30  |     |     |     |
| TTT      | GAT | TCG | TAT | AAT | GTC | TAT | AAA        | ACG        | CCA        | ACT  | ATA | GGC | AGT | TTT | AAG | 144 |
| Phe      | Asp | Ser | Tyr | Asn | Val | Tyr | Lys        | Thr        | Pro        | Thr  | Ile | Gly | Ser | Phe | Lys |     |
|          |     | 35  |     |     |     |     | 40         |            |            |      |     | 45  |     |     |     |     |
| TTT      | TTT | TCA | TCT | AAT | CGT | TTG | GAT        | AAA        | GGG        | GTG  | TTT | TAT | GAT | AAA | AAT | 192 |
| Phe      | Phe | Ser | Ser | Asn | Arg | Leu | Asp        | Lys        | Gly        | Val  | Phe | Tyr | Asp | Lys | Asn |     |
|          | 50  |     |     |     |     | 55  |            |            |            |      | 60  |     |     |     |     |     |
| CGG      | GTG | TAT | TAC | GAT | CGC | TAC | TAT        | TTA        | GAT        | TAT  | AAC | GAT | TTT | AAA | CCA | 240 |
| Arg      | Val | Tyr | Tyr | Asp | Arg | Tyr | Tyr        | Leu        | Asp        | Tyr  | Asn | Asp | Phe | Lys | Pro |     |
| 65       |     |     |     |     | 70  |     |            |            |            | 75   |     |     |     |     | 80  |     |
| AAA      | CTT | TAT | CCC | GTT | GTG | GAA | AAA        | TCG        | GCA        | TCT  | AAA | AAA | TCT | CAA | AAA | 288 |
| Lys      | Leu | Tyr | Pro | Val | Val | Glu | Lys        | Ser        | Ala        | Ser  | Lys | Lys | Ser | Gln | Lys |     |
|          |     |     | 85  |     |     |     |            | 90         |            |      |     |     |     | 95  |     |     |
| GGC      | GAA | AAA | GGG | AAC | GCT | CCT | ATT        | TAT        | TTG        | CAA  | GAA | AGG | CAT | AAA | GCT | 336 |
| Gly      | Glu | Lys | Gly | Asn | Ala | Pro | Ile        | Tyr        | Leu        | Gln  | Glu | Arg | His | Lys | Ala |     |
|          |     |     | 100 |     |     |     |            | 105        |            |      |     |     | 110 |     |     |     |
| AAA      | GAA | AAT | AAA | CAG | CCT | TTA | GAA        | GAA        | AAC        | AAA  | GTT | AAA | CCA | AGA | AAT | 384 |
| Lys      | Glu | Asn | Lys | Gln | Pro | Leu | Glu        | Glu        | Asn        | Lys  | Val | Lys | Pro | Arg | Asn |     |
|          |     | 115 |     |     |     |     | 120        |            |            |      |     | 125 |     |     |     |     |
| AGC      | GGG | TTT | GAA | GAA | GAA | GAG | GTT        | AAA        | ACC        | AGA  | AGG | CCT | GAG | CCT | ATT | 432 |
| Ser      | Gly | Phe | Glu | Glu | Glu | Glu | Val        | Lys        | Thr        | Arg  | Arg | Pro | Glu | Pro | Ile |     |
|          | 130 |     |     |     |     | 135 |            |            |            |      | 140 |     |     |     |     |     |
| AGG      | GAT | CAA | AAT | AAC | GCC | ACC | CAA        | CAA        | GGC        | GAA  | ACA | AAA | AAC | AAT | GAA | 480 |
| Arg      | Asp | Gln | Asn | Asn | Ala | Thr | Gln        | Gln        | Gly        | Glu  | Thr | Lys | Asn | Asn | Glu |     |
| 145      |     |     |     |     | 150 |     |            |            |            | 155  |     |     |     |     | 160 |     |
| AGT      | AAA | AAC | GCT | CCT | GTC | TTA | AAA        | GAA        | AAC        | GCC  | GCT | AAA | AAA | GAA | GTG | 528 |
| Ser      | Lys | Asn | Ala | Pro | Val | Leu | Lys        | Glu        | Asn        | Ala  | Ala | Lys | Lys | Glu | Val |     |
|          |     |     | 165 |     |     |     |            | 170        |            |      |     |     |     | 175 |     |     |
| CCA      | AAA | CCA | AAT | TCT | AAA | GAA | GAA        | AAA        | CGC        | CGC  | TTG | AAA | GAA | GAA | AAG | 576 |
| Pro      | Lys | Pro | Asn | Ser | Lys | Glu | Glu        | Lys        | Arg        | Arg  | Leu | Lys | Glu | Glu | Lys |     |
|          |     |     | 180 |     |     |     |            | 185        |            |      |     |     | 190 |     |     |     |
| AAA      | AAA | GCC | AAA | GCC | GAA | CAA | AGA        | GCG        | AGA        | GAA  | TTT | GAA | CAA | AGA | GCG | 624 |
| Lys      | Lys | Ala | Lys | Ala | Glu | Gln | Arg        | Ala        | Arg        | Glu  | Phe | Glu | Gln | Arg | Ala |     |
|          |     | 195 |     |     |     |     | 200        |            |            |      |     | 205 |     |     |     |     |
| AGA      | GAG | CAT | CAA | GAA | AGA | GAT | GAA        | AAA        | GAG        | CTT  | GAA | GAA | AGA | AGA | AAA | 672 |
| Arg      | Glu | His | Gln | Glu | Arg | Asp | Glu        | Lys        | Glu        | Leu  | Glu | Glu | Arg | Arg | Lys |     |
|          | 210 |     |     |     |     | 215 |            |            |            |      | 220 |     |     |     |     |     |
| GCT      | TTA | GAA | ATG | AAT | AAG | AAG | TAGGCCTATG | CCAGCTAGGC | AATCTTTTAC | AGAT |     |     |     |     |     | 727 |
| Ala      | Leu | Glu | Met | Asn | Lys | Lys |            |            |            |      |     |     |     |     |     |     |
| 225      |     |     |     |     | 230 |     |            |            |            |      |     |     |     |     |     |     |
| TTGAAAAA |     |     |     |     |     |     |            |            |            |      |     |     |     |     |     | 735 |

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Cys | Xaa | Xaa | Ser | Leu | Asn | Thr | Ile | Val | Leu | Asn | His | Asn | Lys | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Ser | Leu | Glu | Lys | Arg | Gly | Tyr | Val | Ile | Glu | Val | Asp | Leu | Asn | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Asp | Ser | Tyr | Asn | Val | Tyr | Lys | Thr | Pro | Thr | Ile | Gly | Ser | Phe | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Phe | Ser | Ser | Asn | Arg | Leu | Asp | Lys | Gly | Val | Phe | Tyr | Asp | Lys | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Val | Tyr | Tyr | Asp | Arg | Tyr | Tyr | Leu | Asp | Tyr | Asn | Asp | Phe | Lys | Pro |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Lys | Leu | Tyr | Pro | Val | Glu | Lys | Ser | Ala | Ser | Lys | Lys | Ser | Gln | Lys |     |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | Glu | Lys | Gly | Asn | Ala | Pro | Ile | Tyr | Leu | Gln | Glu | Arg | His | Lys | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Glu | Asn | Lys | Gln | Pro | Leu | Glu | Glu | Asn | Lys | Val | Lys | Pro | Arg | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Gly | Phe | Glu | Glu | Glu | Glu | Val | Lys | Thr | Arg | Arg | Pro | Glu | Pro | Ile |
|     | 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Arg | Asp | Gln | Asn | Asn | Ala | Thr | Gln | Gln | Gly | Glu | Thr | Lys | Asn | Asn | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Lys | Asn | Ala | Pro | Val | Leu | Lys | Glu | Asn | Ala | Ala | Lys | Lys | Glu | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Pro | Lys | Pro | Asn | Ser | Lys | Glu | Glu | Lys | Arg | Arg | Leu | Lys | Glu | Glu | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Lys | Ala | Lys | Ala | Glu | Gln | Arg | Ala | Arg | Glu | Phe | Glu | Gln | Arg | Ala |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Glu | His | Gln | Glu | Arg | Asp | Glu | Lys | Glu | Leu | Glu | Glu | Arg | Arg | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Leu | Glu | Met | Asn | Lys | Lys |     |     |     |     |     |     |     |     |     |
| 225 |     |     |     |     | 230 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1047 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...1005
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| AGAAAGAAAC CATTCAAGGA ACGCATTGAT TTG ATG AAT AAA CCA TTT TTA ATC | 54  |
| Met Asn Lys Pro Phe Leu Ile                                      |     |
| 1 5                                                              |     |
| TTA CTC ATA GCC CTA ATT GTC TTT AGC GGC TGT AAC ATG AGA AAA TAT  | 102 |
| Leu Leu Ile Ala Leu Ile Val Phe Ser Gly Cys Asn Met Arg Lys Tyr  |     |
| 10 15 20                                                         |     |
| TTC AAA CCC GCT AAA CAC CAA ATT AAA GGC GAA GCG TAT TTC CCT AAC  | 150 |
| Phe Lys Pro Ala Lys His Gln Ile Lys Gly Glu Ala Tyr Phe Pro Asn  |     |
| 25 30 35                                                         |     |
| CAT TTG CAA GAA AGT ATC GTT TCG TCT AAT CGT TAT GGA GCC ATT TTG  | 198 |
| His Leu Gln Glu Ser Ile Val Ser Ser Asn Arg Tyr Gly Ala Ile Leu  |     |
| 40 45 50 55                                                      |     |
| AAA AAT GGA GCG GTT ATA GGC GAT AAA GGT TTA ACG CAG CTA AGA ATC  | 246 |
| Lys Asn Gly Ala Val Ile Gly Asp Lys Gly Leu Thr Gln Leu Arg Ile  |     |
| 60 65 70                                                         |     |
| GGT AAG AAC TTC AAT TAC GAA AGC AGT TTT TTA AAT GAG AGT CAA GGG  | 294 |
| Gly Lys Asn Phe Asn Tyr Glu Ser Ser Phe Leu Asn Glu Ser Gln Gly  |     |
| 75 80 85                                                         |     |
| TTT TTT ATT CTT GCG CAA GAT TGT TTG AAC AAG ATT GAT AAA AAA ACA  | 342 |
| Phe Phe Ile Leu Ala Gln Asp Cys Leu Asn Lys Ile Asp Lys Lys Thr  |     |
| 90 95 100                                                        |     |
| AAC AAA AGC AAG GTG GCT AAG ACT GAA GAA ACG GAA TTG AAA TTA AAG  | 390 |
| Asn Lys Ser Lys Val Ala Lys Thr Glu Glu Thr Glu Leu Lys Leu Lys  |     |
| 105 110 115                                                      |     |
| GGC GTT GAA GCG GAA GTC CAA GAT AAA GTC TGT CAT CAA GTG GAA TTG  | 438 |
| Gly Val Glu Ala Glu Val Gln Asp Lys Val Cys His Gln Val Glu Leu  |     |
| 120 125 130 135                                                  |     |
| ATT AGC AAT AAC CCT AAC GCC AGC CAA CAA TCT ATC GTT ATT CCT TTG  | 486 |
| Ile Ser Asn Asn Pro Asn Ala Ser Gln Gln Ser Ile Val Ile Pro Leu  |     |
| 140 145 150                                                      |     |
| GAG ACT TTT GCC TTG AGC GCA AGC GTT AAA GGG AAT CTT TTA GCG GTG  | 534 |
| Glu Thr Phe Ala Leu Ser Ala Ser Val Lys Gly Asn Leu Leu Ala Val  |     |
| 155 160 165                                                      |     |
| GTG TTA GCG GAC AAT TCA GCG AAC TTA TAC GAC ATC ACT TCT CAA AAA  | 582 |
| Val Leu Ala Asp Asn Ser Ala Asn Leu Tyr Asp Ile Thr Ser Gln Lys  |     |
| 170 175 180                                                      |     |
| TTG CTT TTT AGT GAG AAA GGT TCC CCA AGC ACC ACG ATC AAT TCT TTA  | 630 |
| Leu Leu Phe Ser Glu Lys Gly Ser Pro Ser Thr Thr Ile Asn Ser Leu  |     |
| 185 190 195                                                      |     |
| ATG GCG ATG CCT ATT TTT ATG GAT ACG GTC GTG GTG TTC CCC ATG CTA  | 678 |
| Met Ala Met Pro Ile Phe Met Asp Thr Val Val Val Phe Pro Met Leu  |     |
| 200 205 210 215                                                  |     |

|                                   |            |                   |                   |                   |                   |                   |                   |                   |                   |            |                   |                   |                   |                   |                   |      |
|-----------------------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| GAT<br>Asp                        | GGG<br>Gly | CGC<br>Arg        | TTG<br>Leu        | TTG<br>Leu<br>220 | GTC<br>Val        | GTG<br>Val        | GAT<br>Asp        | TAT<br>Tyr        | GTG<br>Val<br>225 | CAC<br>His | GGA<br>Gly        | AAC<br>Asn        | CCT<br>Pro        | ACG<br>Thr<br>230 | CCT<br>Pro        | 726  |
| ATT<br>Ile                        | AGA<br>Arg | AAC<br>Asn        | ATT<br>Ile<br>235 | GTT<br>Val        | ATC<br>Ile        | AGC<br>Ser        | AGC<br>Ser        | GAT<br>Asp<br>240 | AAG<br>Lys        | TTT<br>Phe | TTT<br>Phe        | AAC<br>Asn        | AAT<br>Asn<br>245 | ATC<br>Ile        | ACC<br>Thr        | 774  |
| TAC<br>Tyr                        | CTT<br>Leu | ATC<br>Ile<br>250 | GTA<br>Val        | GAT<br>Asp        | GGC<br>Gly        | AAT<br>Asn        | AAC<br>Asn<br>255 | ATG<br>Met        | ATC<br>Ile        | GCT<br>Ala | TCT<br>Ser        | ACA<br>Thr<br>260 | GGG<br>Gly        | AAA<br>Lys        | AGG<br>Arg        | 822  |
| ATA<br>Ile<br>265                 | CTC<br>Leu | TCA<br>Ser        | GTA<br>Val        | GTG<br>Val        | AGC<br>Ser        | GGT<br>Gly<br>270 | CAA<br>Gln        | GAG<br>Glu        | TTC<br>Phe        | AAC<br>Asn | TAT<br>Tyr<br>275 | GAT<br>Asp        | GGG<br>Gly        | GAT<br>Asp        | ATT<br>Ile        | 870  |
| GTG<br>Val<br>280                 | GAT<br>Asp | TTG<br>Leu        | CTT<br>Leu        | TAT<br>Tyr        | GAT<br>Asp<br>285 | AAG<br>Lys        | GGG<br>Gly        | ACT<br>Thr        | TTA<br>Leu<br>290 | TAT<br>Tyr | GTG<br>Val        | CTC<br>Leu        | ACG<br>Thr        | CTA<br>Leu        | GAC<br>Asp<br>295 | 918  |
| GGG<br>Gly                        | CAG<br>Gln | ATT<br>Ile        | TTG<br>Leu        | CAA<br>Gln<br>300 | ATG<br>Met        | GAT<br>Asp        | AAG<br>Lys        | AGT<br>Ser        | TTG<br>Leu<br>305 | AGG<br>Arg | GAA<br>Glu        | TTA<br>Leu        | AAC<br>Asn        | AGC<br>Ser<br>310 | GTG<br>Val        | 966  |
| AAA<br>Lys                        | CTG<br>Leu | CCT<br>Pro        | NTC<br>Xaa<br>315 | NTC<br>Xaa        | GCT<br>Ala        | CAA<br>Gln        | CAC<br>His        | GAT<br>Asp<br>320 | TGT<br>Cys        | ATT<br>Ile | AAA<br>Lys        | CCA<br>Pro        | TAATAAATTG        | TA                |                   | 1017 |
| TTCTTTTAGAA AAACGAGGGT ATGTGATAGA |            |                   |                   |                   |                   |                   |                   |                   |                   |            |                   |                   |                   |                   |                   | 1047 |

(2) INFORMATION FOR SEO ID NO:146:

|           |           |            |            |           |           |           |            |            |           |           |           |            |            |           |           |
|-----------|-----------|------------|------------|-----------|-----------|-----------|------------|------------|-----------|-----------|-----------|------------|------------|-----------|-----------|
| Met<br>1  | Asn       | Lys        | Pro        | Phe<br>5  | Leu       | Ile       | Leu        | Leu        | Ile<br>10 | Ala       | Leu       | Ile        | Val        | Phe<br>15 | Ser       |
| Gly       | Cys       | Asn        | Met<br>20  | Arg       | Lys       | Tyr       | Phe        | Lys<br>25  | Pro       | Ala       | Lys       | His        | Gln<br>30  | Ile       | Lys       |
| Gly       | Glu       | Ala<br>35  | Tyr        | Phe       | Pro       | Asn       | His<br>40  | Leu        | Gln       | Glu       | Ser       | Ile<br>45  | Val        | Ser       | Ser       |
| Asn       | Arg<br>50 | Tyr        | Gly        | Ala       | Ile       | Leu<br>55 | Lys        | Asn        | Gly       | Ala       | Val<br>60 | Ile        | Gly        | Asp       | Lys       |
| Gly<br>65 | Leu       | Thr        | Gln        | Leu       | Arg<br>70 | Ile       | Gly        | Lys        | Asn       | Phe<br>75 | Asn       | Tyr        | Glu        | Ser       | Ser<br>80 |
| Phe       | Leu       | Asn        | Glu        | Ser<br>85 | Gln       | Gly       | Phe        | Phe<br>90  | Ile       | Leu       | Ala       | Gln        | Asp<br>95  | Cys       | Leu       |
| Asn       | Lys       | Ile        | Asp<br>100 | Lys       | Lys       | Thr       | Asn        | Lys<br>105 | Ser       | Lys       | Val       | Ala        | Lys<br>110 | Thr       | Glu       |
| Glu       | Thr       | Glu<br>115 | Leu        | Lys       | Leu       | Lys       | Gly<br>120 | Val        | Glu       | Ala       | Glu       | Val<br>125 | Gln        | Asp       | Lys       |







(ii) MOLECULE TYPE: Genomic DNA  
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 38...769  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TTGCAAAAAC TCTCATTA AAA ACAAGGAGC AAAAAAG ATG AAA AAG GCG GGC TTT | 55  |
| Met Lys Lys Ala Gly Phe                                           |     |
| 1 5                                                               |     |
| CTT TTT TTA GCG GTA ATG GCT ATC GTT GTT ATG AGT TTA AAC GCT AAA   | 103 |
| Leu Phe Leu Ala Val Met Ala Ile Val Val Met Ser Leu Asn Ala Lys   |     |
| 10 15 20                                                          |     |
| GAT CCG AAT GTG TTG CGT AAG ATT GTT TTT GAG AAA TGT CTG CCT AAT   | 151 |
| Asp Pro Asn Val Leu Arg Lys Ile Val Phe Glu Lys Cys Leu Pro Asn   |     |
| 25 30 35                                                          |     |
| TAT GAG AAA AAT CAG AAT CCT TCG CCA TGC ATA GAA GTC AAA CCC GAT   | 199 |
| Tyr Glu Lys Asn Gln Asn Pro Ser Pro Cys Ile Glu Val Lys Pro Asp   |     |
| 40 45 50                                                          |     |
| GCC GGC TAT GTG GTT TTA AAA GAT ATT AAC GGC CCG TTG CAA TAT TTG   | 247 |
| Ala Gly Tyr Val Val Leu Lys Asp Ile Asn Gly Pro Leu Gln Tyr Leu   |     |
| 55 60 65 70                                                       |     |
| TTG ATG CCA ACA ACT CAC ATT AGC GGT ATT GAA AGC CCT TTG TTA CTT   | 295 |
| Leu Met Pro Thr Thr His Ile Ser Gly Ile Glu Ser Pro Leu Leu Leu   |     |
| 75 80 85                                                          |     |
| GAT CCT TCT ACG CCT AAC TTT TTT TAT TTA TCC TGG CAA GCG CGT GAT   | 343 |
| Asp Pro Ser Thr Pro Asn Phe Phe Tyr Leu Ser Trp Gln Ala Arg Asp   |     |
| 90 95 100                                                         |     |
| TTT ATG AGT AAA AAA TAC GGC CAA CCC ATT CCT GAT TAT GCG ATT TCT   | 391 |
| Phe Met Ser Lys Lys Tyr Gly Gln Pro Ile Pro Asp Tyr Ala Ile Ser   |     |
| 105 110 115                                                       |     |
| TTG ACG ATT AAC TCT AGC AAA GGG CGA TCG CAA AAC CAT TTT CAT ATC   | 439 |
| Leu Thr Ile Asn Ser Ser Lys Gly Arg Ser Gln Asn His Phe His Ile   |     |
| 120 125 130                                                       |     |
| CAT ATC TCT TGC ATT AGT CTT GAA GCA CGC AAA CAG CTG GAT AAT AAC   | 487 |
| His Ile Ser Cys Ile Ser Leu Glu Ala Arg Lys Gln Leu Asp Asn Asn   |     |
| 135 140 145 150                                                   |     |
| CTA AAA AAA ATC AAC AGC CGT TGG TCG CCA TTA CCG GGC GGT TTG AAT   | 535 |
| Leu Lys Lys Ile Asn Ser Arg Trp Ser Pro Leu Pro Gly Gly Leu Asn   |     |
| 155 160 165                                                       |     |
| GGG CAT AAA TAC TTG GCG CGT CGG GTA ACA GAG AGC GAG TTA GTG CAA   | 583 |
| Gly His Lys Tyr Leu Ala Arg Arg Val Thr Glu Ser Glu Leu Val Gln   |     |
| 170 175 180                                                       |     |

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AAA AGC CCG TTT GTC ATG CTT AAT AAA GAA GTG CCT AAT GCG TAC AAA   | 631 |
| Lys Ser Pro Phe Val Met Leu Asn Lys Glu Val Pro Asn Ala Tyr Lys   |     |
| 185 190 195                                                       |     |
|                                                                   |     |
| CGC ATG GGG GAC TAT GGC TTA GCG GTG GTG CAA CAA AGC GAT AAC TCC   | 679 |
| Arg Met Gly Asp Tyr Gly Leu Ala Val Val Gln Gln Ser Asp Asn Ser   |     |
| 200 205 210                                                       |     |
|                                                                   |     |
| TTT GTC TTA TTA GCG ACA CAA TTT AAC CCA TTG ACT TTA AAT CGC GCT   | 727 |
| Phe Val Leu Leu Ala Thr Gln Phe Asn Pro Leu Thr Leu Asn Arg Ala   |     |
| 215 220 225 230                                                   |     |
|                                                                   |     |
| TCA GCC GAA GAG ATT CAA GAT CAT GAA TGC GCG ATT TTG CAC TAAAGCGAG | 778 |
| Ser Ala Glu Glu Ile Gln Asp His Glu Cys Ala Ile Leu His           |     |
| 235 240                                                           |     |
|                                                                   |     |
| TTAGATTCTT AAGCTTGAGC GATAACCTTT AAAAAGCGTT ATGGGGTGGT GTTGCAAAAC | 838 |
| CC                                                                | 840 |

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Lys | Ala | Gly | Phe | Leu | Phe | Leu | Ala | Val | Met | Ala | Ile | Val | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Met | Ser | Leu | Asn | Ala | Lys | Asp | Pro | Asn | Val | Leu | Arg | Lys | Ile | Val | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Lys | Cys | Leu | Pro | Asn | Tyr | Glu | Lys | Asn | Gln | Asn | Pro | Ser | Pro | Cys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Glu | Val | Lys | Pro | Asp | Ala | Gly | Tyr | Val | Val | Leu | Lys | Asp | Ile | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Pro | Leu | Gln | Tyr | Leu | Leu | Met | Pro | Thr | Thr | His | Ile | Ser | Gly | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Ser | Pro | Leu | Leu | Leu | Asp | Pro | Ser | Thr | Pro | Asn | Phe | Phe | Tyr | Leu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Trp | Gln | Ala | Arg | Asp | Phe | Met | Ser | Lys | Lys | Tyr | Gly | Gln | Pro | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Asp | Tyr | Ala | Ile | Ser | Leu | Thr | Ile | Asn | Ser | Ser | Lys | Gly | Arg | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Asn | His | Phe | His | Ile | His | Ile | Ser | Cys | Ile | Ser | Leu | Glu | Ala | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Gln | Leu | Asp | Asn | Asn | Leu | Lys | Lys | Ile | Asn | Ser | Arg | Trp | Ser | Pro |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |
| Leu | Pro | Gly | Gly | Leu | Asn | Gly | His | Lys | Tyr | Leu | Ala | Arg | Arg | Val | Thr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Ser | Glu | Leu | Val | Gln | Lys | Ser | Pro | Phe | Val | Met | Leu | Asn | Lys | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Pro | Asn | Ala | Tyr | Lys | Arg | Met | Gly | Asp | Tyr | Gly | Leu | Ala | Val | Val |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gln | Gln | Ser | Asp | Asn | Ser | Phe | Val | Leu | Leu | Ala | Thr | Gln | Phe | Asn | Pro |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 210                                                             | 215 | 220 |
| Leu Thr Leu Asn Arg Ala Ser Ala Glu Glu Ile Gln Asp His Glu Cys |     |     |
| 225                                                             | 230 | 235 |
| Ala Ile Leu His                                                 |     | 240 |

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...441
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATATTGAAAG ATAATCAAAA A ATG AAG ACA AGC GCT AAA GTA TTA TTG ACT | 51  |
| Met Lys Thr Ser Ala Lys Val Leu Leu Thr                         |     |
| 1 5 10                                                          |     |
| TTA TTG ATT GTA ATA TCA TTA GGT AAG GGA TTA AAT AGT CTC ATA TCA | 99  |
| Leu Leu Ile Val Ile Ser Leu Gly Lys Gly Leu Asn Ser Leu Ile Ser |     |
| 15 20 25                                                        |     |
| GCT TGG CGT GGC AAA GAT GAT GCG ATC CCC ATT GAA ACA AGA CTC CAT | 147 |
| Ala Trp Arg Gly Lys Asp Asp Ala Ile Pro Ile Glu Thr Arg Leu His |     |
| 30 35 40                                                        |     |
| AAA AAC AAA CTG ACA ATC ATT TCT AAA ACA GAC AGC ATA GAA ATC CAA | 195 |
| Lys Asn Lys Leu Thr Ile Ile Ser Lys Thr Asp Ser Ile Glu Ile Gln |     |
| 45 50 55                                                        |     |
| GAC ATT CAG TTT AAT AGA GAG AAT TGT TCT CAC ACT TAT ACT AGT AAG | 243 |
| Asp Ile Gln Phe Asn Arg Glu Asn Cys Ser His Thr Tyr Thr Ser Lys |     |
| 60 65 70                                                        |     |
| GAT TTG GAA AAA ATT CAA AAA GAT TTA GAA GAG CTT GAA GAA GGA GTG | 291 |
| Asp Leu Glu Lys Ile Gln Lys Asp Leu Glu Glu Leu Glu Glu Gly Val |     |
| 75 80 85 90                                                     |     |
| CCT GAA TTG TTC GAG GAG CTT GAG CGT GAT GAA GAG TCC ATC GCT AAA | 339 |
| Pro Glu Leu Phe Glu Glu Leu Glu Arg Asp Glu Glu Ser Ile Ala Lys |     |
| 95 100 105                                                      |     |
| AAT AAA AAA ACG ATC CAA GAG TAT CAA AAT AAA ATT GCT AAT TTT CAA | 387 |
| Asn Lys Lys Thr Ile Gln Glu Tyr Gln Asn Lys Ile Ala Asn Phe Gln |     |
| 110 115 120                                                     |     |
| AAA TAC TAT AAA GAT ATA AAA GAT ATT GAC GAT TAT TCG GCG TTA ATG | 435 |
| Lys Tyr Tyr Lys Asp Ile Lys Asp Ile Asp Asp Tyr Ser Ala Leu Met |     |





Leu Phe Arg Arg Ile Phe Ala Glu Gly Ser Phe Ser Gln Ser Phe Leu  
 50 55 60  
 Pro Ser Phe Ile Arg Ser Ser Ile Lys Gly Ser Phe Ala Ser Leu Val  
 65 70 75 80  
 Gly Leu Ile Phe Cys Ile Val Leu Phe Met Trp Cys Leu Leu Val Ala  
 85 90 95  
 Leu Asn Pro Leu Trp Leu Ala Lys Leu Leu Ala Tyr Gly Phe Asp Glu  
 100 105 110  
 Glu Thr Leu Lys Leu Cys Ala Pro Ile Val Ala Ile Asn Phe Trp Xaa  
 115 120 125  
 Leu Leu Leu Val Phe Ile Thr Thr Phe Leu Gly Ala Leu Leu Gln Xaa  
 130 135 140  
 Gln Thr Gln Leu Phe Cys Gln Arg Leu  
 145 150

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 39...1016
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TTCTTTGTTC AGATTAATCG TTCTTAAAAG GAAGCGTG ATG CTT AAA ACC TAT CAT | 56  |
| Met Leu Lys Thr Tyr His                                           |     |
| 1 5                                                               |     |
| ATC GCC TTA GCT TGC GTG ATT TTA GCG GTG GTG GTG CTG TTG TTT GGA   | 104 |
| Ile Ala Leu Ala Cys Val Ile Leu Ala Val Val Val Leu Leu Phe Gly   |     |
| 10 15 20                                                          |     |
| GGG GAG TCC TTG AGC TTG GAA GAA TGG CAA GAA GTG TGC CTT AAT GTG   | 152 |
| Gly Glu Ser Leu Ser Leu Glu Glu Trp Gln Glu Val Cys Leu Asn Val   |     |
| 25 30 35                                                          |     |
| AAA AAC CAC TTT TTG CAC AAT GAA GAA CTG AGC TCT TTA AGT ATT ATT   | 200 |
| Lys Asn His Phe Leu His Asn Glu Glu Leu Ser Ser Leu Ser Ile Ile   |     |
| 40 45 50                                                          |     |
| ATT TTA GAA ATA CGA CTA CCA CGA GTG ATT TTA GCG CTC CTG GTG GGA   | 248 |
| Ile Leu Glu Ile Arg Leu Pro Arg Val Ile Leu Ala Leu Leu Val Gly   |     |
| 55 60 65 70                                                       |     |
| GCG AGT TTG TCT GGG AGT GGG GTG GTG ATG CAA ACG ATT TTT AGA AAC   | 296 |
| Ala Ser Leu Ser Gly Ser Gly Val Val Met Gln Thr Ile Phe Arg Asn   |     |
| 75 80 85                                                          |     |
| CCC TTA GTG GAT CCC TTT TTA CTA GGG ATT TCT AGC GGG GCG ATG CTA   | 344 |







| General Information |                                                                       |
|---------------------|-----------------------------------------------------------------------|
| Item                | Value                                                                 |
| Author              | John Doe                                                              |
| Title               | Project X                                                             |
| Date                | 2023-10-27                                                            |
| Version             | 1.0                                                                   |
| Category            | Engineering                                                           |
| Keywords            | Design, Development, Testing                                          |
| Abstract            | Summary of the project goals and objectives.                          |
| Introduction        | Background information and motivation for the project.                |
| Methodology         | Description of the methods and tools used in the project.             |
| Results             | Key findings and outcomes of the project.                             |
| Conclusion          | Summary of the project and final thoughts.                            |
| References          | List of sources and references used in the project.                   |
| Appendix            | Additional data and supporting information.                           |
| Index               | Index of the document.                                                |
| Table of Contents   | Table of Contents of the document.                                    |
| Figure 1            | Figure 1: Diagram illustrating the project structure.                 |
| Figure 2            | Figure 2: Diagram illustrating the project workflow.                  |
| Figure 3            | Figure 3: Diagram illustrating the project timeline.                  |
| Figure 4            | Figure 4: Diagram illustrating the project budget.                    |
| Figure 5            | Figure 5: Diagram illustrating the project risks.                     |
| Figure 6            | Figure 6: Diagram illustrating the project communication plan.        |
| Figure 7            | Figure 7: Diagram illustrating the project stakeholder map.           |
| Figure 8            | Figure 8: Diagram illustrating the project risk register.             |
| Figure 9            | Figure 9: Diagram illustrating the project change log.                |
| Figure 10           | Figure 10: Diagram illustrating the project status report.            |
| Figure 11           | Figure 11: Diagram illustrating the project meeting minutes.          |
| Figure 12           | Figure 12: Diagram illustrating the project decision log.             |
| Figure 13           | Figure 13: Diagram illustrating the project action plan.              |
| Figure 14           | Figure 14: Diagram illustrating the project closure plan.             |
| Figure 15           | Figure 15: Diagram illustrating the project post-mortem.              |
| Figure 16           | Figure 16: Diagram illustrating the project lessons learned.          |
| Figure 17           | Figure 17: Diagram illustrating the project feedback loop.            |
| Figure 18           | Figure 18: Diagram illustrating the project continuous improvement.   |
| Figure 19           | Figure 19: Diagram illustrating the project quality management.       |
| Figure 20           | Figure 20: Diagram illustrating the project risk management.          |
| Figure 21           | Figure 21: Diagram illustrating the project communication management. |
| Figure 22           | Figure 22: Diagram illustrating the project stakeholder management.   |
| Figure 23           | Figure 23: Diagram illustrating the project change management.        |
| Figure 24           | Figure 24: Diagram illustrating the project closure management.       |
| Figure 25           | Figure 25: Diagram illustrating the project post-mortem.              |
| Figure 26           | Figure 26: Diagram illustrating the project lessons learned.          |
| Figure 27           | Figure 27: Diagram illustrating the project feedback loop.            |
| Figure 28           | Figure 28: Diagram illustrating the project continuous improvement.   |
| Figure 29           | Figure 29: Diagram illustrating the project quality management.       |
| Figure 30           | Figure 30: Diagram illustrating the project risk management.          |
| Figure 31           | Figure 31: Diagram illustrating the project communication management. |
| Figure 32           | Figure 32: Diagram illustrating the project stakeholder management.   |
| Figure 33           | Figure 33: Diagram illustrating the project change management.        |
| Figure 34           | Figure 34: Diagram illustrating the project closure management.       |
| Figure 35           | Figure 35: Diagram illustrating the project post-mortem.              |
| Figure 36           | Figure 36: Diagram illustrating the project lessons learned.          |
| Figure 37           | Figure 37: Diagram illustrating the project feedback loop.            |
| Figure 38           | Figure 38: Diagram illustrating the project continuous improvement.   |
| Figure 39           | Figure 39: Diagram illustrating the project quality management.       |
| Figure 40           | Figure 40: Diagram illustrating the project risk management.          |
| Figure 41           | Figure 41: Diagram illustrating the project communication management. |
| Figure 42           | Figure 42: Diagram illustrating the project stakeholder management.   |
| Figure 43           | Figure 43: Diagram illustrating the project change management.        |
| Figure 44           | Figure 44: Diagram illustrating the project closure management.       |
| Figure 45           | Figure 45: Diagram illustrating the project post-mortem.              |
| Figure 46           | Figure 46: Diagram illustrating the project lessons learned.          |
| Figure 47           | Figure 47: Diagram illustrating the project feedback loop.            |
| Figure 48           | Figure 48: Diagram illustrating the project continuous improvement.   |
| Figure 49           | Figure 49: Diagram illustrating the project quality management.       |
| Figure 50           | Figure 50: Diagram illustrating the project risk management.          |
| Figure 51           | Figure 51: Diagram illustrating the project communication management. |
| Figure 52           | Figure 52: Diagram illustrating the project stakeholder management.   |
| Figure 53           | Figure 53: Diagram illustrating the project change management.        |
| Figure 54           | Figure 54: Diagram illustrating the project closure management.       |
| Figure 55           | Figure 55: Diagram illustrating the project post-mortem.              |
| Figure 56           | Figure 56: Diagram illustrating the project lessons learned.          |
| Figure 57           | Figure 57: Diagram illustrating the project feedback loop.            |
| Figure 58           | Figure 58: Diagram illustrating the project continuous improvement.   |
| Figure 59           | Figure 59: Diagram illustrating the project quality management.       |
| Figure 60           | Figure 60: Diagram illustrating the project risk management.          |
| Figure 61           | Figure 61: Diagram illustrating the project communication management. |
| Figure 62           | Figure 62: Diagram illustrating the project stakeholder management.   |
| Figure 63           | Figure 63: Diagram illustrating the project change management.        |
| Figure 64           | Figure 64: Diagram illustrating the project closure management.       |
| Figure 65           | Figure 65: Diagram illustrating the project post-mortem.              |
| Figure 66           | Figure 66: Diagram illustrating the project lessons learned.          |
| Figure 67           | Figure 67: Diagram illustrating the project feedback loop.            |
| Figure 68           | Figure 68: Diagram illustrating the project continuous improvement.   |
| Figure 69           | Figure 69: Diagram illustrating the project quality management.       |
| Figure 70           | Figure 70: Diagram illustrating the project risk management.          |
| Figure 71           | Figure 71: Diagram illustrating the project communication management. |
| Figure 72           | Figure 72: Diagram illustrating the project stakeholder management.   |
| Figure 73           | Figure 73: Diagram illustrating the project change management.        |
| Figure 74           | Figure 74: Diagram illustrating the project closure management.       |
| Figure 75           | Figure 75: Diagram illustrating the project post-mortem.              |
| Figure 76           | Figure 76: Diagram illustrating the project lessons learned.          |
| Figure 77           | Figure 77: Diagram illustrating the project feedback loop.            |
| Figure 78           | Figure 78: Diagram illustrating the project continuous improvement.   |
| Figure 79           | Figure 79: Diagram illustrating the project quality management.       |
| Figure 80           | Figure 80: Diagram illustrating the project risk management.          |
| Figure 81           | Figure 81: Diagram illustrating the project communication management. |
| Figure 82           | Figure 82: Diagram illustrating the project stakeholder management.   |
| Figure 83           | Figure 83: Diagram illustrating the project change management.        |
| Figure 84           | Figure 84: Diagram illustrating the project closure management.       |
| Figure 85           | Figure 85: Diagram illustrating the project post-mortem.              |
| Figure 86           | Figure 86: Diagram illustrating the project lessons learned.          |
| Figure 87           | Figure 87: Diagram illustrating the project feedback loop.            |
| Figure 88           | Figure 88: Diagram illustrating the project continuous improvement.   |
| Figure 89           | Figure 89: Diagram illustrating the project quality management.       |
| Figure 90           | Figure 90: Diagram illustrating the project risk management.          |
| Figure 91           | Figure 91: Diagram illustrating the project communication management. |
| Figure 92           | Figure 92: Diagram illustrating the project stakeholder management.   |
| Figure 93           | Figure 93: Diagram illustrating the project change management.        |
| Figure 94           | Figure 94: Diagram illustrating the project closure management.       |
| Figure 95           | Figure 95: Diagram illustrating the project post-mortem.              |
| Figure 96           | Figure 96: Diagram illustrating the project lessons learned.          |
| Figure 97           | Figure 97: Diagram illustrating the project feedback loop.            |
| Figure 98           | Figure 98: Diagram illustrating the project continuous improvement.   |
| Figure 99           | Figure 99: Diagram illustrating the project quality management.       |
| Figure 100          | Figure 100: Diagram illustrating the project risk management.         |

(D) TOPOLOGY: linear

```
(ix) FEATURE:
```

(D) OTHER INFORMATION:

|                                         |                  |                   |                  |                  |                  |                  |                  |                  |            |                  |                  |                  |                   |                  |                  |     |
|-----------------------------------------|------------------|-------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------|------------------|------------------|------------------|-------------------|------------------|------------------|-----|
| CTAGCTAAAA TCGCCCCAAA AAACGCCAAA ATCGCA |                  |                   |                  |                  |                  |                  |                  |                  |            | ATG<br>Met<br>1  | TTA<br>Leu       | GAC<br>Asp       | TCC<br>Ser        | ACT<br>Thr<br>5  | ACC<br>Thr       | 54  |
| GCT<br>Ala                              | ATC<br>Ile       | GCC<br>Ala        | ATC<br>Ile<br>10 | GCC<br>Ala       | ACG<br>Thr       | CCT<br>Pro       | AGC<br>Ser       | ATC<br>Ile<br>15 | GCC<br>Ala | CCG<br>Pro       | CTA<br>Leu       | GAA<br>Glu       | ATC<br>Ile<br>20  | CCT<br>Pro       | AGT<br>Ser       | 102 |
| AAA<br>Lys                              | AAG<br>Lys       | GGA<br>Gly<br>25  | TCC<br>Ser       | ACT<br>Thr       | AAG<br>Lys       | GGG<br>Gly       | TTT<br>Phe<br>30 | CTA<br>Leu       | AAA<br>Lys | ATC<br>Ile       | GTT<br>Val       | TGC<br>Cys<br>35 | ATC<br>Ile        | ACC<br>Thr       | ACC<br>Thr       | 150 |
| CCA<br>Pro                              | CTC<br>Leu<br>40 | CCA<br>Pro        | GAC<br>Asp       | AAA<br>Lys       | CTC<br>Leu       | GCT<br>Ala<br>45 | CCC<br>Pro       | ACC<br>Thr       | AGG<br>Arg | AGC<br>Ser       | GCT<br>Ala<br>50 | AAA<br>Lys       | ATC<br>Ile        | ACT<br>Thr       | CGT<br>Arg       | 198 |
| GGT<br>Gly<br>55                        | AGT<br>Ser       | CGT<br>Arg        | ATT<br>Ile       | TCT<br>Ser       | AAA<br>Lys<br>60 | ATA<br>Ile       | ATA<br>Ile       | ATA<br>Ile       | CTT<br>Leu | AAA<br>Lys<br>65 | GAG<br>Glu       | CTC<br>Leu       | AGT<br>Ser        | TCT<br>Ser       | TCA<br>Ser<br>70 | 246 |
| TTG<br>Leu                              | TGC<br>Cys       | AAA<br>Lys        | AAG<br>Lys       | TGG<br>Trp<br>75 | TTT<br>Phe       | TTC<br>Phe       | ACA<br>Thr       | TTA<br>Leu<br>80 | AGG<br>Arg | CAC<br>His       | ACT<br>Thr       | TCT<br>Ser       | TGC<br>Cys        | CAT<br>His<br>85 | TCT<br>Ser       | 294 |
| TCC<br>Ser                              | AAG<br>Lys       | CTC<br>Leu        | AAG<br>Lys<br>90 | GAC<br>Asp       | TCC<br>Ser       | CCT<br>Pro       | CCA<br>Pro       | AAC<br>Asn<br>95 | AAC<br>Asn | AGC<br>Ser       | ACC<br>Thr       | ACC<br>Thr       | ACC<br>Thr<br>100 | GCT<br>Ala       | AAA<br>Lys       | 342 |
| ATC<br>Ile                              | ACG<br>Thr       | CAA<br>Gln<br>105 | GCT<br>Ala       | AAG<br>Lys       | GCG<br>Ala       | ATA<br>Ile       | TGATAGGTTT       | TAAGCATCAC       |            |                  | GCTTCCTTTT       |                  |                   | AAGA             |                  | 397 |
| ACGATTAATC TGA                          |                  |                   |                  |                  |                  |                  |                  |                  |            |                  |                  |                  |                   |                  |                  | 410 |

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Met Leu Asp Ser Thr Thr Ala Ile Ala Ile Ala Thr Pro Ser Ile Ala  
1 5 10 15  
Pro Leu Glu Ile Pro Ser Lys Lys Gly Ser Thr Lys Gly Phe Leu Lys  
20 25 30  
Ile Val Cys Ile Thr Thr Pro Leu Pro Asp Lys Leu Ala Pro Thr Arg  
35 40 45  
Ser Ala Lys Ile Thr Arg Gly Ser Arg Ile Ser Lys Ile Ile Ile Leu  
50 55 60  
Lys Glu Leu Ser Ser Ser Leu Cys Lys Lys Trp Phe Phe Thr Leu Arg  
65 70 75 80  
His Thr Ser Cys His Ser Ser Lys Leu Lys Asp Ser Pro Pro Asn Asn  
85 90 95  
Ser Thr Thr Thr Ala Lys Ile Thr Gln Ala Lys Ala Ile  
100 105

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 711 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 39...662

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

AGGAAAAATG GCTGGGGTGC AAGGATTCGA ACCTCGGA ATG CCA GGA CCA AAA CCT 56  
Met Pro Gly Pro Lys Pro  
1 5  
GGT GCC TTA CCG CTT GGC GAC ACC CCA AAA ACT AAA GAA AGC ATT ATA 104  
Gly Ala Leu Pro Leu Gly Asp Thr Pro Lys Thr Lys Glu Ser Ile Ile  
10 15 20  
CAA AAG CTT TTT AAA AAA GTC AAG CTA AAA CGC TAT AAT TTT ATC ATG 152  
Gln Lys Leu Phe Lys Lys Val Lys Leu Lys Arg Tyr Asn Phe Ile Met  
25 30 35  
GAA AAT GGA TTT GAC CCC ATC ATT TAT AAA CGC TAT TTG AAA AAG AAA 200  
Glu Asn Gly Phe Asp Pro Ile Ile Tyr Lys Arg Tyr Leu Lys Lys Lys  
40 45 50  
GAA ACC TTT TTG CTG TTT AAA AAA ATC GCT CAA GCG TCT GCG TTT AAA 248  
Glu Thr Phe Leu Leu Phe Lys Lys Ile Ala Gln Ala Ser Ala Phe Lys  
55 60 65 70

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AAT TTA AAA CTC CAA CTC AAA CGA AGA GAA ATA ATC AAC CGC TAT GTT   | 296 |
| Asn Leu Lys Leu Gln Leu Lys Arg Arg Glu Ile Ile Asn Arg Tyr Val   |     |
| 75 80 85                                                          |     |
| TCT CAA GCT TTG GGG GAT TTA AAA AAA GGG TTT AGA TAC GCT AAA GTA   | 344 |
| Ser Gln Ala Leu Gly Asp Leu Lys Lys Gly Phe Arg Tyr Ala Lys Val   |     |
| 90 95 100                                                         |     |
| GAA CAC CAA ATC CTA AAA ATC TAT TTC ACG CAC CCT AGC TAT TTG AAA   | 392 |
| Glu His Gln Ile Leu Lys Ile Tyr Phe Thr His Pro Ser Tyr Leu Lys   |     |
| 105 110 115                                                       |     |
| GCC TTT AAA ATA GAA GAA GCC TAT TAC ACC AAC CAC CTG AAA GCC CAT   | 440 |
| Ala Phe Lys Ile Glu Glu Ala Tyr Tyr Thr Asn His Leu Lys Ala His   |     |
| 120 125 130                                                       |     |
| TTA AAA GAA ACG CAA AAA ACC CTA AAA GCC CTA GAT TAC CCC TTT GAT   | 488 |
| Leu Lys Glu Thr Gln Lys Thr Leu Lys Ala Leu Asp Tyr Pro Phe Asp   |     |
| 135 140 145 150                                                   |     |
| TTT AAG ACT ATC CAA GCG AGC GTG AAA AAA AGG GCT TAT CAA AAA CCA   | 536 |
| Phe Lys Thr Ile Gln Ala Ser Val Lys Lys Arg Ala Tyr Gln Lys Pro   |     |
| 155 160 165                                                       |     |
| GTT GTT AAA AAA GAA AAA CCC CCT AAA AGC GTG AAT GTC AAT TGC GAA   | 584 |
| Val Val Lys Lys Glu Lys Pro Pro Lys Ser Val Asn Val Asn Cys Glu   |     |
| 170 175 180                                                       |     |
| GGT TTG AGC GAT TTC ACT AAA AAG CAA TTT TTA AAG CTC AAA CGC GCT   | 632 |
| Gly Leu Ser Asp Phe Thr Lys Lys Gln Phe Leu Lys Leu Lys Arg Ala   |     |
| 185 190 195                                                       |     |
| TGT AAC GAT AAT ACG CTG CGC ACG CCC CCT TGAGAGCTGA CCATGCAACT GCC | 685 |
| Cys Asn Asp Asn Thr Leu Arg Thr Pro Pro                           |     |
| 200 205                                                           |     |
| GATCGGGTTT TCGGGGTGC AAGTTT                                       | 711 |

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Pro Gly Pro Lys Pro Gly Ala Leu Pro Leu Gly Asp Thr Pro Lys |  |
| 1 5 10 15                                                       |  |
| Thr Lys Glu Ser Ile Ile Gln Lys Leu Phe Lys Lys Val Lys Leu Lys |  |
| 20 25 30                                                        |  |
| Arg Tyr Asn Phe Ile Met Glu Asn Gly Phe Asp Pro Ile Ile Tyr Lys |  |
| 35 40 45                                                        |  |
| Arg Tyr Leu Lys Lys Lys Glu Thr Phe Leu Leu Phe Lys Lys Ile Ala |  |
| 50 55 60                                                        |  |



GAT CCC CAA TTA GAA ATT GAT GGC CCC TTA CAA TTT GAC GCT TCC ATT 351  
 Asp Pro Gln Leu Glu Ile Asp Gly Pro Leu Gln Phe Asp Ala Ser Ile  
 75 80 85

GAT AAA AGC GTA GCC AAG AAA AAA TGC CTA ACA GCC AAG TGG CTG GGC 399  
 Asp Lys Ser Val Ala Lys Lys Lys Cys Leu Thr Ala Lys Trp Leu Gly  
 90 95 100 105

AAG CTA GCG TTT TTA TTT TCC CGG ATT TAAACGCTGG GAACATCGCT TATAAAG 453  
 Lys Leu Ala Phe Leu Phe Ser Arg Ile  
 110

CGGTGCAACG GAGCGCTAAA GCCGTGGCGA TAG 486

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Cys | Leu | Asp | Thr | Gln | Val | Leu | Val | Phe | Gly | Asp | Cys | Ala | Ile | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Asn | Pro | Ser | Pro | Lys | Glu | Leu | Ala | Glu | Ile | Ala | Thr | Thr | Ser | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Thr | Ala | Lys | Gln | Phe | Asn | Ile | Ala | Pro | Lys | Val | Ala | Leu | Leu | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Ala | Thr | Gly | Asp | Ser | Ala | Gln | Gly | Glu | Met | Ile | Asp | Lys | Ile | Asn |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Ala | Leu | Thr | Ile | Ala | Gln | Lys | Leu | Asp | Pro | Gln | Leu | Glu | Ile | Asp |
|     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Pro | Leu | Gln | Phe | Asp | Ala | Ser | Ile | Asp | Lys | Ser | Val | Ala | Lys | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Cys | Leu | Thr | Ala | Lys | Trp | Leu | Gly | Lys | Leu | Ala | Phe | Leu | Phe | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Ile |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 38...1111
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| AGGGCAGGTT TTCACCCCTA AAAAGATAGT GGATTTC ATG CTC ACT CTC AAA CAC | 55  |
| Met Leu Thr Leu Lys His                                          |     |
| 1 5                                                              |     |
| AAT CAT GGG AGT GTT TTA GAA CCG AGT GCT GGC GAT GGG AGT TTT TTA  | 103 |
| Asn His Gly Ser Val Leu Glu Pro Ser Ala Gly Asp Gly Ser Phe Leu  |     |
| 10 15 20                                                         |     |
| AAG CGC TTA AAA AAG GCC GTA AGG ATT GAA ATC GAT CCT AAA ATC TGC  | 151 |
| Lys Arg Leu Lys Lys Ala Val Arg Ile Glu Ile Asp Pro Lys Ile Cys  |     |
| 25 30 35                                                         |     |
| CCT AAA AAT GCC CTT TGC ATG GAC TTT TTT GAC TAC CCT TTA GAA AAT  | 199 |
| Pro Lys Asn Ala Leu Cys Met Asp Phe Phe Asp Tyr Pro Leu Glu Asn  |     |
| 40 45 50                                                         |     |
| CAA TTT GAC ACC ATT ATT GGT AAC CCG CCC TAT GTC AAG CAC AAG GAT  | 247 |
| Gln Phe Asp Thr Ile Ile Gly Asn Pro Pro Tyr Val Lys His Lys Asp  |     |
| 55 60 65 70                                                      |     |
| ATT GCG CCA AGC ACC AAA GAA AAA CTC CAT TAC AGC CTT TTT GAT GAA  | 295 |
| Ile Ala Pro Ser Thr Lys Glu Lys Leu His Tyr Ser Leu Phe Asp Glu  |     |
| 75 80 85                                                         |     |
| AGG AGT AAT CTC TAC TTG TTT TTC ATA GAA AAA GCG ATC AAG CAT TTA  | 343 |
| Arg Ser Asn Leu Tyr Leu Phe Phe Ile Glu Lys Ala Ile Lys His Leu  |     |
| 90 95 100                                                        |     |
| AAA CCT AAA GGC GAA TTG ATT TTC ATC ACC CCA AGG GAT TTT TTA AAA  | 391 |
| Lys Pro Lys Gly Glu Leu Ile Phe Ile Thr Pro Arg Asp Phe Leu Lys  |     |
| 105 110 115                                                      |     |
| TCC ACT TCT AGC GTG AAA TTA AAC GAA TGG ATT TAT AAA GAA GGC ACG  | 439 |
| Ser Thr Ser Ser Val Lys Leu Asn Glu Trp Ile Tyr Lys Glu Gly Thr  |     |
| 120 125 130                                                      |     |
| ATA ACG CAT TTT TTT GAA CTG GGC GAT CAA AAG GTT TTC CCA AAC GCC  | 487 |
| Ile Thr His Phe Phe Glu Leu Gly Asp Gln Lys Val Phe Pro Asn Ala  |     |
| 135 140 145 150                                                  |     |
| ATG CCT AAT TGC GTG ATT TTT CGT TTT TGT AAG GGT AAT TTC AGT AGA  | 535 |
| Met Pro Asn Cys Val Ile Phe Arg Phe Cys Lys Gly Asn Phe Ser Arg  |     |
| 155 160 165                                                      |     |
| ATC ACC AAC GAT GGT TTG CAA TTT TTG TGC AAA AAA GGC ATT TTG TAT  | 583 |
| Ile Thr Asn Asp Gly Leu Gln Phe Leu Cys Lys Lys Gly Ile Leu Tyr  |     |
| 170 175 180                                                      |     |
| TTC CTC AAC CAA TCT TAC ACG CAA AAA TTA AGC GAG GTT TTT AAG GTT  | 631 |
| Phe Leu Asn Gln Ser Tyr Thr Gln Lys Leu Ser Glu Val Phe Lys Val  |     |
| 185 190 195                                                      |     |
| AAA GTG GGG GCA GTG AGC GGG TGC GAT AAG ATT TTT AAA AAT GAA AAA  | 679 |
| Lys Val Gly Ala Val Ser Gly Cys Asp Lys Ile Phe Lys Asn Glu Lys  |     |
| 200 205 210                                                      |     |





|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Val | Lys | His | Lys | Asp | Ile | Ala | Pro | Ser | Thr | Lys | Glu | Lys | Leu | His |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Tyr | Ser | Leu | Phe | Asp | Glu | Arg | Ser | Asn | Leu | Tyr | Leu | Phe | Phe | Ile | Glu |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Lys | Ala | Ile | Lys | His | Leu | Lys | Pro | Lys | Gly | Glu | Leu | Ile | Phe | Ile | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Arg | Asp | Phe | Leu | Lys | Ser | Thr | Ser | Ser | Val | Lys | Leu | Asn | Glu | Trp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Tyr | Lys | Glu | Gly | Thr | Ile | Thr | His | Phe | Phe | Glu | Leu | Gly | Asp | Gln |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Val | Phe | Pro | Asn | Ala | Met | Pro | Asn | Cys | Val | Ile | Phe | Arg | Phe | Cys |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |
| Lys | Gly | Asn | Phe | Ser | Arg | Ile | Thr | Asn | Asp | Gly | Leu | Gln | Phe | Leu | Cys |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Lys | Lys | Gly | Ile | Leu | Tyr | Phe | Leu | Asn | Gln | Ser | Tyr | Thr | Gln | Lys | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Glu | Val | Phe | Lys | Val | Lys | Val | Gly | Ala | Val | Ser | Gly | Cys | Asp | Lys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Phe | Lys | Asn | Glu | Lys | Tyr | Gly | Asn | Leu | Glu | Phe | Val | Thr | Ser | Ile |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Thr | Lys | Arg | Thr | Asn | Ala | Leu | Glu | Lys | Met | Val | Phe | Val | Asn | Glu | Pro |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     |     | 240 |
| Asn | Asp | Tyr | Leu | Leu | Gln | His | Lys | Asp | Ser | Leu | Met | Gln | Arg | Lys | Ile |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Lys | Lys | Phe | Asn | Glu | Asn | Asn | Trp | Phe | Glu | Trp | Gly | Arg | Met | His | His |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ile | Ser | Pro | Lys | Lys | Arg | Ile | Tyr | Val | Asn | Ala | Lys | Thr | His | Gln | Lys |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asn | Pro | Phe | Phe | Ile | His | Gln | Cys | Pro | Asn | Tyr | Asp | Gly | Ser | Ile | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ala | Leu | Phe | Pro | Tyr | Asn | Gln | Asn | Leu | Asp | Leu | Gln | Asn | Leu | Cys | Asp |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     |     | 320 |
| Lys | Leu | Asn | Ala | Ile | Asn | Trp | Gln | Glu | Leu | Gly | Phe | Val | Cys | Gly | Gly |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Arg | Phe | Leu | Phe | Ser | Gln | Arg | Ser | Leu | Glu | Asn | Ala | Leu | Leu | Pro | Lys |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Asp | Phe | Leu | Asn | Leu | Gly |     |     |     |     |     |     |     |     |     |     |
|     |     | 355 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1130
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

CCTAAAGCGG AGAATAAAGT TACAGAAGTC CTAGCGAGCA AAACAATGTG ATG GCT



|                                                                   |      |
|-------------------------------------------------------------------|------|
| AAT GAT CCC AAC ATG AAC GGG CGT TGC CAA CGA AAT GGC GCT ACG GCG   | 776  |
| Asn Asp Pro Asn Met Asn Gly Arg Cys Gln Arg Asn Gly Ala Thr Ala   |      |
| 230 235 240                                                       |      |
| AAT GTG ATT GGG GTG TAT GCG CAA GCG AAT TAC ACC TTG CAT CCT ATG   | 824  |
| Asn Val Ile Gly Val Tyr Ala Gln Ala Asn Tyr Thr Leu His Pro Met   |      |
| 245 250 255                                                       |      |
| GTA ACT TTA GGG GCA GGG ACT CGT TAT GAT GTC TAT ACT TTA GTG GAT   | 872  |
| Val Thr Leu Gly Ala Gly Thr Arg Tyr Asp Val Tyr Thr Leu Val Asp   |      |
| 260 265 270                                                       |      |
| AAA GAC TGG CAA TTG CAC ATA ACC CAA GGG TTT AGC CCT AGC GCG GCT   | 920  |
| Lys Asp Trp Gln Leu His Ile Thr Gln Gly Phe Ser Pro Ser Ala Ala   |      |
| 275 280 285 290                                                   |      |
| TTA AAT GTC TCG CCT TTA GAA AAT TTG AAT TTC AGG CTT TCT TAT GCG   | 968  |
| Leu Asn Val Ser Pro Leu Glu Asn Leu Asn Phe Arg Leu Ser Tyr Ala   |      |
| 295 300 305                                                       |      |
| TAT GTA ACC AGA GGC CCT ATG CCT GGA GGT TTG GTG TGG ATG CGT CAA   | 1016 |
| Tyr Val Thr Arg Gly Pro Met Pro Gly Gly Leu Val Trp Met Arg Gln   |      |
| 310 315 320                                                       |      |
| GAT AAT TTG CGN CTA CAA CCG CAA TTT AAA GCC AGA AAT TGG GCA AAA   | 1064 |
| Asp Asn Leu Xaa Leu Gln Pro Gln Phe Lys Ala Arg Asn Trp Ala Lys   |      |
| 325 330 335                                                       |      |
| TGT GGA ATT TTA ACA CCG AAT ACA GCA GTC AGT ATT TTG ATT TTA GAG   | 1112 |
| Cys Gly Ile Leu Thr Pro Asn Thr Ala Val Ser Ile Leu Ile Leu Glu   |      |
| 340 345 350                                                       |      |
| CCG CCG GTT TTG TCC AAT TGATTTCTAA TTACATCAAT CAATTTTCTT CAACGCTT | 1168 |
| Pro Pro Val Leu Ser Asn                                           |      |
| 355 360                                                           |      |
| TTTGTAACCA ACTTG                                                  | 1183 |

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Lys | Ile | Asn | Gly | Tyr | Leu | Ser | Glu | Arg | Asp | Ile | Leu | Thr | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Tyr | Asn | Met | Thr | Arg | Asp | Asn | Ala | Asn | Arg | Pro | Leu | Arg | Ala | Asn |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Phe | Thr | Gly | Thr | Phe | Leu | Pro | Tyr | Ser | Cys | Gly | Asp | Phe | Asn | Ala | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Pro | Asn | Glu | Lys | Asn | Pro | Ser | Asp | Cys | Leu | Phe | Glu | Asn | Asp | Ala | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Phe | Lys | Thr | Tyr | Ser | Val | Asn | Leu | Val | His | Asn | Val | Ser | Leu | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Tyr | Glu | Arg | Glu | Gly | Gly | Ser | Arg | Phe | Gly | Asp | Pro | Lys | Leu | Lys | Ile |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Gly | Tyr | Thr | Ser | Ile | Arg | Asn | Val | Gln | Ile | Asp | Pro | Leu | Phe | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Asn | Asp | Ile | Ala | Ala | Ser | Ile | Pro | Phe | Thr | Pro | Asn | Pro | Lys | Leu |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Gly | Glu | Glu | Asn | Glu | Cys | Val | Ala | Gln | Gly | Gly | Ile | Tyr | Asp | Ala | Leu |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Gln | Thr | Cys | Ser | Ile | Thr | Phe | Lys | Ser | Leu | Gly | Gly | Gly | Ser | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | Ala | Asn | Lys | Asn | Leu | Phe | Ile | Ile | Asn | Ser | Gly | Phe | Asn | Ala | Asn |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Ile | His | Thr | Ile | Asp | His | Lys | Asn | Asp | Asn | Leu | Leu | Glu | Tyr | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Asn | Tyr | Gln | Asn | Leu | Thr | Thr | Phe | Asp | Lys | Ala | Ile | Pro | Asn | Ser |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |
| Glu | Leu | Val | Lys | Pro | Gly | Asp | Ala | Pro | Asp | Ala | Cys | Leu | Arg | Val | Thr |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Pro | Asn | Asp | Pro | Asn | Met | Asn | Gly | Arg | Cys | Gln | Arg | Asn | Gly | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Thr | Ala | Asn | Val | Ile | Gly | Val | Tyr | Ala | Gln | Ala | Asn | Tyr | Thr | Leu | His |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Pro | Met | Val | Thr | Leu | Gly | Ala | Gly | Thr | Arg | Tyr | Asp | Val | Tyr | Thr | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Asp | Lys | Asp | Trp | Gln | Leu | His | Ile | Thr | Gln | Gly | Phe | Ser | Pro | Ser |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ala | Ala | Leu | Asn | Val | Ser | Pro | Leu | Glu | Asn | Leu | Asn | Phe | Arg | Leu | Ser |
|     |     |     | 290 |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Tyr | Ala | Tyr | Val | Thr | Arg | Gly | Pro | Met | Pro | Gly | Gly | Leu | Val | Trp | Met |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Arg | Gln | Asp | Asn | Leu | Xaa | Leu | Gln | Pro | Gln | Phe | Lys | Ala | Arg | Asn | Trp |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ala | Lys | Cys | Gly | Ile | Leu | Thr | Pro | Asn | Thr | Ala | Val | Ser | Ile | Leu | Ile |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Leu | Glu | Pro | Pro | Val | Leu | Ser | Asn |     |     |     |     |     |     |     |     |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...387
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

AGACTGAATA AAATCGCACT CGCTCCCGCA ATG ACA ACC TGG AAC ATG GGG CTG

| Met Thr Thr Trp Asn Met Gly Leu            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
|--------------------------------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|
| 1                                          |            |            |            |            |            |            |            | 5          |            |            |            |            |            |            |            |     |
| CCC<br>Pro                                 | AAA<br>Lys | AAC<br>Asn | AAG<br>Lys | TTA<br>Leu | ATG<br>Met | AGC<br>Ser | GAA<br>Glu | CAC<br>His | ACC<br>Thr | ACC<br>Thr | ACC<br>Thr | ACA<br>Thr | ATC<br>Ile | AAA<br>Lys | GCG<br>Ala | 102 |
| 10                                         |            |            |            | 15         |            |            |            | 20         |            |            |            |            |            |            |            |     |
| ATG<br>Met                                 | AAG<br>Lys | AGC<br>Ser | ATT<br>Ile | TTA<br>Leu | CCC<br>Pro | ATA<br>Ile | TTC<br>Phe | GCT<br>Ala | AGA<br>Arg | TCG<br>Ser | TTT<br>Phe | TTA<br>Leu | GTC<br>Val | TTA<br>Leu | AGG<br>Arg | 150 |
| 25                                         |            |            |            | 30         |            |            |            | 35         |            |            |            | 40         |            |            |            |     |
| GCA<br>Ala                                 | TAC<br>Tyr | ACG<br>Thr | CTC<br>Leu | ATC<br>Ile | AAA<br>Lys | CCA<br>Pro | AAG<br>Lys | ACA<br>Thr | ATA<br>Ile | GTT<br>Val | GTC<br>Val | ATG<br>Met | CCC<br>Pro | AAA<br>Lys | GCC<br>Ala | 198 |
| 45                                         |            |            |            | 50         |            |            |            | 55         |            |            |            |            |            |            |            |     |
| TGC<br>Cys                                 | CAA<br>Gln | ATC<br>Ile | GCT<br>Ala | CCT<br>Pro | AAA<br>Lys | CCA<br>Pro | GCT<br>Ala | TTT<br>Phe | GCA<br>Ala | ATC<br>Ile | ACC<br>Thr | ATA<br>Ile | CCC<br>Pro | AAC<br>Asn | AAA<br>Lys | 246 |
| 60                                         |            |            | 65         |            |            | 70         |            |            |            |            |            |            |            |            |            |     |
| GGC<br>Gly                                 | ACT<br>Thr | AGC<br>Ser | GTA<br>Val | ACC<br>Thr | CCT<br>Pro | GAT<br>Asp | AAT<br>Asn | GAA<br>Glu | GTG<br>Val | AAA<br>Lys | GCA<br>Ala | AAC<br>Asn | AGC<br>Ser | ATG<br>Met | AAC<br>Asn | 294 |
| 75                                         |            |            |            | 80         |            |            |            | 85         |            |            |            |            |            |            |            |     |
| AGA<br>Arg                                 | TTC<br>Phe | AAT<br>Asn | CCG<br>Pro | GGT<br>Gly | TTA<br>Leu | GAT<br>Asp | TTA<br>Leu | GAA<br>Glu | AAC<br>Asn | ATC<br>Ile | AAA<br>Lys | CCA<br>Pro | AAA<br>Lys | AAC<br>Asn | GCC<br>Ala | 342 |
| 90                                         |            |            |            | 95         |            |            |            | 100        |            |            |            |            |            |            |            |     |
| GCA<br>Ala                                 | ATT<br>Ile | TCA<br>Ser | GCG<br>Ala | ATA<br>Ile | AAA<br>Lys | AAC<br>Asn | ACC<br>Thr | CAT<br>His | TTA<br>Leu | TAC<br>Tyr | TGC<br>Cys | ACT<br>Thr | ACG<br>Thr | GCT<br>Ala | TGAAA      | 392 |
| 105                                        |            |            |            | 110        |            |            |            | 115        |            |            |            |            |            |            |            |     |
| ATTCATTAAA CCTAGTAACG CCCCAATAGT CGCTAATAA |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            | 431 |

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

|           |     |     |     |          |           |     |     |           |           |           |     |     |           |           |     |
|-----------|-----|-----|-----|----------|-----------|-----|-----|-----------|-----------|-----------|-----|-----|-----------|-----------|-----|
| Met<br>1  | Thr | Thr | Trp | Asn<br>5 | Met       | Gly | Leu | Pro       | Lys<br>10 | Asn       | Lys | Leu | Met       | Ser<br>15 | Glu |
| His       | Thr | Thr | Thr | Thr      | Ile       | Lys | Ala | Met<br>25 | Lys       | Ser       | Ile | Leu | Pro<br>30 | Ile       | Phe |
| Ala       | Arg | Ser | Phe | Leu      | Val       | Leu | Arg | Ala       | Tyr       | Thr       | Leu | Ile | Lys       | Pro       | Lys |
| Thr       | Ile | Val | Val | Met      | Pro       | Lys | Ala | Cys       | Gln       | Ile       | Ala | Pro | Lys       | Pro       | Ala |
| Phe<br>65 | Ala | Ile | Thr | Ile      | Pro<br>70 | Asn | Lys | Gly       | Thr       | Ser<br>75 | Val | Thr | Pro       | Asp<br>80 | Asn |
| Glu       | Val | Lys | Ala | Asn      | Ser       | Met | Asn | Arg       | Phe<br>90 | Asn       | Pro | Gly | Leu       | Asp<br>95 | Leu |
| Glu       | Asn | Ile | Lys | Pro      | Lys       | Asn | Ala | Ala       | Ile       | Ser       | Ala | Ile | Lys       | Asn       | Thr |

100                      105                      110  
 His Leu Tyr Cys Thr Thr Ala  
 115

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 21...599
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

|                                                                 |                                                                            |    |
|-----------------------------------------------------------------|----------------------------------------------------------------------------|----|
| AAGTTTGATA TACTAACAGA                                           | ATG AAT ACT TAT AAA AAC AGC TTG AAT CAC                                    | 50 |
|                                                                 | Met Asn Thr Tyr Lys Asn Ser Leu Asn His                                    |    |
|                                                                 | 1                      5                      10                           |    |
| TTT TTA AAT TTA GTG GAT TGT TTA GAA AAA ATC CCC AAT GTG GGT AAA | 98                                                                         |    |
| Phe Leu Asn Leu Val Asp Cys Leu Glu Lys Ile Pro Asn Val Gly Lys |                                                                            |    |
|                                                                 | 15                      20                      25                         |    |
| AAG TCC GCC TTT AAA ATG GCG TAT CAT TTG GGT TTA GAA AAC CCC TAT | 146                                                                        |    |
| Lys Ser Ala Phe Lys Met Ala Tyr His Leu Gly Leu Glu Asn Pro Tyr |                                                                            |    |
|                                                                 | 30                      35                      40                         |    |
| CTG GCG CTA AAA ATC ACG CAC GCT TTA GAG AAC GCC CTA GAA AAC CTT | 194                                                                        |    |
| Leu Ala Leu Lys Ile Thr His Ala Leu Glu Asn Ala Leu Glu Asn Leu |                                                                            |    |
|                                                                 | 45                      50                      55                         |    |
| AAA ACA TGT TCA TCT TGT AAC GCG CTC AGC GAG AGT GAG GTT TGT GAG | 242                                                                        |    |
| Lys Thr Cys Ser Ser Cys Asn Ala Leu Ser Glu Ser Glu Val Cys Glu |                                                                            |    |
|                                                                 | 60                      65                      70                         |    |
| ATT TGC TCT GAT GAA AGC CGA CAA AAT TCT CAG CTT TGC ATG GTT TTA | 290                                                                        |    |
| Ile Cys Ser Asp Glu Ser Arg Gln Asn Ser Gln Leu Cys Met Val Leu |                                                                            |    |
|                                                                 | 75                      80                      85                      90 |    |
| CAC CCA AGA GAT GTG TTT ATT TTA GAA GAT TTA AAG GAT TTT TTA GGG | 338                                                                        |    |
| His Pro Arg Asp Val Phe Ile Leu Glu Asp Leu Lys Asp Phe Leu Gly |                                                                            |    |
|                                                                 | 95                      100                      105                       |    |
| CGC TAT TAT GTG TTA AAC TCC ATA GAA GAA GTG GAT TTT AAC GCC CTA | 386                                                                        |    |
| Arg Tyr Tyr Val Leu Asn Ser Ile Glu Glu Val Asp Phe Asn Ala Leu |                                                                            |    |
|                                                                 | 110                      115                      120                      |    |
| GAA AAA CGC CTG ATT GAA GAA AAC ATT AAA GAA ATC ATT TTT GCT TTC | 434                                                                        |    |
| Glu Lys Arg Leu Ile Glu Glu Asn Ile Lys Glu Ile Ile Phe Ala Phe |                                                                            |    |
|                                                                 | 125                      130                      135                      |    |



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 26...793
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AAAAAATTCA GGATTAAAT ATAAA ATG AAA AAA GTT TTA TTT TTG TNG GTA  | 52  |
| Met Lys Lys Val Leu Phe Leu Xaa Val                             |     |
| 1 5                                                             |     |
| ATA AGC TTT TTT GGG GGT TTT TTG AAC GCT TCT AGC TTG TAT GAA AAA | 100 |
| Ile Ser Phe Phe Gly Gly Phe Leu Asn Ala Ser Ser Leu Tyr Glu Lys |     |
| 10 15 20 25                                                     |     |
| CTG ATT AAT AAA GAA ACG ATC AGC GTT GGC ACA GAA GGC ATT TAC CCC | 148 |
| Leu Ile Asn Lys Glu Thr Ile Ser Val Gly Thr Glu Gly Ile Tyr Pro |     |
| 30 35 40                                                        |     |
| CCT TTC ACT TAC CAC AAT AAA GAA GGC AAG CTC ACC GGC TAT GAT GTG | 196 |
| Pro Phe Thr Tyr His Asn Lys Glu Gly Lys Leu Thr Gly Tyr Asp Val |     |
| 45 50 55                                                        |     |
| GAA GTG GCT AGG GAG TTG GCC AAA GAG CTT GGC GTG AAG ATC AAA TTC | 244 |
| Glu Val Ala Arg Glu Leu Ala Lys Glu Leu Gly Val Lys Ile Lys Phe |     |
| 60 65 70                                                        |     |
| CAC GAA ACT TCA TGG GAT ATC ATG CTG ACA GGT TTG AAA TCG GGG CGT | 292 |
| His Glu Thr Ser Trp Asp Ile Met Leu Thr Gly Leu Lys Ser Gly Arg |     |
| 75 80 85                                                        |     |
| TTT GAT ATG GTC GCT AAC CAA GTG AGT TTG GCG ACT AAA AAA CGC CAA | 340 |
| Phe Asp Met Val Ala Asn Gln Val Ser Leu Ala Thr Lys Lys Arg Gln |     |
| 90 95 100 105                                                   |     |
| GCG GCT TTT GAT AAA AGC TTG CCT TAT AGC TAT TCA GGC ACG ATC ATG | 388 |
| Ala Ala Phe Asp Lys Ser Leu Pro Tyr Ser Tyr Ser Gly Thr Ile Met |     |
| 110 115 120                                                     |     |
| CTG GTC AGG AAA GAT GAA AAC CGC ATT AAA GAT ATT AAA GAC ATC AAG | 436 |
| Leu Val Arg Lys Asp Glu Asn Arg Ile Lys Asp Ile Lys Asp Ile Lys |     |
| 125 130 135                                                     |     |
| GGT TTG AGA GCG GCT AAC ACT TTA AGC TCC ACT TAT GGG GAA ATC GCT | 484 |
| Gly Leu Arg Ala Ala Asn Thr Leu Ser Ser Thr Tyr Gly Glu Ile Ala |     |
| 140 145 150                                                     |     |
| TTT AAA TAC GAC GCT CAA ATC GTT TCG GTG GAT TCT ATG GCG CAA GCT | 532 |
| Phe Lys Tyr Asp Ala Gln Ile Val Ser Val Asp Ser Met Ala Gln Ala |     |





```

Leu Ser Ser Thr Tyr Gly Glu Ile Ala Phe Lys Tyr Asp Ala Gln Ile
145 150 155 160
Val Ser Val Asp Ser Met Ala Gln Ala Leu Leu Val Ala Gln Lys
 165 170 175
Arg Ala Asp Leu Thr Leu Asn Ser Ser Leu Ala Ile Leu Asn Tyr Leu
 180 185 190
Asn Thr His Lys Asp Asn Pro Phe Lys Ile Ala Trp Glu Ser Lys Glu
 195 200 205
Lys Asp Gly Gly Ala Ser Phe Val Ile Asn Lys His Gln Glu Lys Ala
 210 215 220
Leu Glu Leu Ile Asn Gln Ala Met Gln Arg Leu Ile Asn Lys Gly Val
225 230 235 240
Leu Lys Arg Leu Gly Glu Gln Phe Phe Gly Lys Asp Val Ser Gln Pro
 245 250 255

```

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 23...1372
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

```

CCTAGTTTAT TAAGGAGTTT TT ATG GAA ACG ATT GAT TCG GTG GTG CGT TTG 52
 Met Glu Thr Ile Asp Ser Val Val Arg Leu
 1 5 10

TTA TCT AAT TTG GTG TGG GGG ATT CCC ATG CAA ATT TTA TTA GTA GGC 100
Leu Ser Asn Leu Val Trp Gly Ile Pro Met Gln Ile Leu Leu Val Gly
 15 20 25

ACC GGC TTG TTT TTA ACC TTT TAT CTT AGG GGT TTG CAA TTC AGT AAG 148
Thr Gly Leu Phe Leu Thr Phe Tyr Leu Arg Gly Leu Gln Phe Ser Lys
 30 35 40

ATT TTT TAT GCG ATC AAA ATC CTT TTT GAC AAA GAG TCC CAA TCT AAG 196
Ile Phe Tyr Ala Ile Lys Ile Leu Phe Asp Lys Glu Ser Gln Ser Lys
 45 50 55

GGC GAC ATT TCA CAA TTT TCC GCT CTC ATG CTC TCT TTG GGG GCG ACT 244
Gly Asp Ile Ser Gln Phe Ser Ala Leu Met Leu Ser Leu Gly Ala Thr
 60 65 70

GTA GGC ATT GGG AGT ATC GTA GGC GTA GCG ACC GCT ATT AGC ATC GCA 292
Val Gly Ile Gly Ser Ile Val Gly Val Ala Thr Ala Ile Ser Ile Ala
 75 80 85 90

GGG CCA GGA GCG GTG TTT TGG ATG TGG GTT ACT GGG CTT GTT GGC ATG 340

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Pro | Gly | Ala | Val | Phe | Trp | Met | Trp | Val | Thr | Gly | Leu | Val | Gly | Met |     |
|     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |     |     |
| GCG | ACT | AAG | TAT | TCT | GAG | GGG | ATT | TTA | GCG | GTG | AAA | TAC | CGG | GAA | AAA | 388 |
| Ala | Thr | Lys | Tyr | Ser | Glu | Gly | Ile | Leu | Ala | Val | Lys | Tyr | Arg | Glu | Lys |     |
|     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |     |     |     |
| GGG | GCG | TTT | GGA | TAC | AAC | GGA | GGG | CCC | ATG | TAT | TAC | ATC | AAA | AAC | GGT | 436 |
| Gly | Ala | Phe | Gly | Tyr | Asn | Gly | Gly | Pro | Met | Tyr | Tyr | Ile | Lys | Asn | Gly |     |
|     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |     |     |     |     |
| CTT | AAC | ATG | CCC | AAA | CTC | GCC | ATG | GCG | TTT | GCG | ATT | TTT | ACG | ATT | ATT | 484 |
| Leu | Asn | Met | Pro | Lys | Leu | Ala | Met | Ala | Phe | Ala | Ile | Phe | Thr | Ile | Ile |     |
|     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |     |     |     |     |
| GCA | AGC | ATT | GGC | ACC | GGT | AAC | ATG | ACG | CAA | TCT | AAT | GCG | GTT | TCT | TCC | 532 |
| Ala | Ser | Ile | Gly | Thr | Gly | Asn | Met | Thr | Gln | Ser | Asn | Ala | Val | Ser | Ser |     |
|     |     |     |     |     | 160 |     |     |     |     |     | 165 |     |     |     | 170 |     |
| ATT | TTA | AGC | GAA | CAA | GCG | AAC | CTG | CCT | AAT | TGG | GTT | TCA | GGT | TTA | TTG | 580 |
| Ile | Leu | Ser | Glu | Gln | Ala | Asn | Leu | Pro | Asn | Trp | Val | Ser | Gly | Leu | Leu |     |
|     |     |     |     | 175 |     |     |     |     | 180 |     |     |     |     | 185 |     |     |
| CTC | ACT | CTT | TTA | ACC | GCT | TTC | ATT | GTC | ATA | GGG | GGG | ATC | AAA | TCC | ATT | 628 |
| Leu | Thr | Leu | Leu | Thr | Ala | Phe | Ile | Val | Ile | Gly | Gly | Ile | Lys | Ser | Ile |     |
|     |     |     | 190 |     |     |     |     | 195 |     |     |     |     | 200 |     |     |     |
| GGT | AAA | TTC | ACT | TCT | TAC | TTA | GCT | CCT | GTT | ATG | GTG | CTT | TTA | TAT | TTG | 676 |
| Gly | Lys | Phe | Thr | Ser | Tyr | Leu | Ala | Pro | Val | Met | Val | Leu | Leu | Tyr | Leu |     |
|     |     | 205 |     |     |     |     | 210 |     |     |     |     | 215 |     |     |     |     |
| ATC | GCT | ATT | ATT | TAT | ATT | ATT | GTT | AGC | CAT | TTT | GAT | TTA | GCC | CTT | CAA | 724 |
| Ile | Ala | Ile | Ile | Tyr | Ile | Ile | Val | Ser | His | Phe | Asp | Leu | Ala | Leu | Gln |     |
|     |     | 220 |     |     |     |     | 225 |     |     |     | 230 |     |     |     |     |     |
| GCG | ATC | AAA | CTC | ATT | TTT | GAA | GAA | GCC | TTT | AAC | CCT | AAA | CCC | GTT | GTG | 772 |
| Ala | Ile | Lys | Leu | Ile | Phe | Glu | Glu | Ala | Phe | Asn | Pro | Lys | Pro | Val | Val |     |
|     |     |     |     |     | 240 |     |     |     |     | 245 |     |     |     | 250 |     |     |
| GGC | GGA | GCG | AGC | GGC | GCG | TTG | ATA | GCG | ACG | ATG | ATA | AAA | ACG | GGC | GTG | 820 |
| Gly | Gly | Ala | Ser | Gly | Ala | Leu | Ile | Ala | Thr | Met | Ile | Lys | Thr | Gly | Val |     |
|     |     |     |     | 255 |     |     |     |     | 260 |     |     |     |     | 265 |     |     |
| GCT | AGG | GGG | TTG | TAT | TCT | AAT | GAA | GCG | GGG | TTA | GGG | AGC | TCA | GCC | ATT | 868 |
| Ala | Arg | Gly | Leu | Tyr | Ser | Asn | Glu | Ala | Gly | Leu | Gly | Ser | Ser | Ala | Ile |     |
|     |     |     | 270 |     |     |     |     | 275 |     |     |     |     | 280 |     |     |     |
| ATT | GCC | GCG | AGC | GCT | CAA | ACA | CGC | CAC | CCG | GTG | CGC | CAA | GCC | TTA | GTG | 916 |
| Ile | Ala | Ala | Ser | Ala | Gln | Thr | Arg | His | Pro | Val | Arg | Gln | Ala | Leu | Val |     |
|     |     | 285 |     |     |     |     | 290 |     |     |     |     | 295 |     |     |     |     |
| TCC | ATG | CTC | CAA | ACT | TTT | ATT | GTA | ACC | TTA | ATA | GTG | TGT | TCG | GCA | ACA | 964 |
| Ser | Met | Leu | Gln | Thr | Phe | Ile | Val | Thr | Leu | Ile | Val | Cys | Ser | Ala | Thr |     |

[illegible]

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Met | Trp | Val | Thr | Gly | Leu | Val | Gly | Met | Ala | Thr | Lys | Tyr | Ser | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Ile | Leu | Ala | Val | Lys | Tyr | Arg | Glu | Lys | Gly | Ala | Phe | Gly | Tyr | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Gly | Pro | Met | Tyr | Tyr | Ile | Lys | Asn | Gly | Leu | Asn | Met | Pro | Lys | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Met | Ala | Phe | Ala | Ile | Phe | Thr | Ile | Ile | Ala | Ser | Ile | Gly | Thr | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asn | Met | Thr | Gln | Ser | Asn | Ala | Val | Ser | Ser | Ile | Leu | Ser | Glu | Gln | Ala |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asn | Leu | Pro | Asn | Trp | Val | Ser | Gly | Leu | Leu | Leu | Thr | Leu | Leu | Thr | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Phe | Ile | Val | Ile | Gly | Gly | Ile | Lys | Ser | Ile | Gly | Lys | Phe | Thr | Ser | Tyr |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Ala | Pro | Val | Met | Val | Leu | Leu | Tyr | Leu | Ile | Ala | Ile | Ile | Tyr | Ile |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Val | Ser | His | Phe | Asp | Leu | Ala | Leu | Gln | Ala | Ile | Lys | Leu | Ile | Phe |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Glu | Ala | Phe | Asn | Pro | Lys | Pro | Val | Val | Gly | Gly | Ala | Ser | Gly | Ala |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Ile | Ala | Thr | Met | Ile | Lys | Thr | Gly | Val | Ala | Arg | Gly | Leu | Tyr | Ser |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asn | Glu | Ala | Gly | Leu | Gly | Ser | Ser | Ala | Ile | Ile | Ala | Ala | Ser | Ala | Gln |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Thr | Arg | His | Pro | Val | Arg | Gln | Ala | Leu | Val | Ser | Met | Leu | Gln | Thr | Phe |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ile | Val | Thr | Leu | Ile | Val | Cys | Ser | Ala | Thr | Ala | Ser | Val | Ile | Leu | Met |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ala | Pro | Glu | Tyr | Asn | Thr | Leu | Leu | Pro | Asn | Gly | Glu | Lys | Leu | Ser | Ala |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asn | Leu | Leu | Thr | Leu | Lys | Ser | Thr | Glu | Tyr | Phe | Leu | Gly | Ser | Leu | Gly |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Thr | Val | Val | Ile | Phe | Thr | Thr | Met | Ile | Phe | Phe | Ala | Tyr | Ser | Thr | Ile |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ile | Gly | Trp | Ala | Tyr | Tyr | Gly | Glu | Lys | Cys | Thr | Glu | Tyr | Ala | Phe | Gly |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Glu | Lys | Lys | Val | Lys | Tyr | Tyr | Arg | Leu | Ile | Phe | Leu | Ala | Ser | Val | Met |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Val | Gly | Ala | Met | Ala | Lys | Ile | Asp | Phe | Val | Trp | Asn | Leu | Ala | Asp | Leu |
|     |     |     |     | 405 |     |     |     | 410 |     |     |     |     |     | 415 |     |
| Ser | Asn | Gly | Leu | Met | Ala | Ile | Pro | Asn | Leu | Ile | Ala | Leu | Ile | Leu | Leu |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     | 430 |     |     |     |
| His | Lys | Val | Val | Tyr | Ser | Glu | Thr | Arg | Trp | Tyr | Phe | Ser | Lys | His | Ser |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Asn | Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 49...333  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

|                                                                   |            |            |            |          |             |    |
|-------------------------------------------------------------------|------------|------------|------------|----------|-------------|----|
| TTTAAATTAA                                                        | CCCCGAAATG | GAATTTTAAA | GGGGCTTGGT | TTTTGAGC | ATG AGC TTC | 57 |
|                                                                   |            |            |            |          | Met Ser Phe |    |
|                                                                   |            |            |            |          | 1           |    |
| AGG GTG TCT AAC ACC ACA CCA GGG CAT GAG AGT GGG GCT TTT TTA AAC   | 105        |            |            |          |             |    |
| Arg Val Ser Asn Thr Thr Pro Gly His Glu Ser Gly Ala Phe Leu Asn   |            |            |            |          |             |    |
| 5 10 15                                                           |            |            |            |          |             |    |
| GCA GAA ATA AGC CCA GCA TTC CCA AAA GAA GTG CCG TTT GCG CCA TCG   | 153        |            |            |          |             |    |
| Ala Glu Ile Ser Pro Ala Phe Pro Lys Glu Val Pro Phe Ala Pro Ser   |            |            |            |          |             |    |
| 20 25 30 35                                                       |            |            |            |          |             |    |
| TTT TTT TCT ATC ACG CAG ACC TTA TGC CCT AAC TTG TGC ATA GAA TAC   | 201        |            |            |          |             |    |
| Phe Phe Ser Ile Thr Gln Thr Leu Cys Pro Asn Leu Cys Ile Glu Tyr   |            |            |            |          |             |    |
| 40 45 50                                                          |            |            |            |          |             |    |
| GCA CAA GAA AGC CCT ACA ATC CCA CCG CCT ATG ACC ACG ACC TCT TTT   | 249        |            |            |          |             |    |
| Ala Gln Glu Ser Pro Thr Ile Pro Pro Pro Met Thr Thr Thr Ser Phe   |            |            |            |          |             |    |
| 55 60 65                                                          |            |            |            |          |             |    |
| TTC ATG CTG ATA GTC CCT TTA ATA AAT TAC TTA ATG GCT ATC GCT TCA   | 297        |            |            |          |             |    |
| Phe Met Leu Ile Val Pro Leu Ile Asn Tyr Leu Met Ala Ile Ala Ser   |            |            |            |          |             |    |
| 70 75 80                                                          |            |            |            |          |             |    |
| ATT TCT ACT AAA GCG TCT TTA GGC AGT TTA GCC ACT TGAAAGGTCG CTCTGG | 349        |            |            |          |             |    |
| Ile Ser Thr Lys Ala Ser Leu Gly Ser Leu Ala Thr                   |            |            |            |          |             |    |
| 85 90 95                                                          |            |            |            |          |             |    |
| CCGGATAAGG CTCTGTAA                                               | 367        |            |            |          |             |    |

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ser Phe Arg Val Ser Asn Thr Thr Pro Gly His Glu Ser Gly Ala |  |
| 1 5 10 15                                                       |  |
| Phe Leu Asn Ala Glu Ile Ser Pro Ala Phe Pro Lys Glu Val Pro Phe |  |
| 20 25 30                                                        |  |
| Ala Pro Ser Phe Phe Ser Ile Thr Gln Thr Leu Cys Pro Asn Leu Cys |  |
| 35 40 45                                                        |  |
| Ile Glu Tyr Ala Gln Glu Ser Pro Thr Ile Pro Pro Pro Met Thr Thr |  |
| 50 55 60                                                        |  |
| Thr Ser Phe Phe Met Leu Ile Val Pro Leu Ile Asn Tyr Leu Met Ala |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     | 70  |     | 75  |     | 80  |     |     |     |     |     |     |     |     |
| Ile | Ala | Ser | Ile | Ser | Thr | Lys | Ala | Ser | Leu | Gly | Ser | Leu | Ala | Thr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 36...689
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GCGCACGCTG AATTTAGGGT TTTGAAAGGT TAAAA ATG AAA TTT AAA TTT TTG  | 53  |
| Met Lys Phe Lys Phe Leu                                         |     |
| 1 5                                                             |     |
| AAT ATG GAT AAT GAA AGC GGT TTT ATT TTG ATT GAA AAA GAA TTG AAA | 101 |
| Asn Met Asp Asn Glu Ser Gly Phe Ile Leu Ile Glu Lys Glu Leu Lys |     |
| 10 15 20                                                        |     |
| CGA TTA AAC ATT CTC GCT CAA GTC AAA GAA GAT TGC ATT GAA TTA AAA | 149 |
| Arg Leu Asn Ile Leu Ala Gln Val Lys Glu Asp Cys Ile Glu Leu Lys |     |
| 25 30 35                                                        |     |
| GGC GAA AAC ACA GAA CAA GCG AGA ATT TAT CTT AAA ACG CTT TTT AAC | 197 |
| Gly Glu Asn Thr Glu Gln Ala Arg Ile Tyr Leu Lys Thr Leu Phe Asn |     |
| 40 45 50                                                        |     |
| TCC AAT ATT GTA GAA TTA GAC GAT CAT CAA AAA AGT GCA AAC GCT TTA | 245 |
| Ser Asn Ile Val Glu Leu Asp Asp His Gln Lys Ser Ala Asn Ala Leu |     |
| 55 60 65 70                                                     |     |
| ATA GAG CGC TTG AAA TCT TTA GAT TTA AAA ATT GCG GTG GCT GAA AGC | 293 |
| Ile Glu Arg Leu Lys Ser Leu Asp Leu Lys Ile Ala Val Ala Glu Ser |     |
| 75 80 85                                                        |     |
| TGC TCT GGG GGG CTA TTA TCG CAT GCA TTC ACT TCC ATT AGC GGG GCT | 341 |
| Cys Ser Gly Gly Leu Leu Ser His Ala Phe Thr Ser Ile Ser Gly Ala |     |
| 90 95 100                                                       |     |
| TCA GCG GTT TTT ATG GGG GGT ATT GTG TGC TAC AAT GAA GAG GTT AAG | 389 |
| Ser Ala Val Phe Met Gly Gly Ile Val Cys Tyr Asn Glu Glu Val Lys |     |
| 105 110 115                                                     |     |
| CGC GAA TTA TTG AAG GTC AAT GCC ACG ACT TTA AAA GTC TTT GGG GTT | 437 |
| Arg Glu Leu Leu Lys Val Asn Ala Thr Thr Leu Lys Val Phe Gly Val |     |
| 120 125 130                                                     |     |

[illegible]



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Val | Ala | Gly | Pro | Asn | Gly | Gly | Asn | Lys | Ala | Asn | Pro | Val | Gly | Thr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Tyr | Ile | Gly | Ala | Gln | Lys | Leu | Gly | Ser | Gln | Ala | Leu | Ile | Asp | Arg |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Cys | Phe | Phe | Glu | Gly | Asn | Arg | Glu | Ser | Ile | Gln | Asn | Lys | Ser | Val | Glu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| His | Ala | Leu | Asn | Met | Leu | Ala | Arg | Met | Leu |     |     |     |     |     |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 28...657  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

|         |         |          |             |         |         |         |         |     |    |
|---------|---------|----------|-------------|---------|---------|---------|---------|-----|----|
| AAATTC  | TCTAAA  | AAAATAAA | AGG AAAATCA | ATG AAA | TTT TTG | GAT CAA | GAA AAA | AGA | 54 |
|         |         |          |             | Met Lys | Phe Leu | Asp Gln | Glu Lys | Arg |    |
|         |         |          |             | 1       |         | 5       |         |     |    |
| AGA CAA | TTA TTA | AAC GAG  | CGC CAT     | TCT TGC | AAG ATG | TTT GAT | AGC CAT | 102 |    |
| Arg Gln | Leu Leu | Asn Glu  | Arg Arg     | His Ser | Cys Lys | Met Phe | Asp Ser |     |    |
| 10      |         | 15       |             |         | 20      |         | 25      |     |    |
| TAT GAG | TTT TCT | AGC ACA  | GAA TTA     | GAA GAA | ATC GCT | GAA ATC | GCC AGG | 150 |    |
| Tyr Glu | Phe Ser | Thr Thr  | Glu Leu     | Glu Glu | Ile Ala | Glu Ile | Ala Arg |     |    |
|         |         | 30       |             | 35      |         |         | 40      |     |    |
| CTA TCG | CCA AGC | TCT TAC  | AAC ACG     | CAG CCA | TGG CAT | TTT GTG | ATG GTT | 198 |    |
| Leu Ser | Pro Ser | Ser Tyr  | Asn Thr     | Gln Gln | Pro Trp | His Phe | Val Met |     |    |
|         |         | 45       |             | 50      |         |         | 55      |     |    |
| ACT GAT | AAG GAT | TTA AAA  | AAA CAA     | ATT GCA | GCG CAC | AGC ATC | TAT TTC | 246 |    |
| Thr Asp | Lys Asp | Leu Lys  | Lys Gln     | Ile Ala | Ala His | Ser Tyr | Phe Asn |     |    |
|         | 60      |          | 65          |         | 70      |         |         |     |    |
| GAA GAG | ATG ATT | AAA AGC  | GCT TCA     | GCG TTA | ATG GTG | GTA TGC | TCT TTA | 294 |    |
| Glu Glu | Met Ile | Lys Ser  | Ala Ala     | Ser Leu | Met Met | Val Val | Cys Ser |     |    |
| 75      |         | 80       |             |         | 85      |         |         |     |    |
| AGA CCC | AGC GAG | TTG TTA  | CCA CAC     | GGC CAC | TAC ATG | CAA AAT | CTC TAT | 342 |    |
| Arg Pro | Ser Glu | Leu Leu  | Pro His     | Gly His | Tyr Met | Gln Asn | Leu Tyr |     |    |
| 90      |         | 95       |             |         | 100     |         | 105     |     |    |
| CCG GAG | TCT TAT | AAA GTT  | AGA GTG     | ATC CCC | TCT TTT | GCT CAA | ATG CTT | 390 |    |
| Pro Glu | Ser Tyr | Lys Val  | Arg Val     | Ile Ile | Pro Ser | Phe Ala | Gln Met |     |    |
|         |         | 110      |             | 115     |         |         | 120     |     |    |

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GGC GTG AGA TTC AAC CAC AGC ATG CAA AGA TTA GAA AGC TAT ATT TTA | 438 |
| Gly Val Arg Phe Asn His Ser Met Gln Arg Leu Glu Ser Tyr Ile Leu |     |
| 125 130 135                                                     |     |
| GAG CAA TGC TAT ATC GCT GTG GGG CAA ATT TGC ATG GGC GTG AGC TTA | 486 |
| Glu Gln Cys Tyr Ile Ala Val Gly Gln Ile Cys Met Gly Val Ser Leu |     |
| 140 145 150                                                     |     |
| ATG GGA TTG GAT AGT TGC ATT ATT GGA GGC TTT GAT CCT TTA AAG GTG | 534 |
| Met Gly Leu Asp Ser Cys Ile Ile Gly Gly Phe Asp Pro Leu Lys Val |     |
| 155 160 165                                                     |     |
| GGC GAA GTT TTA GAA GAG CGT ATC AAT AAG CCT AAA ATC GCA TGC TTG | 582 |
| Gly Glu Val Leu Glu Glu Arg Ile Asn Lys Pro Lys Ile Ala Cys Leu |     |
| 170 175 180 185                                                 |     |
| ATC GCT TTG GGC AAG AGG GTG GCA GAA GCG AGT CAA AAA TCA AGA AAA | 630 |
| Ile Ala Leu Gly Lys Arg Val Ala Glu Ala Ser Gln Lys Ser Arg Lys |     |
| 190 195 200                                                     |     |
| TCA AAA GTT GAT GCG ATT ACT TGG TTG TGATTAAACA AAATCAAAAA CTTT  | 681 |
| Ser Lys Val Asp Ala Ile Thr Trp Leu                             |     |
| 205 210                                                         |     |

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Phe | Leu | Asp | Gln | Glu | Lys | Arg | Arg | Gln | Leu | Leu | Asn | Glu | Arg |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| His | Ser | Cys | Lys | Met | Phe | Asp | Ser | His | Tyr | Glu | Phe | Ser | Ser | Thr | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Leu | Glu | Glu | Ile | Ala | Glu | Ile | Ala | Arg | Leu | Ser | Pro | Ser | Ser | Tyr | Asn |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Thr | Gln | Pro | Trp | His | Phe | Val | Met | Val | Thr | Asp | Lys | Asp | Leu | Lys | Lys |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Gln | Ile | Ala | Ala | His | Ser | Tyr | Phe | Asn | Glu | Glu | Met | Ile | Lys | Ser | Ala |
|     |     |     |     |     |     |     |     | 70  |     |     |     |     |     | 80  |     |
| Ser | Ala | Leu | Met | Val | Val | Cys | Ser | Leu | Arg | Pro | Ser | Glu | Leu | Leu | Pro |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 95  |     |
| His | Gly | His | Tyr | Met | Gln | Asn | Leu | Tyr | Pro | Glu | Ser | Tyr | Lys | Val | Arg |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 110 |     |
| Val | Ile | Pro | Ser | Phe | Ala | Gln | Met | Leu | Gly | Val | Arg | Phe | Asn | His | Ser |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 125 |     |
| Met | Gln | Arg | Leu | Glu | Ser | Tyr | Ile | Leu | Glu | Gln | Cys | Tyr | Ile | Ala | Val |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 140 |     |
| Gly | Gln | Ile | Cys | Met | Gly | Val | Ser | Leu | Met | Gly | Leu | Asp | Ser | Cys | Ile |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 160 |     |
| Ile | Gly | Gly | Phe | Asp | Pro | Leu | Lys | Val | Gly | Glu | Val | Leu | Glu | Glu | Arg |



|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| AAC<br>Asn | AAC<br>Asn | TTG<br>Leu | TTG<br>Leu | GGC<br>Gly | TTG<br>Leu | AAA<br>Lys | TTA<br>Leu | AAA<br>Lys | CTC<br>Leu | CCT<br>Pro | GAA<br>Glu | GAC<br>Asp | ATG<br>Met | AAT<br>Asn | CCC<br>Pro | 500  |
| 120125130  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| ACC<br>Thr | ACA<br>Thr | GCT<br>Ala | ATC<br>Ile | CCC<br>Pro | ACT<br>Thr | TAT<br>Tyr | TGC<br>Cys | TTA<br>Leu | AAG<br>Lys | GGT<br>Gly | AAA<br>Lys | AGA<br>Arg | GAA<br>Glu | GTT<br>Val | TTA<br>Leu | 548  |
| 135140145  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| ATG<br>Met | GGG<br>Gly | TTT<br>Phe | TCT<br>Ser | CAA<br>Gln | AAT<br>Asn | GGG<br>Gly | GGC<br>Gly | ATG<br>Met | GTG<br>Val | GAA<br>Glu | TTG<br>Leu | CCA<br>Pro | CAT<br>His | CTC<br>Leu | GCT<br>Ala | 596  |
| 155160165  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| TTT<br>Phe | GAC<br>Asp | CAT<br>His | CAG<br>Gln | TTT<br>Phe | TTA<br>Leu | AAC<br>Asn | TCC<br>Ser | CTT<br>Leu | GGC<br>Gly | TTT<br>Phe | AAT<br>Asn | TTG<br>Leu | AAA<br>Lys | GAG<br>Glu | ATC<br>Ile | 644  |
| 170175180  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| ATG<br>Met | CCT<br>Pro | TTC<br>Phe | ATG<br>Met | CTT<br>Leu | TTA<br>Leu | AGC<br>Ser | GCT<br>Ala | CCT<br>Pro | AGC<br>Ser | GTG<br>Val | CCT<br>Pro | TTT<br>Phe | GAA<br>Glu | TTT<br>Phe | TTA<br>Leu | 692  |
| 185190195  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| TGC<br>Cys | TTC<br>Phe | ATA<br>Ile | GAC<br>Asp | ACG<br>Thr | CCT<br>Pro | GGT<br>Gly | TTT<br>Phe | AAC<br>Asn | TCC<br>Ser | GCC<br>Ala | AAG<br>Lys | CAA<br>Gln | GGC<br>Gly | TAT<br>Tyr | ACG<br>Thr | 740  |
| 200205210  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GGT<br>Gly | GGG<br>Gly | GAT<br>Asp | AAA<br>Lys | GAA<br>Glu | GCC<br>Ala | TCT<br>Ser | AAA<br>Lys | GAA<br>Glu | TCC<br>Ser | CTA<br>Leu | AAA<br>Lys | CAC<br>His | GCC<br>Ala | AAA<br>Lys | CAC<br>His | 788  |
| 215220225  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| ATT<br>Ile | CTG<br>Leu | TGG<br>Trp | CTC<br>Leu | ATT<br>Ile | AGT<br>Ser | TGC<br>Cys | GAG<br>Glu | AGT<br>Ser | GGG<br>Gly | GAG<br>Glu | ATT<br>Ile | CAC<br>His | GAA<br>Glu | GAT<br>Asp | GAT<br>Asp | 836  |
| 235240245  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| TTA<br>Leu | GAA<br>Glu | TAT<br>Tyr | TTG<br>Leu | CAA<br>Gln | GAA<br>Glu | TTA<br>Leu | TAC<br>Tyr | GAA<br>Glu | GAA<br>Glu | GGC<br>Gly | AAG<br>Lys | CAG<br>Gln | GTT<br>Val | TTT<br>Phe | ATC<br>Ile | 884  |
| 250255260  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GTA<br>Val | TTG<br>Leu | AGT<br>Ser | AGG<br>Arg | GCT<br>Ala | GAT<br>Asp | AGG<br>Arg | CGC<br>Arg | ACA<br>Thr | AAA<br>Lys | AGG<br>Arg | CAA<br>Gln | TTA<br>Leu | GAA<br>Glu | GAA<br>Glu | GTC<br>Val | 932  |
| 265270275  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GTT<br>Val | ATT<br>Ile | AAA<br>Lys | ATT<br>Ile | AAA<br>Lys | GAG<br>Glu | ACT<br>Thr | TTA<br>Leu | AAA<br>Lys | GAT<br>Asp | AAT<br>Asn | GGC<br>Gly | ATT<br>Ile | GAA<br>Glu | TTT<br>Phe | TTA<br>Leu | 980  |
| 280285290  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GGG<br>Gly | ATT<br>Ile | GGT<br>Gly | GCT<br>Ala | TAT<br>Tyr | AGT<br>Ser | TCT<br>Ser | ACA<br>Thr | AGG<br>Arg | TAT<br>Tyr | CAA<br>Gln | GAA<br>Glu | TAT<br>Tyr | AAA<br>Lys | GAA<br>Glu | TTC<br>Phe | 1028 |
| 295300305  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| AGC<br>Ser | GAA<br>Glu | AAA<br>Lys | AGC<br>Ser | AAA<br>Lys | GTT<br>Val | TTT<br>Phe | AAC<br>Asn | TCG<br>Ser | CTT<br>Leu | GAG<br>Glu | GAA<br>Glu | TTT<br>Phe | CTA<br>Leu | ATG<br>Met | AAG<br>Lys | 1076 |
| 315320325  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| TTA<br>Leu | AAT<br>Asn | CAA<br>Gln | AGG<br>Arg | AGC<br>Ser | GAG<br>Glu | AAA<br>Lys | CAA<br>Gln | AAC<br>Asn | GAA<br>Glu | ATT<br>Ile | TTA<br>Leu | GGA<br>Gly | TAT<br>Tyr | TTA<br>Leu | TAC<br>Tyr | 1124 |
| 330335340  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GAG<br>Glu | GTG<br>Val | CAT<br>His | TCC<br>Ser | ATG<br>Met | TAT<br>Tyr | GAA<br>Glu | AAG<br>Lys | GCT<br>Ala | ATT<br>Ile | GAG<br>Glu | CAA<br>Gln | GAC<br>Asp | GCT<br>Ala | AAC<br>Asn | CAA<br>Gln | 1172 |

| 345                                                               | 350 | 355 |      |
|-------------------------------------------------------------------|-----|-----|------|
| TTC AAA CGC TAC CAA AGC GAA TTG CAT TCT GTT AGA TTG GAT TTG ATG   |     |     | 1220 |
| Phe Lys Arg Tyr Gln Ser Glu Leu His Ser Val Arg Leu Asp Leu Met   |     |     |      |
| 360                                                               | 365 | 370 |      |
| CAA AAA GGC TTT GAT GAT TTT AGC GAT AAA ATT TTT AGA AGA ATT GAG   |     |     | 1268 |
| Gln Lys Gly Phe Asp Asp Phe Ser Asp Lys Ile Phe Arg Arg Ile Glu   |     |     |      |
| 375                                                               | 380 | 385 | 390  |
| AAT TTA GAA AAA GAA TTT TCC GAG CAA GAG CGA TCC AAA AGA GAG AGT   |     |     | 1316 |
| Asn Leu Glu Lys Glu Phe Ser Glu Gln Glu Arg Ser Lys Arg Glu Ser   |     |     |      |
| 395                                                               | 400 | 405 |      |
| TTA GCG CGA TTG AAT GAA GTG ATT GAC TTG TTT AAA GAA GGT ATT GAT   |     |     | 1364 |
| Leu Ala Arg Leu Asn Glu Val Ile Asp Leu Phe Lys Glu Gly Ile Asp   |     |     |      |
| 410                                                               | 415 | 420 |      |
| AAG GTT TTT GAT CGC GTG AGC GCT TTC ACT TGG GAA AAA TAC AAA GAA   |     |     | 1412 |
| Lys Val Phe Asp Arg Val Ser Ala Phe Thr Trp Glu Lys Tyr Lys Glu   |     |     |      |
| 425                                                               | 430 | 435 |      |
| CAA AAT GAC GAT GAA GAG GAC GAT GAT TGAAGAAAAC TACAAAGAAG AGCGTTA |     |     | 1466 |
| Gln Asn Asp Asp Glu Glu Asp Asp Asp                               |     |     |      |
| 440                                                               | 445 |     |      |
| CACCGAAAGG GTGAATCAAG GCGG                                        |     |     | 1490 |

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Val | Asn | Phe | Phe | Lys | Gly | Ile | Phe | Asn | Asp | Asn | Ser | Arg | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Asn | His | Gln | Asp | Asn | His | Gln | Asn | Asn | His | Gln | Val | Gly | Leu | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Arg | Tyr | Asp | Leu | Ile | Ala | Arg | Ile | Leu | Asn | Ala | Arg | Ile | Glu | Asn |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Gly | Leu | Glu | Glu | Tyr | Gln | Ser | Val | Leu | Asp | Asn | Glu | Phe | Leu | Glu |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Ala | Ser | Gly | Val | Asp | Ser | Leu | Lys | Glu | Lys | Glu | Ile | Ala | Leu | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Leu | Gln | Glu | Ile | Gln | Lys | Glu | Leu | Gln | Leu | Val | Ala | Ser | Tyr | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ser | Leu | Phe | Gln | Lys | Thr | Ile | Val | Ala | Val | Gly | Gly | Gly | Phe | Ser | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Lys | Ser | Thr | Phe | Leu | Asn | Asn | Leu | Leu | Gly | Leu | Lys | Leu | Lys | Leu |
|     |     |     | 115 |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Pro | Glu | Asp | Met | Asn | Pro | Thr | Thr | Ala | Ile | Pro | Thr | Tyr | Cys | Leu | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Lys | Arg | Glu | Val | Leu | Met | Gly | Phe | Ser | Gln | Asn | Gly | Gly | Met | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Glu | Leu | Pro | His | Leu | Ala | Phe | Asp | His | Gln | Phe | Leu | Asn | Ser | Leu | Gly |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe | Asn | Leu | Lys | Glu | Ile | Met | Pro | Phe | Met | Leu | Leu | Ser | Ala | Pro | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Pro | Phe | Glu | Phe | Leu | Cys | Phe | Ile | Asp | Thr | Pro | Gly | Phe | Asn | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ala | Lys | Gln | Gly | Tyr | Thr | Gly | Gly | Asp | Lys | Glu | Ala | Ser | Lys | Glu | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Lys | His | Ala | Lys | His | Ile | Leu | Trp | Leu | Ile | Ser | Cys | Glu | Ser | Gly |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Ile | His | Glu | Asp | Leu | Glu | Tyr | Leu | Gln | Glu | Leu | Tyr | Glu | Glu |     |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Gly | Lys | Gln | Val | Phe | Ile | Val | Leu | Ser | Arg | Ala | Asp | Arg | Arg | Thr | Lys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Arg | Gln | Leu | Glu | Glu | Val | Val | Ile | Lys | Ile | Lys | Glu | Thr | Leu | Lys | Asp |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asn | Gly | Ile | Glu | Phe | Leu | Gly | Ile | Gly | Ala | Tyr | Ser | Ser | Thr | Arg | Tyr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gln | Glu | Tyr | Lys | Glu | Phe | Ser | Glu | Lys | Ser | Lys | Val | Phe | Asn | Ser | Leu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Glu | Glu | Phe | Leu | Met | Lys | Leu | Asn | Gln | Arg | Ser | Glu | Lys | Gln | Asn | Glu |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Ile | Leu | Gly | Tyr | Leu | Tyr | Glu | Val | His | Ser | Met | Tyr | Glu | Lys | Ala | Ile |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Glu | Gln | Asp | Ala | Asn | Gln | Phe | Lys | Arg | Tyr | Gln | Ser | Glu | Leu | His | Ser |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Val | Arg | Leu | Asp | Leu | Met | Gln | Lys | Gly | Phe | Asp | Asp | Phe | Ser | Asp | Lys |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ile | Phe | Arg | Arg | Ile | Glu | Asn | Leu | Glu | Lys | Glu | Phe | Ser | Glu | Gln | Glu |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Arg | Ser | Lys | Arg | Glu | Ser | Leu | Ala | Arg | Leu | Asn | Glu | Val | Ile | Asp | Leu |
|     |     |     | 405 |     |     |     |     | 410 |     |     |     |     |     | 415 |     |
| Phe | Lys | Glu | Gly | Ile | Asp | Lys | Val | Phe | Asp | Arg | Val | Ser | Ala | Phe | Thr |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Trp | Glu | Lys | Tyr | Lys | Glu | Gln | Asn | Asp | Asp | Glu | Glu | Asp | Asp | Asp |     |
|     | 435 |     |     |     |     | 440 |     |     |     |     |     | 445 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1718 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 28...1674
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

ATTTTAGTTT TTAATTTTAA AGGATTG ATG ATG GTT TTA CGC ACA CAG ACA AAT

Met Met Val Leu Arg Thr Gln Thr Asn  
1 5

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TTT GTG GAG TTT TTA GAA CAG GTT TTA GAA GTT TTA AAA GAA GTG GAG | 102 |
| Phe Val Glu Phe Leu Glu Gln Val Leu Glu Val Leu Lys Glu Val Glu |     |
| 10 15 20 25                                                     |     |
| ATC GAT AAA ACA GAA TGC TCC ACG CTT TTA GCA AGC GTT CAA AAA CAA | 150 |
| Ile Asp Lys Thr Glu Cys Ser Thr Leu Leu Ala Ser Val Gln Lys Gln |     |
| 30 35 40                                                        |     |
| CAG CTA GTG ATA CCC GTT GTG GGG AAT TTT AGC GCA GGG AAA AGC ACG | 198 |
| Gln Leu Val Ile Pro Val Val Gly Asn Phe Ser Ala Gly Lys Ser Thr |     |
| 45 50 55                                                        |     |
| CTA TTA AAC CGC TTT TTA GGC AGC AGC GTT TTG CCT ACC GGT ATC ACG | 246 |
| Leu Leu Asn Arg Phe Leu Gly Ser Ser Val Leu Pro Thr Gly Ile Thr |     |
| 60 65 70                                                        |     |
| CCA GAG ACT TCT TTA GCC ACT GAG TTG CAC TAT AGC GCT AAG GAA CGC | 294 |
| Pro Glu Thr Ser Leu Ala Thr Glu Leu His Tyr Ser Ala Lys Glu Arg |     |
| 75 80 85                                                        |     |
| ATA GAG GCT TTT TCA AAC AAT GAT GAA AAA ACA GAG AGT TTT GAA CTG | 342 |
| Ile Glu Ala Phe Ser Asn Asn Asp Glu Lys Thr Glu Ser Phe Glu Leu |     |
| 90 95 100 105                                                   |     |
| AAT GAG CAA AGT TTT GAA GCG ATT AAA GAG AAT GCC ACG AAG TAT TCC | 390 |
| Asn Glu Gln Ser Phe Glu Ala Ile Lys Glu Asn Ala Thr Lys Tyr Ser |     |
| 110 115 120                                                     |     |
| TAC CTT AAG GTT TAT TTG AAT AAT GAA GCT TTG AAA AAC AGC GCT CCT | 438 |
| Tyr Leu Lys Val Tyr Leu Asn Asn Glu Ala Leu Lys Asn Ser Ala Pro |     |
| 125 130 135                                                     |     |
| TTA GTG TTT GTG GAT ATG CCA GGC TTT GAT AGC CCC ATT TCA AGC CAC | 486 |
| Leu Val Phe Val Asp Met Pro Gly Phe Asp Ser Pro Ile Ser Ser His |     |
| 140 145 150                                                     |     |
| ACC CAT GCC ATT TTG GAA TAT TTA GAA AGG GGC GTG CAT TTT GTC ATT | 534 |
| Thr His Ala Ile Leu Glu Tyr Leu Glu Arg Gly Val His Phe Val Ile |     |
| 155 160 165                                                     |     |
| CTC ACA AGC GTA GAA GAG GGC AAT CTC ACT AAA CGC ATG GTT AGG GAG | 582 |
| Leu Thr Ser Val Glu Glu Gly Asn Leu Thr Lys Arg Met Val Arg Glu |     |
| 170 175 180 185                                                 |     |
| TTA AAA AAC CTT TTA GAG TTT GAC AAA GGC CTT AGC TTT ATT TTG AGT | 630 |
| Leu Lys Asn Leu Leu Glu Phe Asp Lys Gly Leu Ser Phe Ile Leu Ser |     |
| 190 195 200                                                     |     |
| AAA ACG AAT TTA AGA ACG CCT TCG CAA GTG GGA GAA ATC TCT CAC TAC | 678 |
| Lys Thr Asn Leu Arg Thr Pro Ser Gln Val Gly Glu Ile Ser His Tyr |     |
| 205 210 215                                                     |     |
| ATT CAA GAT CAA ATC CAG GAT CAC CTT GAT TTG ACA ACG CAC CTC ATC | 726 |
| Ile Gln Asp Gln Ile Gln Asp His Leu Asp Leu Thr Thr His Leu Ile |     |
| 220 225 230                                                     |     |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| CAT<br>His | TCC<br>Ser | AAT<br>Asn | AAA<br>Lys | GAC<br>Asp | AAT<br>Asn | AAC<br>Asn | GCC<br>Ala | CTT<br>Leu | TTA<br>Leu | GAG<br>Glu | GTA<br>Val | GCG<br>Ala | GAT<br>Asp | AAA<br>Lys | ATA<br>Ile | 774  |
| 235240245  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GAC<br>Asp | GCT<br>Ala | GAA<br>Glu | AAG<br>Lys | CTT<br>Leu | TTT<br>Phe | AGC<br>Ser | GCT<br>Ala | TTG<br>Leu | TAT<br>Tyr | TTG<br>Leu | AAA<br>Lys | CGA<br>Arg | TTG<br>Leu | AAG<br>Lys | TTT<br>Phe | 822  |
| 250255260  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| TTA<br>Leu | AAT<br>Asn | TCT<br>Ser | AAG<br>Lys | TTA<br>Leu | CAA<br>Gln | AAT<br>Asn | AGC<br>Ser | CTA<br>Leu | AAA<br>Lys | AGC<br>Ser | GTG<br>Val | ATG<br>Met | GAA<br>Glu | AGC<br>Ser | TTT<br>Phe | 870  |
| 270275280  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GAT<br>Asp | TAT<br>Tyr | TCT<br>Ser | AAA<br>Lys | GAA<br>Glu | AAG<br>Lys | GCT<br>Ala | TTA<br>Leu | GAA<br>Glu | GAA<br>Glu | ATA<br>Ile | CAA<br>Gln | GCT<br>Ala | TTG<br>Leu | GAT<br>Asp | TTG<br>Leu | 918  |
| 285290295  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GGC<br>Gly | GTT<br>Val | AAA<br>Lys | GAC<br>Asp | ATT<br>Ile | GAA<br>Glu | AAA<br>Lys | ACC<br>Thr | TAT<br>Tyr | GAA<br>Glu | AAA<br>Lys | TTA<br>Leu | AGG<br>Arg | GCT<br>Ala | AAT<br>Asn | TTA<br>Leu | 966  |
| 300305310  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GAA<br>Glu | GAA<br>Glu | GAA<br>Glu | TAT<br>Tyr | TCT<br>Ser | AGC<br>Ser | GTG<br>Val | GCT<br>Ala | GTG<br>Val | GGA<br>Gly | TCG<br>Ser | GTG<br>Val | GTT<br>Val | AAA<br>Lys | AAA<br>Lys | GTA<br>Val | 1014 |
| 315320325  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GTA<br>Val | GAA<br>Glu | GAG<br>Glu | GTT<br>Val | AGG<br>Arg | GAT<br>Asp | CAA<br>Gln | AAA<br>Lys | TCC<br>Ser | TAT<br>Tyr | TTA<br>Leu | GCC<br>Ala | TCT<br>Ser | TTA<br>Leu | ATC<br>Ile | AAC<br>Asn | 1062 |
| 330335340  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| AAG<br>Lys | CCT<br>Pro | AAC<br>Asn | GAG<br>Glu | TTC<br>Phe | AAT<br>Asn | AGC<br>Ser | GAA<br>Glu | ATA<br>Ile | GAA<br>Glu | AGC<br>Ser | ATC<br>Ile | ATG<br>Met | CAA<br>Gln | CAA<br>Gln | AGC<br>Ser | 1110 |
| 350355360  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| TTG<br>Leu | ATC<br>Ile | AAA<br>Lys | AAC<br>Asn | GCT<br>Ala | AAA<br>Lys | TTA<br>Leu | GAG<br>Glu | ATT<br>Ile | GAA<br>Glu | AAG<br>Lys | ATC<br>Ile | AAC<br>Asn | CTT<br>Leu | TCT<br>Ser | TTT<br>Phe | 1158 |
| 365370375  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| TCA<br>Ser | AAA<br>Lys | GAT<br>Asp | TTC<br>Phe | CAT<br>His | GCG<br>Ala | GAA<br>Glu | TTT<br>Phe | GAA<br>Glu | AGC<br>Ser | CTG<br>Leu | AAC<br>Asn | AAG<br>Lys | CTT<br>Leu | TCT<br>Ser | AGC<br>Ser | 1206 |
| 380385390  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GAT<br>Asp | CTG<br>Leu | TCT<br>Ser | GTG<br>Val | AAT<br>Asn | TTA<br>Leu | GAG<br>Glu | CAT<br>His | GGG<br>Gly | ATT<br>Ile | GAA<br>Glu | TTA<br>Leu | GGG<br>Gly | ATC<br>Ile | AAC<br>Asn | GCT<br>Ala | 1254 |
| 395400405  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| TTA<br>Leu | AGC<br>Ser | GTG<br>Val | ATT<br>Ile | TTT<br>Phe | TCC<br>Ser | AAG<br>Lys | AAT<br>Asn | CCG<br>Pro | GTT<br>Val | ACA<br>Thr | AGG<br>Arg | CCA<br>Pro | TTC<br>Phe | GCG<br>Ala | CTG<br>Leu | 1302 |
| 410415420  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| ATT<br>Ile | TTG<br>Leu | CAA<br>Gln | GGG<br>Gly | TTA<br>Leu | AAA<br>Lys | TCT<br>Ser | CTT<br>Leu | TTA<br>Leu | AAA<br>Lys | GAT<br>Asp | TTA<br>Leu | CTG<br>Leu | ACA<br>Thr | TTG<br>Leu | TTG<br>Leu | 1350 |
| 430435440  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| CCT<br>Pro | AAT<br>Asn | ATC<br>Ile | ATC<br>Ile | GCT<br>Ala | TCA<br>Ser | TTC<br>Phe | TTT<br>Phe | AGG<br>Arg | AAT<br>Asn | GAA<br>Glu | GAA<br>Glu | AAA<br>Lys | GAG<br>Glu | CGG<br>Arg | GCG<br>Ala | 1398 |
| 445450455  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| AAA<br>Lys | TTA<br>Leu | GAA<br>Glu | AAT<br>Asn | CTG<br>Leu | ATT<br>Ile | GAA<br>Glu | GTC<br>Val | AGA<br>Arg | GTG<br>Val | ATT<br>Ile | CCA<br>Pro | GAA<br>Glu | ATC<br>Ile | CAA<br>Gln | TAC<br>Tyr | 1446 |



| 460                                                               | 465 | 470 |      |
|-------------------------------------------------------------------|-----|-----|------|
| AAG CTT AAA AAA GTT TTA CCG GGA TTG TTT AAT GAA GCT TTG CAA AAT   |     |     | 1494 |
| Lys Leu Lys Lys Val Leu Pro Gly Leu Phe Asn Glu Ala Leu Gln Asn   |     |     |      |
| 475                                                               | 480 | 485 |      |
| TCC CTA AAA TCT CTA AAA GAT CGG TGC GAG CTA GAA ATC ACG CAT AAA   |     |     | 1542 |
| Ser Leu Lys Ser Leu Lys Asp Arg Cys Glu Leu Glu Ile Thr His Lys   |     |     |      |
| 490                                                               | 495 | 500 | 505  |
| AAA CAA GAA ATC GCG CTC GCT CAA AAG GAA AAA GAA AAA CAC CTA AAC   |     |     | 1590 |
| Lys Gln Glu Ile Ala Leu Ala Gln Lys Glu Lys Glu Lys His Leu Asn   |     |     |      |
|                                                                   | 510 | 515 | 520  |
| GAT TTA GAA GAT CAA AAA CAA ATC TTA GAA AAT AAG ATC AAC GCT TTA   |     |     | 1638 |
| Asp Leu Glu Asp Gln Lys Gln Ile Leu Glu Asn Lys Ile Asn Ala Leu   |     |     |      |
|                                                                   | 525 | 530 | 535  |
| AGC GAT TTA GAA CAA CAA TAT TTA AAG GAT CAA CAA TGAACGAGCA AGAACT |     |     | 1690 |
| Ser Asp Leu Glu Gln Gln Tyr Leu Lys Asp Gln Gln                   |     |     |      |
|                                                                   | 540 | 545 |      |
| CATTCAAAAA AGCGCTTTAA TTGAAAAA                                    |     |     | 1718 |

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Val | Leu | Arg | Thr | Gln | Thr | Asn | Phe | Val | Glu | Phe | Leu | Glu | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Leu | Glu | Val | Leu | Lys | Glu | Val | Glu | Ile | Asp | Lys | Thr | Glu | Cys | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Leu | Leu | Ala | Ser | Val | Gln | Lys | Gln | Gln | Leu | Val | Ile | Pro | Val | Val |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Gly | Asn | Phe | Ser | Ala | Gly | Lys | Ser | Thr | Leu | Leu | Asn | Arg | Phe | Leu | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Ser | Val | Leu | Pro | Thr | Gly | Ile | Thr | Pro | Glu | Thr | Ser | Leu | Ala | Thr |
|     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Glu | Leu | His | Tyr | Ser | Ala | Lys | Glu | Arg | Ile | Glu | Ala | Phe | Ser | Asn | Asn |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Glu | Lys | Thr | Glu | Ser | Phe | Glu | Leu | Asn | Glu | Gln | Ser | Phe | Glu | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Lys | Glu | Asn | Ala | Thr | Lys | Tyr | Ser | Tyr | Leu | Lys | Val | Tyr | Leu | Asn |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Asn | Glu | Ala | Leu | Lys | Asn | Ser | Ala | Pro | Leu | Val | Phe | Val | Asp | Met | Pro |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Phe | Asp | Ser | Pro | Ile | Ser | Ser | His | Thr | His | Ala | Ile | Leu | Glu | Tyr |
|     |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Leu | Glu | Arg | Gly | Val | His | Phe | Val | Ile | Leu | Thr | Ser | Val | Glu | Glu | Gly |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |



(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...348
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

TCTTTTCTT CATTCTAAA GAATGAAGCG ATG ATA TTA GGC AAC AAT GTC AGT 54  
Met Ile Leu Gly Asn Asn Val Ser  
1 5

AAA TCT TTT AAA AGA GAT TTT AAC CCT TGC AAA ATC AGC GCG AAT GGC 102  
Lys Ser Phe Lys Arg Asp Phe Asn Pro Cys Lys Ile Ser Ala Asn Gly  
10 15 20

CTT GTA ACC GGA TTC TTG GAA AAA ATC ACG CTT AAA GCG TTG ATC CCT 150  
Leu Val Thr Gly Phe Leu Glu Lys Ile Thr Leu Lys Ala Leu Ile Pro  
25 30 35 40

AAT TCA ATC CCA TGC TCT AAA TTC ACA GAC AGA TCG CTA GAA AGC TTG 198  
Asn Ser Ile Pro Cys Ser Lys Phe Thr Asp Arg Ser Leu Glu Ser Leu  
45 50 55

TTC AGG CTT TCA AAT TCC GCA TGG AAA TCT TTT GAA AAA GAA AGG TTG 246  
Phe Arg Leu Ser Asn Ser Ala Trp Lys Ser Phe Glu Lys Glu Arg Leu  
60 65 70

ATC TTT TCA ATC TCT AAT TTA GCG TTT TTG ATC AAG CTT TGT TGC ATG 294  
Ile Phe Ser Ile Ser Asn Leu Ala Phe Leu Ile Lys Leu Cys Cys Met  
75 80 85

ATG CTT TCT ATT TCG CTA TTG AAC TCG TTA GGC TTG TTG ATT AAA GAG 342  
Met Leu Ser Ile Ser Leu Leu Asn Ser Leu Gly Leu Leu Ile Lys Glu  
90 95 100

GCT AAA TAGGATTTTT GA 360  
Ala Lys  
105

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Met Ile Leu Gly Asn Asn Val Ser Lys Ser Phe Lys Arg Asp Phe Asn  
1 5 10 15  
Pro Cys Lys Ile Ser Ala Asn Gly Leu Val Thr Gly Phe Leu Glu Lys  
20 25 30



|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| GAG CGC TTG AGC AGC GTG ATG AAA GAT TTA CCC GTG GGG GTT GAG GGG<br>Glu Arg Leu Ser Ser Val Met Lys Asp Leu Pro Val Gly Val Glu Gly<br>115 120 125     | 444  |
| GGC ATG GCG CCC ATT GTT ACG CCG CTA TCA GAT ATC TTT ATG TTC ACT<br>Gly Met Ala Pro Ile Val Thr Pro Leu Ser Asp Ile Phe Met Phe Thr<br>130 135 140     | 492  |
| ATT GAT GGC AAT ATC ACT GAG ATA GAA AAA CGA CAG CTT TTA GAT TTT<br>Ile Asp Gly Asn Ile Thr Glu Ile Glu Lys Arg Gln Leu Leu Asp Phe<br>145 150 155 160 | 540  |
| GTG ATC CGC CCA CAA TTA AGA ATG ATT AGC GGC GTA GCA GAT GTC AAT<br>Val Ile Arg Pro Gln Leu Arg Met Ile Ser Gly Val Ala Asp Val Asn<br>165 170 175     | 588  |
| TCC ATT GGA GGC TTT AGC AGA GCG TTT GTG ATC GTG CCG GAT TTT AAT<br>Ser Ile Gly Gly Phe Ser Arg Ala Phe Val Ile Val Pro Asp Phe Asn<br>180 185 190     | 636  |
| GAC ATG GCA AGG CTT GGG GTG AGT ATT TCT GAT TTA GAA TCG GCT GTG<br>Asp Met Ala Arg Leu Gly Val Ser Ile Ser Asp Leu Glu Ser Ala Val<br>195 200 205     | 684  |
| AGA GTG AAT TTA AGA AAC AGC GGA GCG GGG CGC GTG GAT AGA GAT GGC<br>Arg Val Asn Leu Arg Asn Ser Gly Ala Gly Arg Val Asp Arg Asp Gly<br>210 215 220     | 732  |
| GAA ACC TTT TTA GTC AAA ATC CAA ACC GCT TCT TTG AGT TTA GAA GAC<br>Glu Thr Phe Leu Val Lys Ile Gln Thr Ala Ser Leu Ser Leu Glu Asp<br>225 230 235 240 | 780  |
| ATT GGC AAA ATC ACC GTT TCC ACT AAT TTA GGG CAT TTG CAC ATT AAG<br>Ile Gly Lys Ile Thr Val Ser Thr Asn Leu Gly His Leu His Ile Lys<br>245 250 255     | 828  |
| GAT TTT GCG AAA GTC ATC AGC CAG TCT CGC ACC CGT TTG GGG TTT GTT<br>Asp Phe Ala Lys Val Ile Ser Gln Ser Arg Thr Arg Leu Gly Phe Val<br>260 265 270     | 876  |
| ACT AAA GAT GGC GTG GGC GAG ACC ACA GAA GGC TTG GTG CTT TCT TTA<br>Thr Lys Asp Gly Val Gly Glu Thr Thr Glu Gly Leu Val Leu Ser Leu<br>275 280 285     | 924  |
| AAA GAC GCT AAC ACC AAA GAA ATC ATC ACT CAA GTG TAT CAA AAA CTA<br>Lys Asp Ala Asn Thr Lys Glu Ile Ile Thr Gln Val Tyr Gln Lys Leu<br>290 295 300     | 972  |
| GAA GAA TTA AAA CCC TTT TTA CCG AAT GGC GTG TCC ATT AAT GTT TTT<br>Glu Glu Leu Lys Pro Phe Leu Pro Asn Gly Val Ser Ile Asn Val Phe<br>305 310 315 320 | 1020 |
| TAT GAT CGC TCA GAA TTT ACG CAA AAA GCC ATT GCC ACC GTT TCT AAA<br>Tyr Asp Arg Ser Glu Phe Thr Gln Lys Ala Ile Ala Thr Val Ser Lys<br>325 330 335     | 1068 |
| ACC CTC ATT GAA GCC GTT GTT TTA ATC ATC ATC ACG CTC TTT TTA TTT<br>Thr Leu Ile Glu Ala Val Val Leu Ile Ile Ile Thr Leu Phe Leu Phe                    | 1116 |





| 805                                             |     |     |      |     |     |     |     |     |      | 810 |     |            |        |     | 815  |      |  |  |  |  |
|-------------------------------------------------|-----|-----|------|-----|-----|-----|-----|-----|------|-----|-----|------------|--------|-----|------|------|--|--|--|--|
| CGC                                             | GAT | TTG | AAA  | TCT | TTT | GTA | GAA | GAG | GCT  | AAA | AAA | GTG        | ATC    | GCT | CAA  | 2556 |  |  |  |  |
| Arg                                             | Asp | Leu | Lys  | Ser | Phe | Val | Glu | Glu | Ala  | Lys | Lys | Val        | Ile    | Ala | Gln  |      |  |  |  |  |
|                                                 |     |     | 820  |     |     |     | 825 |     |      |     |     |            | 830    |     |      |      |  |  |  |  |
| AAC                                             | ATC | AAA | CTC  | CCT | CCC | AGC | TAC | TAT | ATC  | ACT | TAT | GGG        | GGG    | CAG | TTT  | 2604 |  |  |  |  |
| Asn                                             | Ile | Lys | Leu  | Pro | Pro | Ser | Tyr | Tyr | Ile  | Thr | Tyr | Gly        | Gly    | Gln | Phe  |      |  |  |  |  |
|                                                 |     |     | 835  |     |     |     | 840 |     |      |     |     |            | 845    |     |      |      |  |  |  |  |
| GAA                                             | AAC | CAG | CAA  | CGG | GCC | AAT | AAA | AGG | CTC  | TCC | ACC | GTT        | ATC    | CCT | TTA  | 2652 |  |  |  |  |
| Glu                                             | Asn | Gln | Gln  | Arg | Ala | Asn | Lys | Arg | Leu  | Ser | Thr | Val        | Ile    | Pro | Leu  |      |  |  |  |  |
|                                                 |     |     | 850  |     |     |     | 855 |     |      |     |     |            | 860    |     |      |      |  |  |  |  |
| AGC                                             | ATC | TTA | GCG  | ATT | TTT | TTC | ATT | CTT | TTT  | TTC | ACT | TTT        | AAA    | AGC | ATT  | 2700 |  |  |  |  |
| Ser                                             | Ile | Leu | Ala  | Ile | Phe | Phe | Ile | Leu | Phe  | Phe | Thr | Phe        | Lys    | Ser | Ile  |      |  |  |  |  |
|                                                 |     |     | 865  |     |     |     | 870 |     |      |     |     |            | 875    |     |      |      |  |  |  |  |
| CCT                                             | TTA | GCC | TTG  | CTC | ATT | CTT | TTG | AAT | ATC  | CCT | TTT | GCG        | GTT    | ACC | GGA  | 2748 |  |  |  |  |
| Pro                                             | Leu | Ala | Leu  | Leu | Ile | Leu | Leu | Asn | Ile  | Pro | Phe | Ala        | Val    | Thr | Gly  |      |  |  |  |  |
|                                                 |     |     | 885  |     |     |     |     |     | 890  |     |     |            |        |     | 895  |      |  |  |  |  |
| GGC                                             | CTT | ATT | GCG  | TTG | TTT | GCG | GTC | GGG | GAG  | TAT | ATT | TCA        | GTG    | CCA | GCG  | 2796 |  |  |  |  |
| Gly                                             | Leu | Ile | Ala  | Leu | Phe | Ala | Val | Gly | Glu  | Tyr | Ile | Ser        | Val    | Pro | Ala  |      |  |  |  |  |
|                                                 |     |     | 900  |     |     |     |     |     | 905  |     |     |            |        |     | 910  |      |  |  |  |  |
| AGC                                             | GTG | GGC | TTT  | ATC | GCT | CTT | TTT | GGG | ATT  | GCG | GTT | TTA        | AAT    | GGC | GTG  | 2844 |  |  |  |  |
| Ser                                             | Val | Gly | Phe  | Ile | Ala | Leu | Phe | Gly | Ile  | Ala | Val | Leu        | Asn    | Gly | Val  |      |  |  |  |  |
|                                                 |     |     | 915  |     |     |     |     |     | 920  |     |     |            |        |     | 925  |      |  |  |  |  |
| GTG                                             | ATG | ATA | GGC  | TAT | TTT | AAA | GAG | CTT | CTC  | TTG | CAA | GGG        | AAA    | AGC | GTA  | 2892 |  |  |  |  |
| Val                                             | Met | Ile | Gly  | Tyr | Phe | Lys | Glu | Leu | Leu  | Leu | Gln | Gly        | Lys    | Ser | Val  |      |  |  |  |  |
|                                                 |     |     | 930  |     |     |     |     |     | 935  |     |     |            |        |     | 940  |      |  |  |  |  |
| GAA                                             | GAA | TGC | GTT  | TTA | TTG | GGC | GCT | AAA | AGG  | CGT | TTG | AGA        | CCG    | GTT | TTA  | 2940 |  |  |  |  |
| Glu                                             | Glu | Cys | Val  | Leu | Leu | Gly | Ala | Lys | Arg  | Arg | Leu | Arg        | Pro    | Val | Leu  |      |  |  |  |  |
|                                                 |     |     | 945  |     |     |     |     |     | 950  |     |     |            |        |     | 955  |      |  |  |  |  |
| ATG                                             | ACC | GCT | TGC  | ATT | GCC | GGT | TTG | GGT | TTG  | CTC | CCT | TTA        | TTA    | TTT | TCT  | 2988 |  |  |  |  |
| Met                                             | Thr | Ala | Cys  | Ile | Ala | Gly | Leu | Gly | Leu  | Leu | Pro | Leu        | Leu    | Phe | Ser  |      |  |  |  |  |
|                                                 |     |     | 965  |     |     |     |     |     | 970  |     |     |            |        |     | 975  |      |  |  |  |  |
| CAT                                             | AGC | GTG | GGA  | TCA | GAA | GTC | CAA | AAA | CCT  | TTA | GCG | ATC        | GTG    | GTG | CTT  | 3036 |  |  |  |  |
| His                                             | Ser | Val | Gly  | Ser | Glu | Val | Gln | Lys | Pro  | Leu | Ala | Ile        | Val    | Val | Leu  |      |  |  |  |  |
|                                                 |     |     | 980  |     |     |     |     |     | 985  |     |     |            |        |     | 990  |      |  |  |  |  |
| GGA                                             | GGC | TTG | GTT  | ACC | TCA | AGC | GCT | CTA | ACC  | TTA | CTC | CTA        | CTG    | CCG | CCA  | 3084 |  |  |  |  |
| Gly                                             | Gly | Leu | Val  | Thr | Ser | Ser | Ala | Leu | Thr  | Leu | Leu | Leu        | Leu    | Pro | Pro  |      |  |  |  |  |
|                                                 |     |     | 995  |     |     |     |     |     | 1000 |     |     |            |        |     | 1005 |      |  |  |  |  |
| ATG                                             | TTT | ATG | CTC  | ATC | GCT | AAA | AAG | ATT | AAA  | ATC | GTT | TGAGTTAAAG | GATTTC |     |      | 3136 |  |  |  |  |
| Met                                             | Phe | Met | Leu  | Ile | Ala | Lys | Lys | Ile | Lys  | Ile | Val |            |        |     |      |      |  |  |  |  |
|                                                 |     |     | 1010 |     |     |     |     |     | 1015 |     |     |            |        |     | 1020 |      |  |  |  |  |
| ACATGCTCGC TTTAGAAATT TATATTGATA TTTGTTTGAA AGA |     |     |      |     |     |     |     |     |      |     |     |            |        |     | 3179 |      |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:188:



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1020 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Leu | Ala | Ser | Ile | Ile | Glu | Phe | Ser | Leu | Arg | Gln | Arg | Val | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ile | Val | Gly | Ala | Ile | Leu | Ile | Leu | Phe | Phe | Gly | Thr | Tyr | Ser | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Asn | Thr | Pro | Val | Asp | Ala | Phe | Pro | Asp | Ile | Ser | Pro | Thr | Gln | Val |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Lys | Ile | Ile | Leu | Lys | Leu | Pro | Gly | Ser | Ser | Pro | Glu | Glu | Met | Glu | Asn |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Asn | Ile | Val | Arg | Pro | Leu | Glu | Leu | Glu | Leu | Gly | Leu | Lys | Gly | Gln |     |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Lys | Ser | Leu | Arg | Ser | Val | Ser | Lys | Tyr | Ser | Ile | Ser | Asp | Ile | Thr | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asp | Phe | Asp | Asp | Ser | Val | Asp | Ile | Tyr | Leu | Ala | Arg | Asn | Ile | Val | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Arg | Leu | Ser | Ser | Val | Met | Lys | Asp | Leu | Pro | Val | Gly | Val | Glu | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Met | Ala | Pro | Ile | Val | Thr | Pro | Leu | Ser | Asp | Ile | Phe | Met | Phe | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Asp | Gly | Asn | Ile | Thr | Glu | Ile | Glu | Lys | Arg | Gln | Leu | Leu | Asp | Phe |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Val | Ile | Arg | Pro | Gln | Leu | Arg | Met | Ile | Ser | Gly | Val | Ala | Asp | Val | Asn |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ser | Ile | Gly | Gly | Phe | Ser | Arg | Ala | Phe | Val | Ile | Val | Pro | Asp | Phe | Asn |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asp | Met | Ala | Arg | Leu | Gly | Val | Ser | Ile | Ser | Asp | Leu | Glu | Ser | Ala | Val |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Val | Asn | Leu | Arg | Asn | Ser | Gly | Ala | Gly | Arg | Val | Asp | Arg | Asp | Gly |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Glu | Thr | Phe | Leu | Val | Lys | Ile | Gln | Thr | Ala | Ser | Leu | Ser | Leu | Glu | Asp |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Ile | Gly | Lys | Ile | Thr | Val | Ser | Thr | Asn | Leu | Gly | His | Leu | His | Ile | Lys |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Asp | Phe | Ala | Lys | Val | Ile | Ser | Gln | Ser | Arg | Thr | Arg | Leu | Gly | Phe | Val |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Thr | Lys | Asp | Gly | Val | Gly | Glu | Thr | Thr | Glu | Gly | Leu | Val | Leu | Ser | Leu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Lys | Asp | Ala | Asn | Thr | Lys | Glu | Ile | Ile | Thr | Gln | Val | Tyr | Gln | Lys | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Glu | Glu | Leu | Lys | Pro | Phe | Leu | Pro | Asn | Gly | Val | Ser | Ile | Asn | Val | Phe |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Tyr | Asp | Arg | Ser | Glu | Phe | Thr | Gln | Lys | Ala | Ile | Ala | Thr | Val | Ser | Lys |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Thr | Leu | Ile | Glu | Ala | Val | Val | Leu | Ile | Ile | Ile | Thr | Leu | Phe | Leu | Phe |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Leu | Gly | Asn | Leu | Arg | Ala | Ser | Val | Ala | Val | Gly | Val | Ile | Leu | Pro | Leu |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Ser | Leu | Ser | Val | Ala | Phe | Ile | Phe | Ile | Lys | Phe | Ser | Asp | Leu | Thr | Leu |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |





(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 33...638
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

|                                                                 |                             |     |
|-----------------------------------------------------------------|-----------------------------|-----|
| AAGCTTATAA AATCATCAAA AAGAGTGCTG AA                             | ATG AAT GTT TTA ATC AGA TTG | 53  |
|                                                                 | Met Asn Val Leu Ile Arg Leu |     |
|                                                                 | 1 5                         |     |
| TGC TTT ATT TTT TTG ATT GGG TTT TTT GGC GCG AAT AAA ACC CTA AAC |                             | 101 |
| Cys Phe Ile Phe Leu Ile Gly Phe Phe Gly Ala Asn Lys Thr Leu Asn |                             |     |
|                                                                 | 10 15 20                    |     |
| GCA ACA GCC ATT CTT TCT CTT GAC TTT GGC TCT TTT TCC ATG CCA ATC |                             | 149 |
| Ala Thr Ala Ile Leu Ser Leu Asp Phe Gly Ser Phe Ser Met Pro Ile |                             |     |
|                                                                 | 25 30 35                    |     |
| ACT GCC AAT TTC TCA GAT GGT GCG TTA AAT GTA TTC AAA TGG TTT GAA |                             | 197 |
| Thr Ala Asn Phe Ser Asp Gly Ala Leu Asn Val Phe Lys Trp Phe Glu |                             |     |
|                                                                 | 40 45 50 55                 |     |
| AAA CAC CCA TCA GTG GGT GTT AAA GTT GGT CGG CTT GCA AAT CAA GAC |                             | 245 |
| Lys His Pro Ser Val Gly Val Lys Val Gly Arg Leu Ala Asn Gln Asp |                             |     |
|                                                                 | 60 65 70                    |     |
| GAC ACT ATC TTT ACT CTA GTT TTC ATT GTG ATA GTT GTC GCA ATA ATT |                             | 293 |
| Asp Thr Ile Phe Thr Leu Val Phe Ile Val Ile Val Val Ala Ile Ile |                             |     |
|                                                                 | 75 80 85                    |     |
| GCC CTT ATC GCT ATT TTT ATA AGG AGT ATA TTA CTA AAC ACA ATT TTT |                             | 341 |
| Ala Leu Ile Ala Ile Phe Ile Arg Ser Ile Leu Leu Asn Thr Ile Phe |                             |     |
|                                                                 | 90 95 100                   |     |
| GTA GGA TCG CTC ATA GGA TCC TTA TGG TTG TAT ATG GTA GGG TTT TAT |                             | 389 |
| Val Gly Ser Leu Ile Gly Ser Leu Trp Leu Tyr Met Val Gly Phe Tyr |                             |     |
|                                                                 | 105 110 115                 |     |
| TAT TTT TAT GGT GTT CCC TTT TTG AGT TAT TTG AGC GGT TGT TAT GAA |                             | 437 |
| Tyr Phe Tyr Gly Val Pro Phe Leu Ser Tyr Leu Ser Gly Cys Tyr Glu |                             |     |
|                                                                 | 120 125 130 135             |     |
| TCG TTT TCT TTC TCC GCA TGC TAT CCT CAT AGT TTG CAG CTA CTC CCC |                             | 485 |
| Ser Phe Ser Phe Ser Ala Cys Tyr Pro His Ser Leu Gln Leu Leu Pro |                             |     |
|                                                                 | 140 145 150                 |     |



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 65...280
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

```
AATTCAGAA GGCAAAAAT TATCTTTTTT CCTCGAATCA ATCATTAGGT TATTTTTTGG 60
TTTT ATG ATA GTT TCT TTT ATT GCC GTT CCA TGC TAC TAT GTT TTA TTG 109
Met Ile Val Ser Phe Ile Ala Val Pro Cys Tyr Tyr Val Leu Leu
 1 5 10 15

GCG ATG GAA TAC CAA ATA GCC TAT GAA CAC CCA GGA GAA TTA ATA AGC 157
Ala Met Glu Tyr Gln Ile Ala Tyr Glu His Pro Gly Glu Leu Ile Ser
 20 25 30

ACG ATT GGT TTT GTT GCG TTA GCA GTG CTT GTG TAT TAC TTA TGG GGT 205
Thr Ile Gly Phe Val Ala Leu Ala Val Leu Val Tyr Tyr Leu Trp Gly
 35 40 45

AAA TGG GAG AAG TTG CTA TGG GGC GCA CCT TCC AAT CAA GAG CAA CAA 253
Lys Trp Glu Lys Leu Leu Trp Gly Ala Pro Ser Asn Gln Glu Gln Gln
 50 55 60

CTC TCC AAT CAA GGC AAC CAA AAT CAA TGATTGTGAT TGATCGCTAG GTCAATC 307
Leu Ser Asn Gln Gly Asn Gln Asn Gln
 65 70

TGA 310
```

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

```
Met Ile Val Ser Phe Ile Ala Val Pro Cys Tyr Tyr Val Leu Leu Ala
 1 5 10 15
Met Glu Tyr Gln Ile Ala Tyr Glu His Pro Gly Glu Leu Ile Ser Thr
 20 25 30
Ile Gly Phe Val Ala Leu Ala Val Leu Val Tyr Tyr Leu Trp Gly Lys
 35 40 45
Trp Glu Lys Leu Leu Trp Gly Ala Pro Ser Asn Gln Glu Gln Gln Leu
```



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Val | Ser | Met | Asn | Cys | Ile | Gly | Ser | Lys | Tyr | Lys | Leu | Ile | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Ile | Gln | Glu | Asn | Ile | His | Ala | Val | Val | Gly | Gln | Pro | Phe | Gly | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Phe | Leu | Arg | Ser | Val | Arg | Trp | Asp | Gly | Tyr | Arg | Gly | Val | Cys | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Trp | Ser | Leu | Gly | Ser | Thr | Leu | Lys | Asn | Ile | Phe | Ser | Leu | Asp | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Leu | Lys | Ala | Asn | Gln | Val | Ile | Pro | Lys | Asp | Ala |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...872
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

|                                                                 |            |            |            |            |         |    |
|-----------------------------------------------------------------|------------|------------|------------|------------|---------|----|
| AAAATTAAGT                                                      | TGTTTGATCG | CTTTTAAACG | ATTTTAAAAA | GGAAAAATTT | ATG GAT | 56 |
|                                                                 |            |            |            |            | Met Asp |    |
|                                                                 |            |            |            |            | 1       |    |
| GAA ATT AAA ACG CTG TTA GTG GAT TTT TTT CCG CAG GCA AAG CAT TTT | 104        |            |            |            |         |    |
| Glu Ile Lys Thr Leu Leu Val Asp Phe Phe Pro Gln Ala Lys His Phe |            |            |            |            |         |    |
| 5 10 15                                                         |            |            |            |            |         |    |
| GGG ATA ATC TTA ATC AAG GCT ATT GTT GTC TTT TGT ATA GGT TTT TAT | 152        |            |            |            |         |    |
| Gly Ile Ile Leu Ile Lys Ala Ile Val Val Phe Cys Ile Gly Phe Tyr |            |            |            |            |         |    |
| 20 25 30                                                        |            |            |            |            |         |    |
| TTT TCA TTT TTC TTA CAA AAA AAA ACC ATG AAA TTT TTA TCC AAA AAG | 200        |            |            |            |         |    |
| Phe Ser Phe Phe Leu Gln Lys Lys Thr Met Lys Phe Leu Ser Lys Lys |            |            |            |            |         |    |
| 35 40 45 50                                                     |            |            |            |            |         |    |
| GAT GAG ATT TTA GCG AAT TTT GTC GCA CAG GTT ACT TTT ATC TTA ATC | 248        |            |            |            |         |    |
| Asp Glu Ile Leu Ala Asn Phe Val Ala Gln Val Thr Phe Ile Leu Ile |            |            |            |            |         |    |
| 55 60 65                                                        |            |            |            |            |         |    |
| CTT ATC ATC ACC ACA ATC ATT GCG CTC AGC ACG CTA GGC GTG CAA ACC | 296        |            |            |            |         |    |
| Leu Ile Ile Thr Thr Ile Ile Ala Leu Ser Thr Leu Gly Val Gln Thr |            |            |            |            |         |    |
| 70 75 80                                                        |            |            |            |            |         |    |
| ACC TCT ATT ATC ACT GTT TTA GGA ACG GTA GGG ATT GCT GTG GCG TTG | 344        |            |            |            |         |    |
| Thr Ser Ile Ile Thr Val Leu Gly Thr Val Gly Ile Ala Val Ala Leu |            |            |            |            |         |    |
| 85 90 95                                                        |            |            |            |            |         |    |







|                   |                   |                   |                   |            |                   |                   |                  |                   |                   |                   |                       |                   |            |                   |                   |     |
|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|------------------|-------------------|-------------------|-------------------|-----------------------|-------------------|------------|-------------------|-------------------|-----|
| TCA<br>Ser        | CTT<br>Leu        | GCT<br>Ala<br>5   | GGG<br>Gly        | GGA<br>Gly | TTG<br>Leu        | AGT<br>Ser        | GGT<br>Gly<br>10 | AGA<br>Arg        | GCG<br>Ala        | TGG<br>Trp        | GGA<br>Gly            | GAA<br>Glu<br>15  | ATG<br>Met | TTG<br>Leu        | TGT<br>Cys        | 105 |
| AAA<br>Lys        | ATG<br>Met<br>20  | GTA<br>Val        | AAC<br>Asn        | GAT<br>Asp | AGT<br>Ser        | AAT<br>Asn<br>25  | TAT<br>Tyr       | GAA<br>Glu        | AGC<br>Ser        | GAG<br>Glu        | CAA<br>Gln<br>30      | GCT<br>Ala        | CTT<br>Leu | TTA<br>Leu        | GCA<br>Ala        | 153 |
| ACA<br>Thr<br>35  | GGC<br>Gly        | AAT<br>Asn        | AGC<br>Ser        | TCA<br>Ser | GAA<br>Glu<br>40  | GAG<br>Glu        | CAA<br>Gln       | AAA<br>Lys        | CGA<br>Arg        | AGA<br>Arg<br>45  | TTT<br>Phe            | TTG<br>Leu        | CTT<br>Leu | AGA<br>Arg        | GTA<br>Val<br>50  | 201 |
| AAG<br>Lys        | AAA<br>Lys        | AAG<br>Lys        | GTT<br>Val<br>55  | AAT<br>Asn | GAT<br>Asp        | AAT<br>Asn        | AGG<br>Arg       | CAG<br>Gln        | TTA<br>Leu<br>60  | AAA<br>Lys        | AAG<br>Lys            | AAA<br>Lys        | CTT<br>Leu | GAC<br>Asp<br>65  | CCA<br>Pro        | 249 |
| TTT<br>Phe        | CTA<br>Leu        | AAA<br>Lys<br>70  | AGA<br>Arg        | CTT<br>Leu | GAT<br>Asp        | GTC<br>Val        | CTA<br>Leu<br>75 | CAA<br>Gln        | ACT<br>Thr        | GAG<br>Glu        | TTT<br>Phe            | GGT<br>Gly<br>80  | GTA<br>Val | ACT<br>Thr        | GAC<br>Asp        | 297 |
| CCT<br>Pro        | ACA<br>Thr<br>85  | GCT<br>Ala        | AAC<br>Asn        | CAT<br>His | AAT<br>Asn        | AAG<br>Lys        | CAA<br>Gln<br>90 | GGG<br>Gly        | ATA<br>Ile        | CAT<br>His        | TAT<br>Tyr            | TGC<br>Cys<br>95  | ACA<br>Thr | GAA<br>Glu        | AAT<br>Asn        | 345 |
| AAA<br>Lys        | AAG<br>Lys<br>100 | ACA<br>Thr        | GGT<br>Gly        | AAA<br>Lys | TGC<br>Cys        | GAC<br>Asp<br>105 | CCT<br>Pro       | ATT<br>Ile        | GAT<br>Asp        | AAT<br>Asn        | GTA<br>Val<br>110     | TTT<br>Phe        | AGG<br>Arg | ACA<br>Thr        | ACT<br>Thr        | 393 |
| CGC<br>Arg<br>115 | TTA<br>Leu        | GAT<br>Asp        | AAC<br>Asn        | GAA<br>Glu | TTA<br>Leu<br>120 | GAA<br>Glu        | CAA<br>Gln       | GAA<br>Glu        | ATC<br>Ile        | CAA<br>Gln<br>125 | ACG<br>Thr            | CTC<br>Leu        | ACA<br>Thr | CTT<br>Leu        | GAT<br>Asp<br>130 | 441 |
| TTA<br>Leu        | ACC<br>Thr        | AAA<br>Lys        | GCC<br>Ala<br>135 | CCC<br>Pro | AAT<br>Asn        | AAA<br>Lys        | GAC<br>Asp       | GCT<br>Ala<br>140 | CAA<br>Gln        | AGC<br>Ser        | CAA<br>Gln            | GCC<br>Ala        | TAC<br>Tyr | GCA<br>Ala<br>145 | AAT<br>Asn        | 489 |
| TTC<br>Phe        | AAT<br>Asn        | CAA<br>Gln<br>150 | AGG<br>Arg        | ATT<br>Ile | AAA<br>Lys        | TTA<br>Leu        | CTT<br>Leu       | ACT<br>Thr<br>155 | CTA<br>Leu        | AAA<br>Lys        | TAT<br>Tyr            | TTA<br>Leu<br>160 | AAA<br>Lys | GAA<br>Glu        | ATT<br>Ile        | 537 |
| ACC<br>Thr        | AAT<br>Asn<br>165 | CAA<br>Gln        | ATG<br>Met        | CTC<br>Leu | TTT<br>Phe        | TTA<br>Leu<br>170 | AAT<br>Asn       | CAA<br>Gln        | ACA<br>Thr        | ATG<br>Met        | GCA<br>Ala<br>175     | ATG<br>Met        | CAA<br>Gln | AGC<br>Ser        | GAG<br>Glu        | 585 |
| ATT<br>Ile<br>180 | ATG<br>Met        | GCA<br>Ala        | GAT<br>Asp        | GAT<br>Asp | TAT<br>Tyr        | TTT<br>Phe<br>185 | AGG<br>Arg       | CAA<br>Gln        | AAT<br>Asn        | AAT<br>Asn        | GAT<br>Asp<br>190     | GGC<br>Gly        | TTT<br>Phe | GGG<br>Gly        | AAA<br>Lys        | 633 |
| GAA<br>Glu<br>195 | GAA<br>Glu        | AAC<br>Asn        | CAT<br>His        | ATA<br>Ile | GAC<br>Asp<br>200 | AAA<br>Lys        | CAA<br>Gln       | TTA<br>Leu        | ACG<br>Thr        | CAA<br>Gln<br>205 | AAA<br>Lys            | AGA<br>Arg        | ATA<br>Ile | AAC<br>Asn        | GAA<br>Glu<br>210 | 681 |
| AGA<br>Arg        | GAA<br>Glu        | AGA<br>Arg        | GCC<br>Ala<br>215 | AGA<br>Arg | ATA<br>Ile        | TAC<br>Tyr        | TTT<br>Phe       | CAA<br>Gln        | AAC<br>Asn<br>220 | CCT<br>Pro        | AAT<br>Asn            | GTT<br>Val        | AAA<br>Lys | TTT<br>Phe<br>225 | GAC<br>Asp        | 729 |
| CAA<br>Gln        | TTT<br>Phe        | GGT<br>Gly        | TTT<br>Phe        | CCC<br>Pro | ATT<br>Ile        | TTT<br>Phe        | AGT<br>Ser       | ATA<br>Ile        | TGG<br>Trp        | GAT<br>Asp        | TAAGGGTTTA GTGATGAGAG |                   |            |                   |                   | 782 |

ATAGAATAAG TATTTTTTTTTT CCAAAC TATT CCTATTTTAG TGGTAGTGTT G

833

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Ser | Leu | Ala | Gly | Gly | Leu | Ser | Gly | Arg | Ala | Trp | Gly | Glu | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Cys | Lys | Met | Val | Asn | Asp | Ser | Asn | Tyr | Glu | Ser | Glu | Gln | Ala | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ala | Thr | Gly | Asn | Ser | Ser | Glu | Glu | Gln | Lys | Arg | Arg | Phe | Leu | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Val | Lys | Lys | Lys | Val | Asn | Asp | Asn | Arg | Gln | Leu | Lys | Lys | Lys | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Asp | Pro | Phe | Leu | Lys | Arg | Leu | Asp | Val | Leu | Gln | Thr | Glu | Phe | Gly | Val |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Thr | Asp | Pro | Thr | Ala | Asn | His | Asn | Lys | Gln | Gly | Ile | His | Tyr | Cys | Thr |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Glu | Asn | Lys | Lys | Thr | Gly | Lys | Cys | Asp | Pro | Ile | Asp | Asn | Val | Phe | Arg |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Thr | Thr | Arg | Leu | Asp | Asn | Glu | Leu | Glu | Gln | Glu | Ile | Gln | Thr | Leu | Thr |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Leu | Asp | Leu | Thr | Lys | Ala | Pro | Asn | Lys | Asp | Ala | Gln | Ser | Gln | Ala | Tyr |
|     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Ala | Asn | Phe | Asn | Gln | Arg | Ile | Lys | Leu | Leu | Thr | Leu | Lys | Tyr | Leu | Lys |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |
| Glu | Ile | Thr | Asn | Gln | Met | Leu | Phe | Leu | Asn | Gln | Thr | Met | Ala | Met | Gln |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ser | Glu | Ile | Met | Ala | Asp | Asp | Tyr | Phe | Arg | Gln | Asn | Asn | Asp | Gly | Phe |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Gly | Lys | Glu | Glu | Asn | His | Ile | Asp | Lys | Gln | Leu | Thr | Gln | Lys | Arg | Ile |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Asn | Glu | Arg | Glu | Arg | Ala | Arg | Ile | Tyr | Phe | Gln | Asn | Pro | Asn | Val | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Asp | Gln | Phe | Gly | Phe | Pro | Ile | Phe | Ser | Ile | Trp | Asp |     |     |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 63...311  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

```

TCAAACCAAA ACCAACACAA AATTTGCTAA ACTACAATCA AATCAATTTA GGGAGGATAA 60
AA ATG TCA TTT GCC CCT ATG TTA TTA GCT ACA ATC AAT AAC TCT ATT 107
 Met Ser Phe Ala Pro Met Leu Leu Ala Thr Ile Asn Asn Ser Ile
 1 5 10 15

GGC AAT AAA GAT AAG CAT GTG AGT TTA GAG TAT CTT ATA GGG CTT TTT 155
Gly Asn Lys Asp Lys His Val Ser Leu Glu Tyr Leu Ile Gly Leu Phe
 20 25 30

ATG GAT AAA AAA ACA ACT AAT CTA AGC AAT ACT GAC AAG TAT ATT ATA 203
Met Asp Lys Lys Thr Thr Asn Leu Ser Asn Thr Asp Lys Tyr Ile Ile
 35 40 45

GGC ACA ATT CAA ACA GAG GCA CTA GAG CAA GAA ATA GAA TGG TTT TCA 251
Gly Thr Ile Gln Thr Glu Ala Leu Glu Gln Glu Ile Glu Trp Phe Ser
 50 55 60

CAA GAC TAT CAC ATT CCT ATG GAG AAT ATT TTA CAT GTC CTT TCT ATC 299
Gln Asp Tyr His Ile Pro Met Glu Asn Ile Leu His Val Leu Ser Ile
 65 70 75

AAT CCC TAT CAA TGAAAAGAGC CTTAGTTTTA TCAAAAACAA CTTTCAAGCT 351
Asn Pro Tyr Gln
80

```

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

```

Met Ser Phe Ala Pro Met Leu Leu Ala Thr Ile Asn Asn Ser Ile Gly
 1 5 10 15
Asn Lys Asp Lys His Val Ser Leu Glu Tyr Leu Ile Gly Leu Phe Met
 20 25 30
Asp Lys Lys Thr Thr Asn Leu Ser Asn Thr Asp Lys Tyr Ile Ile Gly
 35 40 45
Thr Ile Gln Thr Glu Ala Leu Glu Gln Glu Ile Glu Trp Phe Ser Gln
 50 55 60
Asp Tyr His Ile Pro Met Glu Asn Ile Leu His Val Leu Ser Ile Asn
 65 70 75 80
Pro Tyr Gln

```

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1934 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 67...1866
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

```
AAACATAGGG CAAATCTAGT TGGCACAAAA ACAGCTAGTC CTGTGCTTAT TAAAAACATA 60
GGGCAA ATG AAA CGC TCC CAC TTA GAA AAT GCC CTA AAT TAT GCT TTA 108
Met Lys Arg Ser His Leu Glu Asn Ala Leu Asn Tyr Ala Leu
 1 5 10

GAA AAT AGC GAA ACA GCT TAC AAT GAA ATG TTT TTA GAA TGC GAT AAG 156
Glu Asn Ser Glu Thr Ala Tyr Asn Glu Met Phe Leu Glu Cys Asp Lys
 15 20 25 30

CAA TTC ATC TTA GAG AGT TGG CTC AAT GAC TTT GAT TTG ACT AAA GAT 204
Gln Phe Ile Leu Glu Ser Trp Leu Asn Asp Phe Asp Leu Thr Lys Asp
 35 40 45

TAT AAC GAG ACT ATG CAC TTA GTT TTT TCT ATC AAA GAT AAG CCA GAT 252
Tyr Asn Glu Thr Met His Leu Val Phe Ser Ile Lys Asp Lys Pro Asp
 50 55 60

GAA GAG ACA ATG CAA GGG CTT TTA CAT TCT ACT TGG GAG AGC TTA AAA 300
Glu Glu Thr Met Gln Gly Leu Leu His Ser Thr Trp Glu Ser Leu Lys
 65 70 75

ATA AGA TTG CCT GAA TAC AAG TTT GCC CTT GTG CCA CAC GCT CAT CAA 348
Ile Arg Leu Pro Glu Tyr Lys Phe Ala Leu Val Pro His Ala His Gln
 80 85 90

GAC CAT GCC CAT ATC CAT TGT TTT ATC AAT AAG ACT AAT CAG CTC ACA 396
Asp His Ala His Ile His Cys Phe Ile Asn Lys Thr Asn Gln Leu Thr
 95 100 105 110

CGA AGA AGA CTG CGT TTT AAG GGG CAT GAA GAT TGT AAA GAA TTT TTT 444
Arg Arg Arg Leu Arg Phe Lys Gly His Glu Asp Cys Lys Glu Phe Phe
 115 120 125

AAT GAA TTA AGA AGT GAG TTT GCT TAT AGG TTG AAT GAC CAC TTA TTG 492
Asn Glu Leu Arg Ser Glu Phe Ala Tyr Arg Leu Asn Asp His Leu Leu
 130 135 140

AGC GAA GAA TAC TTG TAT GTC AAT GAG CCA AAA CTT AAA GAG CTA GAC 540
Ser Glu Glu Tyr Leu Tyr Val Asn Glu Pro Lys Leu Lys Glu Leu Asp
 145 150 155
```

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| AAT ATC AAA CAA CAA TTA CAA GAC TTG GAA AAA GAA GAA AAA GCC TTA<br>Asn Ile Lys Gln Gln Leu Gln Asp Leu Glu Lys Glu Glu Lys Ala Leu<br>160 165 170     | 588  |
| GAA CAA ATC AAA TCC CCA CAA GAT GAG TGG GAC TTA AAC AAG GCT TTA<br>Glu Gln Ile Lys Ser Pro Gln Asp Glu Trp Asp Leu Asn Lys Ala Leu<br>175 180 185 190 | 636  |
| CAA AGC GAG TAT TTA CAA GAA CTC AAA TAT AAA AAC AAA GCA AAA GCC<br>Gln Ser Glu Tyr Leu Gln Glu Leu Lys Tyr Lys Asn Lys Ala Lys Ala<br>195 200 205     | 684  |
| CTA GAC ATT CAA AAT AAC CAC AGC ACC CCT TTA AAA CAA AAG ATT TCT<br>Leu Asp Ile Gln Asn Asn His Ser Thr Pro Leu Lys Gln Lys Ile Ser<br>210 215 220     | 732  |
| GAA TTT AAA ATC GCT CTG TTT AAT CAC AAA GAC ACA AGC GAT GAT GAA<br>Glu Phe Lys Ile Ala Leu Phe Asn His Lys Asp Thr Ser Asp Asp Glu<br>225 230 235     | 780  |
| AAA GAA CAG CTA GAT ATT GAC AGG ATA GAT AAG AGA AAA CCA GTA AGC<br>Lys Glu Gln Leu Asp Ile Asp Arg Ile Asp Lys Arg Lys Pro Val Ser<br>240 245 250     | 828  |
| GAA CAC TTA AAA AAC ACT AAC AAA CAC GAG CTA TAC GAA CTC TTA GGC<br>Glu His Leu Lys Asn Thr Asn Lys His Glu Leu Tyr Glu Leu Leu Gly<br>255 260 265 270 | 876  |
| TTT TAT CAA AAA GAA TTA GAT AAA AAA CAA AAC CAT TCA GCC TTT AAG<br>Phe Tyr Gln Lys Glu Leu Asp Lys Lys Gln Asn His Ser Ala Phe Lys<br>275 280 285     | 924  |
| AAT TTT GCT ATT CTC AAT GGT TTA GAC AGA GAC TTT GAA AGA GAG ACT<br>Asn Phe Ala Ile Leu Asn Gly Leu Asp Arg Asp Phe Glu Arg Glu Thr<br>290 295 300     | 972  |
| AAT GGC TAT TCT GTT TTA AAG AAA AAA GAA ATG CTT TTA AAT AAG CTT<br>Asn Gly Tyr Ser Val Leu Lys Lys Lys Glu Met Leu Leu Asn Lys Leu<br>305 310 315     | 1020 |
| GAA CAC CTA GAC AAA CGC CTT TTA GAT AAA AAC TCA CAC TTA CTA TTA<br>Glu His Leu Asp Lys Arg Leu Leu Asp Lys Asn Ser His Leu Leu Leu<br>320 325 330     | 1068 |
| GCC CAG CTA AGA AAT GAA GTT AAA ACC AAG CAA AAC ATC CAA TAC AAC<br>Ala Gln Leu Arg Asn Glu Val Lys Thr Lys Gln Asn Ile Gln Tyr Asn<br>335 340 345 350 | 1116 |
| ACT CTA ACT AAT CCT ATT CTT TTA GCC AAA GCC TTA GAA CTT TCT AAA<br>Thr Leu Thr Asn Pro Ile Leu Leu Ala Lys Ala Leu Glu Leu Ser Lys<br>355 360 365     | 1164 |
| GAT AAA CGC CCC ACT CTC AAA ACT TTT AAA AAC GCT TAT TTT AGT GCT<br>Asp Lys Arg Pro Thr Leu Lys Thr Phe Lys Asn Ala Tyr Phe Ser Ala<br>370 375 380     | 1212 |
| AGA AAA TAT CAA TTC ATG CTA GAG AGC TTT AAA ACT AAG CAA AAT GAC<br>Arg Lys Tyr Gln Phe Met Leu Glu Ser Phe Lys Thr Lys Gln Asn Asp                    | 1260 |

| 385                                                                                                                                                   | 390 | 395 |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----|------|
| CCC ACT TAC AAG CTT AAT GAT AAC ACT TAT GAG CTA GTG AGT AAG CAA<br>Pro Thr Tyr Lys Leu Asn Asp Asn Thr Tyr Glu Leu Val Ser Lys Gln<br>400 405 410     |     |     | 1308 |
| CTA CAA GAC TAT CAA AAC ACC ATG CTT TTA TTA GCC AAA GAG AGA TTA<br>Leu Gln Asp Tyr Gln Asn Thr Met Leu Leu Leu Ala Lys Glu Arg Leu<br>415 420 425 430 |     |     | 1356 |
| CTT TTT TTA GAA CAA GAT TTA AAA CAA AAA GAA GAA GAG TTT GAA AGA<br>Leu Phe Leu Glu Gln Asp Leu Lys Gln Lys Glu Glu Glu Phe Glu Arg<br>435 440 445     |     |     | 1404 |
| GCC AAA GAA CAT TAT GTG AAA TCT TCA AAA CAT TAT AGA GAA ACT TCA<br>Ala Lys Glu His Tyr Val Lys Ser Ser Lys His Tyr Arg Glu Thr Ser<br>450 455 460     |     |     | 1452 |
| TTG TCT CCA AAA GAA AAA CAA GGC TTT CTC AAA CAA ATT AAA CAA TTT<br>Leu Ser Pro Lys Glu Lys Gln Gly Phe Leu Lys Gln Ile Lys Gln Phe<br>465 470 475     |     |     | 1500 |
| TCT AAA ATT TCT AAG GAT ATT CTC TAT ACT TGT AAT GAG ATC ATA GGA<br>Ser Lys Ile Ser Lys Asp Ile Leu Tyr Thr Cys Asn Glu Ile Ile Gly<br>480 485 490     |     |     | 1548 |
| GCT AAT AGG TTT TTA ACC CAC TAT GAC AAC CTA AAC CTT GAA AAA GTC<br>Ala Asn Arg Phe Leu Thr His Tyr Asp Asn Leu Asn Leu Glu Lys Val<br>495 500 505 510 |     |     | 1596 |
| CTA GAA CAC GCT AAA GAT ACT AAG CTA GAG CAA AAA GAA ATT CAA GCT<br>Leu Glu His Ala Lys Asp Thr Lys Leu Glu Gln Lys Glu Ile Gln Ala<br>515 520 525     |     |     | 1644 |
| ATC ACA AAA GAG CCT AAT AAC GAT GAG CCT TGG ATT GAG TTT GGT AAA<br>Ile Thr Lys Glu Pro Asn Asn Asp Glu Pro Trp Ile Glu Phe Gly Lys<br>530 535 540     |     |     | 1692 |
| AAA GAA CAA GCT AGA GCT AAA GCA CAC TAT CAA GCT ATG CTA GAA AAA<br>Lys Glu Gln Ala Arg Ala Lys Ala His Tyr Gln Ala Met Leu Glu Lys<br>545 550 555     |     |     | 1740 |
| GAA AAA GCT AAA GAA TTA GCT AAA CAA CAA GCT AAC ACC TTG CAC TCT<br>Glu Lys Ala Lys Glu Leu Ala Lys Gln Gln Ala Asn Thr Leu His Ser<br>560 565 570     |     |     | 1788 |
| AAT GAG CTT GAT GAT GAC CCT AAA GCT CAT GCT GGA TTA AAA CAA AAT<br>Asn Glu Leu Asp Asp Asp Pro Lys Ala His Ala Gly Leu Lys Gln Asn<br>575 580 585 590 |     |     | 1836 |
| GAC AAC ACA AAC TTT AAA GGG CGT AAT AGA TAATGCTCTC AAGCGATGAT TGC<br>Asp Asn Thr Asn Phe Lys Gly Arg Asn Arg<br>595 600                               |     |     | 1889 |
| CTTTAATGTT CTTAATAAAG AATATACCCT TTGAAAGGGG TTTAT                                                                                                     |     |     | 1934 |

(2) INFORMATION FOR SEQ ID NO:202:



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Arg | Ser | His | Leu | Glu | Asn | Ala | Leu | Asn | Tyr | Ala | Leu | Glu | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Glu | Thr | Ala | Tyr | Asn | Glu | Met | Phe | Leu | Glu | Cys | Asp | Lys | Gln | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Leu | Glu | Ser | Trp | Leu | Asn | Asp | Phe | Asp | Leu | Thr | Lys | Asp | Tyr | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Thr | Met | His | Leu | Val | Phe | Ser | Ile | Lys | Asp | Lys | Pro | Asp | Glu | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Met | Gln | Gly | Leu | Leu | His | Ser | Thr | Trp | Glu | Ser | Leu | Lys | Ile | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Pro | Glu | Tyr | Lys | Phe | Ala | Leu | Val | Pro | His | Ala | His | Gln | Asp | His |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | His | Ile | His | Cys | Phe | Ile | Asn | Lys | Thr | Asn | Gln | Leu | Thr | Arg | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Leu | Arg | Phe | Lys | Gly | His | Glu | Asp | Cys | Lys | Glu | Phe | Phe | Asn | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Arg | Ser | Glu | Phe | Ala | Tyr | Arg | Leu | Asn | Asp | His | Leu | Leu | Ser | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Tyr | Leu | Tyr | Val | Asn | Glu | Pro | Lys | Leu | Lys | Glu | Leu | Asp | Asn | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Gln | Gln | Leu | Gln | Asp | Leu | Glu | Lys | Glu | Glu | Lys | Ala | Leu | Glu | Gln |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Lys | Ser | Pro | Gln | Asp | Glu | Trp | Asp | Leu | Asn | Lys | Ala | Leu | Gln | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Tyr | Leu | Gln | Glu | Leu | Lys | Tyr | Lys | Asn | Lys | Ala | Lys | Ala | Leu | Asp |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Gln | Asn | Asn | His | Ser | Thr | Pro | Leu | Lys | Gln | Lys | Ile | Ser | Glu | Phe |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Lys | Ile | Ala | Leu | Phe | Asn | His | Lys | Asp | Thr | Ser | Asp | Asp | Glu | Lys | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gln | Leu | Asp | Ile | Asp | Arg | Ile | Asp | Lys | Arg | Lys | Pro | Val | Ser | Glu | His |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Lys | Asn | Thr | Asn | Lys | His | Glu | Leu | Tyr | Glu | Leu | Leu | Gly | Phe | Tyr |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Gln | Lys | Glu | Leu | Asp | Lys | Lys | Gln | Asn | His | Ser | Ala | Phe | Lys | Asn | Phe |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ala | Ile | Leu | Asn | Gly | Leu | Asp | Arg | Asp | Phe | Glu | Arg | Glu | Thr | Asn | Gly |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Tyr | Ser | Val | Leu | Lys | Lys | Lys | Glu | Met | Leu | Leu | Asn | Lys | Leu | Glu | His |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Leu | Asp | Lys | Arg | Leu | Leu | Asp | Lys | Asn | Ser | His | Leu | Leu | Leu | Ala | Gln |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Leu | Arg | Asn | Glu | Val | Lys | Thr | Lys | Gln | Asn | Ile | Gln | Tyr | Asn | Thr | Leu |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     |     | 350 |     |     |
| Thr | Asn | Pro | Ile | Leu | Leu | Ala | Lys | Ala | Leu | Glu | Leu | Ser | Lys | Asp | Lys |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |
| Arg | Pro | Thr | Leu | Lys | Thr | Phe | Lys | Asn | Ala | Tyr | Phe | Ser | Ala | Arg | Lys |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |



|                   |                   |                   |                   |                   |                   |                   |                                      |                   |                   |                   |                   |                   |                   |                   |                   |     |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| GAA<br>Glu        | AAG<br>Lys        | TTT<br>Phe<br>45  | GCT<br>Ala        | AAA<br>Lys        | AAT<br>Asn        | TTA<br>Leu        | ACC<br>Thr<br>50                     | CAA<br>Gln        | CTG<br>Leu        | ACA<br>Thr        | CAA<br>Gln        | GAA<br>Glu<br>55  | GAA<br>Glu        | TTC<br>Phe        | ATG<br>Met        | 195 |
| CGT<br>Arg        | TTA<br>Leu<br>60  | AGA<br>Arg        | GAG<br>Glu        | CCA<br>Pro        | CAA<br>Gln        | AAA<br>Lys<br>65  | CAA<br>Gln                           | GTG<br>Val        | GTC<br>Val        | ATC<br>Ile<br>70  | AAA<br>Lys        | AAC<br>Asn        | ATA<br>Ile        | GGC<br>Gly        | AAT<br>Asn        | 243 |
| ATG<br>Met<br>75  | ACA<br>Thr        | CGC<br>Arg        | CTG<br>Leu        | CAT<br>His<br>80  | TCA<br>Ser        | AAA<br>Lys        | AGA<br>Arg                           | GCG<br>Ala        | ATG<br>Met<br>85  | GAT<br>Asp        | TAT<br>Tyr        | ATC<br>Ile        | GCT<br>Ala        | AAA<br>Lys<br>90  | CAT<br>His        | 291 |
| GGT<br>Gly        | GAG<br>Glu        | CTA<br>Leu        | GTG<br>Val        | AGA<br>Arg<br>95  | GAT<br>Asp        | GAA<br>Glu        | TTT<br>Phe                           | TTT<br>Phe<br>100 | AAT<br>Asn        | GAA<br>Glu        | GTT<br>Val        | AAT<br>Asn        | TAT<br>Tyr        | AAT<br>Asn<br>105 | GAC<br>Asp        | 339 |
| ATA<br>Ile        | GCA<br>Ala        | GAG<br>Glu        | CAA<br>Gln<br>110 | TGG<br>Trp        | AAT<br>Asn        | GAG<br>Glu        | CAA<br>Gln<br>115                    | TTT<br>Phe<br>115 | GAA<br>Glu        | AAA<br>Lys        | TTA<br>Leu        | TTA<br>Leu<br>120 | GAA<br>Glu<br>120 | AAT<br>Asn        | AAG<br>Lys        | 387 |
| AGC<br>Ser        | CGT<br>Arg<br>125 | GTT<br>Val        | AAA<br>Lys        | AAT<br>Asn        | TGC<br>Cys        | GCT<br>Ala        | TTA<br>Leu<br>130                    | CAT<br>His        | CTA<br>Leu        | GTG<br>Val        | TTT<br>Phe<br>135 | AGC<br>Ser<br>135 | ATT<br>Ile        | GAT<br>Asp        | GAA<br>Glu        | 435 |
| AAT<br>Asn<br>140 | TGT<br>Cys        | AAT<br>Asn        | GAA<br>Glu        | AAA<br>Lys        | AAT<br>Asn<br>145 | TTA<br>Leu        | AAA<br>Lys                           | GCT<br>Ala        | TTG<br>Leu        | GAA<br>Glu        | TTA<br>Leu<br>150 | AGC<br>Ser        | GTG<br>Val        | TAT<br>Tyr        | CAA<br>Gln        | 483 |
| ACA<br>Thr<br>155 | CTC<br>Leu        | ACT<br>Thr        | AAC<br>Asn        | ACG<br>Thr<br>160 | CTA<br>Leu        | GGT<br>Gly        | TAT<br>Tyr                           | GAT<br>Asp        | TAT<br>Tyr<br>165 | CCT<br>Pro        | TTT<br>Phe        | ATA<br>Ile        | ATG<br>Met        | AAA<br>Lys        | CTC<br>Leu<br>170 | 531 |
| CAT<br>His        | ACA<br>Thr        | CAC<br>His        | CAA<br>Gln<br>175 | AAC<br>Asn        | AAT<br>Asn        | CCG<br>Pro        | CAT<br>His                           | GCG<br>Ala<br>180 | CAT<br>His        | GTG<br>Val        | ATT<br>Ile        | ATC<br>Ile        | AAC<br>Asn        | AAA<br>Lys<br>185 | ACT<br>Thr        | 579 |
| AAC<br>Asn        | AAA<br>Lys        | ATT<br>Ile<br>190 | ACC<br>Thr        | AAT<br>Asn        | AAG<br>Lys        | CAA<br>Gln        | CTA<br>Leu<br>195                    | TGC<br>Cys        | TTT<br>Phe<br>195 | AAT<br>Asn        | TCT<br>Ser        | AAA<br>Lys<br>200 | GAC<br>Asp        | AGC<br>Ser        | TGT<br>Cys        | 627 |
| AAA<br>Lys        | GAG<br>Glu        | TTT<br>Phe<br>205 | TAC<br>Tyr        | CAC<br>His        | ACA<br>Thr        | CTA<br>Leu<br>210 | AGA<br>Arg                           | GAA<br>Glu        | ACA<br>Thr<br>215 | TTT<br>Phe        | AAA<br>Lys<br>215 | GAT<br>Asp        | TAT<br>Tyr        | TTA<br>Leu        | TTT<br>Phe        | 675 |
| GCT<br>Ala        | AAC<br>Asn<br>220 | TCA<br>Ser        | AAA<br>Lys        | GGC<br>Gly        | GAA<br>Glu        | TTG<br>Leu<br>225 | CAA<br>Gln                           | TAT<br>Tyr        | TCT<br>Ser        | AAC<br>Asn<br>230 | ACG<br>Thr        | CCT<br>Pro        | AAT<br>Asn        | ATT<br>Ile        | TAT<br>Tyr        | 723 |
| AAG<br>Lys<br>235 | GCG<br>Ala        | ATT<br>Ile        | AAA<br>Lys        | GAC<br>Asp<br>240 | ATA<br>Ile        | GAA<br>Glu        | ACA<br>Thr                           | GAG<br>Glu        | CTA<br>Leu<br>245 | GAT<br>Asp        | GCA<br>Ala        | CTA<br>Leu        | GAA<br>Glu        | AAC<br>Asn        | AGG<br>Arg<br>250 | 771 |
| CTA<br>Leu        | GAA<br>Glu        | ACA<br>Thr        | ATA<br>Ile        | AGA<br>Arg<br>255 | GTT<br>Val        | TTA<br>Leu        | GGC<br>Gly                           | ATG<br>Met<br>260 | AAA<br>Lys        | ACT<br>Thr        | ATT<br>Ile        | TTT<br>Phe        | ATA<br>Ile<br>265 | AAG<br>Lys        | TTT<br>Phe        | 819 |
| TGG<br>Trp        | GTA<br>Val        | GTG<br>Val        | CAA<br>Gln        | CTT<br>Leu        | CTC<br>Leu        | AAA<br>Lys        | TAGAAAGTTT GAAAAAAGA GAAAATGCCC TATT |                   |                   |                   |                   |                   |                   |                   |                   | 874 |

TGATCATTTA

## (2) INFORMATION FOR SEQ ID NO:204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

```

Met Ala Leu Glu Lys Ser Tyr Ser Lys Asn Phe Glu Ser Asp Glu Leu
 1 5 10 15
Phe Asp Tyr Glu Ile Ile Lys Pro Lys Lys Thr Leu Lys Ile Gln Tyr
 20 25 30
Thr Tyr Ala Lys Arg Tyr Tyr Lys Glu Val Glu Lys Phe Ala Lys Asn
 35 40 45
Leu Thr Gln Leu Thr Gln Glu Phe Met Arg Leu Arg Glu Pro Gln
 50 55 60
Lys Gln Val Val Ile Lys Asn Ile Gly Asn Met Thr Arg Leu His Ser
65 70 75 80
Lys Arg Ala Met Asp Tyr Ile Ala Lys His Gly Glu Leu Val Arg Asp
 85 90 95
Glu Phe Phe Asn Glu Val Asn Tyr Asn Asp Ile Ala Glu Gln Trp Asn
 100 105 110
Glu Gln Phe Glu Lys Leu Leu Glu Asn Lys Ser Arg Val Lys Asn Cys
 115 120 125
Ala Leu His Leu Val Phe Ser Ile Asp Glu Asn Cys Asn Glu Lys Asn
 130 135 140
Leu Lys Ala Leu Glu Leu Ser Val Tyr Gln Thr Leu Thr Asn Thr Leu
145 150 155 160
Gly Tyr Asp Tyr Pro Phe Ile Met Lys Leu His Thr His Gln Asn Asn
 165 170 175
Pro His Ala His Val Ile Ile Asn Lys Thr Asn Lys Ile Thr Asn Lys
 180 185 190
Gln Leu Cys Phe Asn Ser Lys Asp Ser Cys Lys Glu Phe Tyr His Thr
 195 200 205
Leu Arg Glu Thr Phe Lys Asp Tyr Leu Phe Ala Asn Ser Lys Gly Glu
 210 215 220
Leu Gln Tyr Ser Asn Thr Pro Asn Ile Tyr Lys Ala Ile Lys Asp Ile
225 230 235 240
Glu Thr Glu Leu Asp Ala Leu Glu Asn Arg Leu Glu Thr Ile Arg Val
 245 250 255
Leu Gly Met Lys Thr Ile Phe Ile Lys Phe Trp Val Val Gln Leu Leu
 260 265 270
Lys

```

## (2) INFORMATION FOR SEQ ID NO:205:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 49...519  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATAAACAACC ATGACAAACT AACGGACTTT AAGCAATACC AAACAGAC ATG AAA GAA  | 57  |
| Met Lys Glu                                                       |     |
| 1                                                                 |     |
| TTA CTA GGG ATA GAA ATA GAT GAA GAG CTG GAT ACT AAA CGA CTT ATC   | 105 |
| Leu Leu Gly Ile Glu Ile Asp Glu Glu Leu Asp Thr Lys Arg Leu Ile   |     |
| 5 10 15                                                           |     |
| CCT ACT TAT TCC AAA TTG TAT TCT TTA AAA AAA TAC TCT AAA AAA TTT   | 153 |
| Pro Thr Tyr Ser Lys Leu Tyr Ser Leu Lys Lys Tyr Ser Lys Lys Phe   |     |
| 20 25 30 35                                                       |     |
| AAA AGA TTA CAA AGA AAA CAA AGC CGT AGG GTG TTA AAG TCT AAA CAA   | 201 |
| Lys Arg Leu Gln Arg Lys Gln Ser Arg Arg Val Leu Lys Ser Lys Gln   |     |
| 40 45 50                                                          |     |
| AAC AAA ACC AAA TTA GGA GGT AAT TTT TAC AAA ACC CAA AAG AAA TTA   | 249 |
| Asn Lys Thr Lys Leu Gly Gly Asn Phe Tyr Lys Thr Gln Lys Lys Leu   |     |
| 55 60 65                                                          |     |
| AAC CAA GCC TTT GAC AAG TCT AGT CAT CAA AAA ACA GAC AGA TAC CAT   | 297 |
| Asn Gln Ala Phe Asp Lys Ser Ser His Gln Lys Thr Asp Arg Tyr His   |     |
| 70 75 80                                                          |     |
| AAA ATC ACA AGC GAA CTT TCA AAG CAA TTT GAA TTG ATA GTA GTT GAA   | 345 |
| Lys Ile Thr Ser Glu Leu Ser Lys Gln Phe Glu Leu Ile Val Val Glu   |     |
| 85 90 95                                                          |     |
| GAT TTG CAA GTA AAA AAC ATG ACT AAA AGA GCT AAA CTC AAA AAT GTT   | 393 |
| Asp Leu Gln Val Lys Asn Met Thr Lys Arg Ala Lys Leu Lys Asn Val   |     |
| 100 105 110 115                                                   |     |
| AAA CAA AAG AGT GGG CTT AAT CAA TCT ATT TTA AAC GCT TCA TTC TAT   | 441 |
| Lys Gln Lys Ser Gly Leu Asn Gln Ser Ile Leu Asn Ala Ser Phe Tyr   |     |
| 120 125 130                                                       |     |
| CAA ATC ATC TCT TTT TTA GAC TAC AAA CAA CAG CAT AAT GGC AAA TTG   | 489 |
| Gln Ile Ile Ser Phe Leu Asp Tyr Lys Gln Gln His Asn Gly Lys Leu   |     |
| 135 140 145                                                       |     |
| TTA GTG AAA GTT TCC CCC ACA ATA TAC GAG TAAAACTTGC CATTGTTGTG GGA | 542 |
| Leu Val Lys Val Ser Pro Thr Ile Tyr Glu                           |     |
| 150 155                                                           |     |
| ATATCAACCA CAAGC                                                  | 557 |

| 1. <i>Chlorophyll a</i> (mg/g) |  | 2. <i>Chlorophyll b</i> (mg/g) |  | 3. <i>Chlorophyll a+b</i> (mg/g) |  | 4. <i>Carotenoids</i> (mg/g) |  | 5. <i>Protein</i> (mg/g) |  | 6. <i>Starch</i> (mg/g) |  | 7. <i>Cellulose</i> (mg/g) |  | 8. <i>Hemicellulose</i> (mg/g) |  | 9. <i>Lignin</i> (mg/g) |  | 10. <i>Phenolics</i> (mg/g) |  | 11. <i>Flavonoids</i> (mg/g) |  | 12. <i>Anthracenes</i> (mg/g) |  | 13. <i>Terpenes</i> (mg/g) |  | 14. <i>Alkaloids</i> (mg/g) |  | 15. <i>Saponins</i> (mg/g) |  | 16. <i>Glycosides</i> (mg/g) |  | 17. <i>Enzymes</i> (mg/g) |  | 18. <i>Antioxidants</i> (mg/g) |  | 19. <i>Antibiotics</i> (mg/g) |  | 20. <i>Antifungals</i> (mg/g) |  | 21. <i>Antiparasitics</i> (mg/g) |  | 22. <i>Anticancer</i> (mg/g) |  | 23. <i>Antiviral</i> (mg/g) |  | 24. <i>Antibacterial</i> (mg/g) |  | 25. <i>Antimicrobial</i> (mg/g) |  | 26. <i>Antipollutants</i> (mg/g) |  | 27. <i>Anticorrosive</i> (mg/g) |  | 28. <i>Anticatalytic</i> (mg/g) |  | 29. <i>Anticorrosive</i> (mg/g) |  | 30. <i>Anticatalytic</i> (mg/g) |  | 31. <i>Anticorrosive</i> (mg/g) |  | 32. <i>Anticatalytic</i> (mg/g) |  | 33. <i>Anticorrosive</i> (mg/g) |  | 34. <i>Anticatalytic</i> (mg/g) |  | 35. <i>Anticorrosive</i> (mg/g) |  | 36. <i>Anticatalytic</i> (mg/g) |  | 37. <i>Anticorrosive</i> (mg/g) |  | 38. <i>Anticatalytic</i> (mg/g) |  | 39. <i>Anticorrosive</i> (mg/g) |  | 40. <i>Anticatalytic</i> (mg/g) |  | 41. <i>Anticorrosive</i> (mg/g) |  | 42. <i>Anticatalytic</i> (mg/g) |  | 43. <i>Anticorrosive</i> (mg/g) |  | 44. <i>Anticatalytic</i> (mg/g) |  | 45. <i>Anticorrosive</i> (mg/g) |  | 46. <i>Anticatalytic</i> (mg/g) |  | 47. <i>Anticorrosive</i> (mg/g) |  | 48. <i>Anticatalytic</i> (mg/g) |  | 49. <i>Anticorrosive</i> (mg/g) |  | 50. <i>Anticatalytic</i> (mg/g) |  | 51. <i>Anticorrosive</i> (mg/g) |  | 52. <i>Anticatalytic</i> (mg/g) |  | 53. <i>Anticorrosive</i> (mg/g) |  | 54. <i>Anticatalytic</i> (mg/g) |  | 55. <i>Anticorrosive</i> (mg/g) |  | 56. <i>Anticatalytic</i> (mg/g) |  | 57. <i>Anticorrosive</i> (mg/g) |  | 58. <i>Anticatalytic</i> (mg/g) |  | 59. <i>Anticorrosive</i> (mg/g) |  | 60. <i>Anticatalytic</i> (mg/g) |  | 61. <i>Anticorrosive</i> (mg/g) |  | 62. <i>Anticatalytic</i> (mg/g) |  | 63. <i>Anticorrosive</i> (mg/g) |  | 64. <i>Anticatalytic</i> (mg/g) |  | 65. <i>Anticorrosive</i> (mg/g) |  | 66. <i>Anticatalytic</i> (mg/g) |  | 67. <i>Anticorrosive</i> (mg/g) |  | 68. <i>Anticatalytic</i> (mg/g) |  | 69. <i>Anticorrosive</i> (mg/g) |  | 70. <i>Anticatalytic</i> (mg/g) |  | 71. <i>Anticorrosive</i> (mg/g) |  | 72. <i>Anticatalytic</i> (mg/g) |  | 73. <i>Anticorrosive</i> (mg/g) |  | 74. <i>Anticatalytic</i> (mg/g) |  | 75. <i>Anticorrosive</i> (mg/g) |  | 76. <i>Anticatalytic</i> (mg/g) |  | 77. <i>Anticorrosive</i> (mg/g) |  | 78. <i>Anticatalytic</i> (mg/g) |  | 79. <i>Anticorrosive</i> (mg/g) |  | 80. <i>Anticatalytic</i> (mg/g) |  | 81. <i>Anticorrosive</i> (mg/g) |  | 82. <i>Anticatalytic</i> (mg/g) |  | 83. <i>Anticorrosive</i> (mg/g) |  | 84. <i>Anticatalytic</i> (mg/g) |  | 85. <i>Anticorrosive</i> (mg/g) |  | 86. <i>Anticatalytic</i> (mg/g) |  | 87. <i>Anticorrosive</i> (mg/g) |  | 88. <i>Anticatalytic</i> (mg/g) |  | 89. <i>Anticorrosive</i> (mg/g) |  | 90. <i>Anticatalytic</i> (mg/g) |  | 91. <i>Anticorrosive</i> (mg/g) |  | 92. <i>Anticatalytic</i> (mg/g) |  | 93. <i>Anticorrosive</i> (mg/g) |  | 94. <i>Anticatalytic</i> (mg/g) |  | 95. <i>Anticorrosive</i> (mg/g) |  | 96. <i>Anticatalytic</i> (mg/g) |  | 97. <i>Anticorrosive</i> (mg/g) |  | 98. <i>Anticatalytic</i> (mg/g) |  | 99. <i>Anticorrosive</i> (mg/g) |  | 100. <i>Anticatalytic</i> (mg/g) |  | 101. <i>Anticorrosive</i> (mg/g) |  | 102. <i>Anticatalytic</i> (mg/g) |  | 103. <i>Anticorrosive</i> (mg/g) |  | 104. <i>Anticatalytic</i> (mg/g) |  | 105. <i>Anticorrosive</i> (mg/g) |  | 106. <i>Anticatalytic</i> (mg/g) |  | 107. <i>Anticorrosive</i> (mg/g) |  | 108. <i>Anticatalytic</i> (mg/g) |  | 109. <i>Anticorrosive</i> (mg/g) |  | 110. <i>Anticatalytic</i> (mg/g) |  | 111. <i>Anticorrosive</i> (mg/g) |  | 112. <i>Anticatalytic</i> (mg/g) |  | 113. <i>Anticorrosive</i> (mg/g) |  | 114. <i>Anticatalytic</i> (mg/g) |  | 115. <i>Anticorrosive</i> (mg/g) |  | 116. <i>Anticatalytic</i> (mg/g) |  | 117. <i>Anticorrosive</i> (mg/g) |  | 118. <i>Anticatalytic</i> (mg/g) |  | 119. <i>Anticorrosive</i> (mg/g) |  | 120. <i>Anticatalytic</i> (mg/g) |  | 121. <i>Anticorrosive</i> (mg/g) |  | 122. <i>Anticatalytic</i> (mg/g) |  | 123. <i>Anticorrosive</i> (mg/g) |  | 124. <i>Anticatalytic</i> (mg/g) |  | 125. <i>Anticorrosive</i> (mg/g) |  | 126. <i>Anticatalytic</i> (mg/g) |  | 127. <i>Anticorrosive</i> (mg/g) |  | 128. <i>Anticatalytic</i> (mg/g) |  | 129. <i>Anticorrosive</i> (mg/g) |  | 130. <i>Anticatalytic</i> (mg/g) |  | 131. <i>Anticorrosive</i> (mg/g) |  | 132. <i>Anticatalytic</i> (mg/g) |  | 133. <i>Anticorrosive</i> (mg/g) |  | 134. <i>Anticatalytic</i> (mg/g) |  | 135. <i>Anticorrosive</i> (mg/g) |  | 136. <i>Anticatalytic</i> (mg/g) |  | 137. <i>Anticorrosive</i> (mg/g) |  | 138. <i>Anticatalytic</i> (mg/g) |  | 139. <i>Anticorrosive</i> (mg/g) |  | 140. <i>Anticatalytic</i> (mg/g) |  | 141. <i>Anticorrosive</i> (mg/g) |  | 142. <i>Anticatalytic</i> (mg/g) |  | 143. <i>Anticorrosive</i> (mg/g) |  | 144. <i>Anticatalytic</i> (mg/g) |  | 145. <i>Anticorrosive</i> (mg/g) |  | 146. <i>Anticatalytic</i> (mg/g) |  | 147. <i>Anticorrosive</i> (mg/g) |  | 148. <i>Anticatalytic</i> (mg/g) |  | 149. <i>Anticorrosive</i> (mg/g) |  | 150. <i>Anticatalytic</i> (mg/g) |  | 151. <i>Anticorrosive</i> (mg/g) |  | 152. <i>Anticatalytic</i> (mg/g) |  | 153. <i>Anticorrosive</i> (mg/g) |  | 154. <i>Anticatalytic</i> (mg/g) |  | 155. <i>Anticorrosive</i> (mg/g) |  | 156. <i>Anticatalytic</i> (mg/g) |  | 157. <i>Anticorrosive</i> (mg/g) |  | 158. <i>Anticatalytic</i> (mg/g) |  | 159. <i>Anticorrosive</i> (mg/g) |  | 160. <i>Anticatalytic</i> (mg/g) |  | 161. <i>Anticorrosive</i> (mg/g) |  | 162. <i>Anticatalytic</i> (mg/g)</ |  |
|--------------------------------|--|--------------------------------|--|----------------------------------|--|------------------------------|--|--------------------------|--|-------------------------|--|----------------------------|--|--------------------------------|--|-------------------------|--|-----------------------------|--|------------------------------|--|-------------------------------|--|----------------------------|--|-----------------------------|--|----------------------------|--|------------------------------|--|---------------------------|--|--------------------------------|--|-------------------------------|--|-------------------------------|--|----------------------------------|--|------------------------------|--|-----------------------------|--|---------------------------------|--|---------------------------------|--|----------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|------------------------------------|--|
|--------------------------------|--|--------------------------------|--|----------------------------------|--|------------------------------|--|--------------------------|--|-------------------------|--|----------------------------|--|--------------------------------|--|-------------------------|--|-----------------------------|--|------------------------------|--|-------------------------------|--|----------------------------|--|-----------------------------|--|----------------------------|--|------------------------------|--|---------------------------|--|--------------------------------|--|-------------------------------|--|-------------------------------|--|----------------------------------|--|------------------------------|--|-----------------------------|--|---------------------------------|--|---------------------------------|--|----------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|---------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|----------------------------------|--|------------------------------------|--|

- (A) LENGTH: 157 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

|            |            |            |            |           |            |            |            |            |           |            |            |            |            |           |           |
|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|-----------|
| Met<br>1   | Lys        | Glu        | Leu        | Leu<br>5  | Gly        | Ile        | Glu        | Ile        | Asp<br>10 | Glu        | Glu        | Leu        | Asp<br>15  | Thr       | Lys       |
| Arg        | Leu        | Ile        | Pro<br>20  | Thr       | Tyr        | Ser        | Lys        | Leu<br>25  | Tyr       | Ser        | Leu        | Lys        | Lys<br>30  | Tyr       | Ser       |
| Lys        | Lys        | Phe<br>35  | Lys        | Arg       | Leu        | Gln        | Arg<br>40  | Lys        | Gln       | Ser        | Arg        | Arg<br>45  | Val        | Leu       | Lys       |
| Ser        | Lys<br>50  | Gln        | Asn        | Lys       | Thr        | Lys<br>55  | Leu        | Gly        | Gly       | Asn        | Phe<br>60  | Tyr        | Lys        | Thr       | Gln       |
| Lys<br>65  | Lys        | Leu        | Asn        | Gln       | Ala<br>70  | Phe        | Asp        | Lys        | Ser       | Ser<br>75  | His        | Gln        | Lys        | Thr       | Asp<br>80 |
| Arg        | Tyr        | His        | Lys        | Ile<br>85 | Thr        | Ser        | Glu        | Leu        | Ser<br>90 | Lys        | Gln        | Phe        | Glu        | Leu<br>95 | Ile       |
| Val        | Val        | Glu        | Asp<br>100 | Leu       | Gln        | Val        | Lys        | Asn<br>105 | Met       | Thr        | Lys        | Arg        | Ala<br>110 | Lys       | Leu       |
| Lys        | Asn        | Val<br>115 | Lys        | Gln       | Lys        | Ser        | Gly<br>120 | Leu        | Asn       | Gln        | Ser        | Ile<br>125 | Leu        | Asn       | Ala       |
| Ser        | Phe<br>130 | Tyr        | Gln        | Ile       | Ile        | Ser<br>135 | Phe        | Leu        | Asp       | Tyr        | Lys<br>140 | Gln        | Gln        | His       | Asn       |
| Gly<br>145 | Lys        | Leu        | Leu        | Val       | Lys<br>150 | Val        | Ser        | Pro        | Thr       | Ile<br>155 | Tyr        | Glu        |            |           |           |

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 889 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 52...843  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

ATTACATTCT TTTTGATTTC TATTGAAAAA TTTAATATTA AGAGGACTTT T ATG AAA 57  
Met Lys  
1

AAA TCA AAT GAC AAT AAC GCA CTC GCC AGA AGT CAA AGG GAG TTG TTT 105  
Lys Ser Asn Asp Asn Asn Ala Leu Ala Arg Ser Gln Arg Glu Leu Phe  
5 10 15



245

250

255

AAA AAT CTT TTA TCC CAC TAGCGCGAAA AACTCCGTCC TTTAGGGCGG AGATGTAA 881  
 Lys Asn Leu Leu Ser His  
 260

GCGTTTAG

889

## (2) INFORMATION FOR SEQ ID NO:208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Met Lys Lys Ser Asn Asp Asn Asn Ala Leu Ala Arg Ser Gln Arg Glu  
 1 5 10 15  
 Leu Phe Val Gly Ile Arg Asp Phe Ile Val Phe Lys Phe Lys Arg Met  
 20 25 30  
 Val Val Phe Asn Gly Val Arg Asp Phe Thr Lys Met Arg Phe Leu Ser  
 35 40 45  
 Ile Glu Leu Glu Lys Cys Glu Asn Ile Lys Asp Leu Glu Lys Leu Cys  
 50 55 60  
 His Thr Ile Tyr Asn Gln Gly Thr Lys His Ile Leu Met Met Arg Val  
 65 70 75 80  
 Leu Phe Leu Phe Phe Asp Tyr Phe Cys Lys His Leu Lys Val Lys Arg  
 85 90 95  
 Leu Arg Leu Leu Asn Glu Glu Met Leu Val Asn Phe Leu Phe Glu Leu  
 100 105 110  
 Ala Lys Gln Arg Lys Ile Asn Ser Met Ala Lys Tyr Val Met Tyr Ile  
 115 120 125  
 Arg Gln Phe Phe Asp Tyr Leu Asp Arg Thr Lys His Tyr Glu Phe Tyr  
 130 135 140  
 Phe Ser Leu Lys Asn Ile Ala Phe Ala Lys His Lys Asp Asn Leu Pro  
 145 150 155 160  
 Lys His Leu Asn Ser Lys Asp Leu Lys Ser Phe Ile Tyr Thr Leu Ile  
 165 170 175  
 Asn Tyr Arg Thr Arg Ser Ser Tyr Glu Lys Arg Asn Lys Cys Ile Leu  
 180 185 190  
 Leu Leu Ile Ile Leu Gly Gly Leu Arg Lys Ser Glu Val Phe Asn Leu  
 195 200 205  
 Glu Leu Arg Asn Ile Val Leu Glu Lys Glu His Tyr Ile Leu Leu Ile  
 210 215 220  
 Lys Gly Lys Asn Asn Lys Glu Arg Lys Ala Phe Ile Lys Ile Ala Gln  
 225 230 235 240  
 Thr Asp Ile Asp Thr Leu Ala Pro Leu Ile Arg Ile Leu Leu Glu Ser  
 245 250 255  
 Ile Ala Lys Asn Leu Leu Ser His  
 260

## (2) INFORMATION FOR SEQ ID NO:209:

## (i) SEQUENCE CHARACTERISTICS:



(A) LENGTH: 546 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 75...530  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| TTGACAGAGT | GGATTTTTTT | ATTTCTAACG | CTATTATTTA | TGGGCGTTCT | GTCGTGGGGG | 60  |
| GATTTCACAC | GTTT       | ATG        | CGA        | TTA        | AAA        | 110 |
|            | Met        | Arg        | Leu        | Lys        | Pro        |     |
|            | 1          |            |            | 5          |            |     |
|            |            |            |            |            | Leu        |     |
|            |            |            |            |            | Asn        |     |
|            |            |            |            |            | Asn        |     |
|            |            |            |            |            | Ile        |     |
|            |            |            |            |            | Tyr        |     |
|            |            |            |            |            | 10         |     |
| ACA        | GCC        | ACC        | GTG        | TTA        | GCG        | 158 |
| Thr        | Ala        | Thr        | Val        | Leu        | Ala        |     |
|            | 15         |            |            |            | Phe        |     |
|            |            |            |            |            | Val        |     |
|            |            |            |            |            | Val        |     |
|            |            |            |            |            | Gly        |     |
|            |            |            |            |            | Ala        |     |
|            |            |            |            |            | Gln        |     |
|            |            |            |            |            | Glu        |     |
|            |            |            |            |            | Ala        |     |
|            |            |            |            |            | Ala        |     |
|            |            |            |            |            | Lys        |     |
|            |            |            |            |            | 20         |     |
| CGC        | ATG        | CAA        | AAA        | ATA        | GGC        | 206 |
| Arg        | Met        | Gln        | Lys        | Ile        | Gly        |     |
|            | 30         |            |            |            | Gly        |     |
|            |            |            |            |            | Gly        |     |
|            |            |            |            |            | Gly        |     |
|            |            |            |            |            | Ala        |     |
|            |            |            |            |            | Ile        |     |
|            |            |            |            |            | Val        |     |
|            |            |            |            |            | Ser        |     |
|            |            |            |            |            | Leu        |     |
|            |            |            |            |            | Ser        |     |
|            |            |            |            |            | Ser        |     |
|            |            |            |            |            | Thr        |     |
|            |            |            |            |            | 40         |     |
| GGG        | AAT        | CTA        | GTT        | TAT        | ATG        | 254 |
| Gly        | Asn        | Leu        | Val        | Tyr        | Met        |     |
|            | 45         |            |            |            | Pro        |     |
|            |            |            |            |            | Asn        |     |
|            |            |            |            |            | Tyr        |     |
|            |            |            |            |            | Ala        |     |
|            |            |            |            |            | Gly        |     |
|            |            |            |            |            | His        |     |
|            |            |            |            |            | Gly        |     |
|            |            |            |            |            | Asn        |     |
|            |            |            |            |            | Ser        |     |
|            |            |            |            |            | Lys        |     |
|            |            |            |            |            | 60         |     |
| AAC        | GCC        | GTA        | GAA        | ACC        | ATG        | 302 |
| Asn        | Ala        | Val        | Glu        | Thr        | Met        |     |
|            |            |            |            |            | Val        |     |
|            |            |            |            |            | Lys        |     |
|            |            |            |            |            | Tyr        |     |
|            |            |            |            |            | Ala        |     |
|            |            |            |            |            | Ala        |     |
|            |            |            |            |            | Val        |     |
|            |            |            |            |            | Asp        |     |
|            |            |            |            |            | Leu        |     |
|            |            |            |            |            | Gly        |     |
|            |            |            |            |            | Glu        |     |
|            |            |            |            |            | 75         |     |
| TTT        | AAC        | ATT        | AGA        | GTG        | AAT        | 350 |
| Phe        | Asn        | Ile        | Arg        | Val        | Asn        |     |
|            |            |            |            |            | Ala        |     |
|            |            |            |            |            | Val        |     |
|            |            |            |            |            | Ser        |     |
|            |            |            |            |            | Gly        |     |
|            |            |            |            |            | Gly        |     |
|            |            |            |            |            | Pro        |     |
|            |            |            |            |            | Ile        |     |
|            |            |            |            |            | Asp        |     |
|            |            |            |            |            | Thr        |     |
|            |            |            |            |            | Asp        |     |
|            |            |            |            |            | 90         |     |
| GCT        | TTG        | AAA        | GCC        | TTC        | CCT        | 398 |
| Ala        | Leu        | Lys        | Ala        | Phe        | Pro        |     |
|            |            |            |            |            | Asp        |     |
|            |            |            |            |            | Tyr        |     |
|            |            |            |            |            | Val        |     |
|            |            |            |            |            | Glu        |     |
|            |            |            |            |            | Ile        |     |
|            |            |            |            |            | Lys        |     |
|            |            |            |            |            | Glu        |     |
|            |            |            |            |            | Lys        |     |
|            |            |            |            |            | Val        |     |
|            |            |            |            |            | Glu        |     |
|            |            |            |            |            | 105        |     |
| GAG        | CAA        | TCG        | CCC        | CTA        | AAA        | 446 |
| Glu        | Gln        | Ser        | Pro        | Leu        | Lys        |     |
|            |            |            |            |            | Arg        |     |
|            |            |            |            |            | Met        |     |
|            |            |            |            |            | Gly        |     |
|            |            |            |            |            | Asn        |     |
|            |            |            |            |            | Pro        |     |
|            |            |            |            |            | Asn        |     |
|            |            |            |            |            | Asp        |     |
|            |            |            |            |            | Leu        |     |
|            |            |            |            |            | Ala        |     |
|            |            |            |            |            | Gly        |     |
|            |            |            |            |            | 110        |     |
| GCG        | GCT        | TAT        | TTT        | TTA        | TGC        | 494 |
| Ala        | Ala        | Tyr        | Phe        | Leu        | Cys        |     |
|            |            |            |            |            | Asp        |     |
|            |            |            |            |            | Glu        |     |
|            |            |            |            |            | Thr        |     |
|            |            |            |            |            | Gln        |     |
|            |            |            |            |            | Ser        |     |
|            |            |            |            |            | Gly        |     |
|            |            |            |            |            | Trp        |     |
|            |            |            |            |            | Leu        |     |
|            |            |            |            |            | Thr        |     |
|            |            |            |            |            | Gly        |     |
|            |            |            |            |            | 140        |     |
| CAA        | ACG        | ATC        | GTT        | GTA        | GAT        | 546 |
| Gln        | Thr        | Ile        | Val        | Val        | Asp        |     |
|            |            |            |            |            | Gly        |     |
|            |            |            |            |            | Gly        |     |
|            |            |            |            |            | Thr        |     |
|            |            |            |            |            | Thr        |     |
|            |            |            |            |            | Phe        |     |
|            |            |            |            |            | Lys        |     |
|            |            |            |            |            | 145        |     |
|            |            |            |            |            | 150        |     |

546

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

```

Met Arg Leu Lys Pro Lys Gly Leu Asn Asn Ile Tyr Thr Ala Thr Val
 1 5 10 15
Leu Ala Phe Val Val Gly Ala Gln Glu Ala Ala Lys Arg Met Gln Lys
 20 25 30
Ile Gly Gly Gly Ala Ile Val Ser Leu Ser Ser Thr Gly Asn Leu Val
 35 40 45
Tyr Met Pro Asn Tyr Ala Gly His Gly Asn Ser Lys Asn Ala Val Glu
 50 55 60
Thr Met Val Lys Tyr Ala Ala Val Asp Leu Gly Glu Phe Asn Ile Arg
 65 70 75 80
Val Asn Ala Val Ser Gly Gly Pro Ile Asp Thr Asp Ala Leu Lys Ala
 85 90 95
Phe Pro Asp Tyr Val Glu Ile Lys Glu Lys Val Glu Glu Gln Ser Pro
100 105 110
Leu Lys Arg Met Gly Asn Pro Asn Asp Leu Ala Gly Ala Ala Tyr Phe
115 120 125
Leu Cys Asp Glu Thr Gln Ser Gly Trp Leu Thr Gly Gln Thr Ile Val
130 135 140
Val Asp Gly Gly Thr Thr Phe Lys
145 150

```

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 2...616
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

```

A AGA TAT TTC TTG CAA AAC ATT ATC CAC ATC CAC CAA AAC AAA GAG TTG 49
 Arg Tyr Phe Leu Gln Asn Ile Ile His Ile His Gln Asn Lys Glu Leu
 1 5 10 15

CAA TTC ATT AAA AAA TGC TTG TTG GGC TAT TTT TTC GCC CCT TTG TGT 97
 Gln Phe Ile Lys Lys Cys Leu Leu Gly Tyr Phe Phe Ala Pro Leu Cys
 20 25 30

```

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGG GCT ATT CTG TTA GTG CTT TTT ATT GTT TCA AGC GGG GCA AAA TCG   | 145 |
| Gly Ala Ile Leu Leu Val Leu Phe Ile Val Ser Ser Gly Ala Lys Ser   |     |
| 35 40 45                                                          |     |
| TTT CAA ATT TCT AAT CTC TTT AAC AAT CAA CTA GCC TAT ATC GTT TTG   | 193 |
| Phe Gln Ile Ser Asn Leu Phe Asn Asn Gln Leu Ala Tyr Ile Val Leu   |     |
| 50 55 60                                                          |     |
| TTG TCT CTT TTT TTG TGC GCG CTT GGG TTT ATT GCC GGA GCG ATT GGT   | 241 |
| Leu Ser Leu Phe Leu Cys Ala Leu Gly Phe Ile Ala Gly Ala Ile Gly   |     |
| 65 70 75 80                                                       |     |
| TTT TAT AGG CTT TCT AAA ATC ACA CGC CAT CTG AGT TTT TTT GAA AAT   | 289 |
| Phe Tyr Arg Leu Ser Lys Ile Thr Arg His Leu Ser Phe Phe Glu Asn   |     |
| 85 90 95                                                          |     |
| TTC GCT TTC AGT TTT TTA GCG GTG ATT TTA TGC GCT ATT TTA AGC TAT   | 337 |
| Phe Ala Phe Ser Phe Leu Ala Val Ile Leu Cys Ala Ile Leu Ser Tyr   |     |
| 100 105 110                                                       |     |
| CTT GTC CCT AAC GCC AGT AAC GCT CTT TCG CTA ATC GGT AAT GGC GTT   | 385 |
| Leu Val Pro Asn Ala Ser Asn Ala Leu Ser Leu Ile Gly Asn Gly Val   |     |
| 115 120 125                                                       |     |
| TCT ATT TTT TAT TTG CAC AAA CTC TAT AGA GAA TTG AGC CTT TAC ACG   | 433 |
| Ser Ile Phe Tyr Leu His Lys Leu Tyr Arg Glu Leu Ser Leu Tyr Thr   |     |
| 130 135 140                                                       |     |
| CAA GAA AGG TTT TTT TTA AGC GGG TTT AGG TTG TTG CTT TTT AGT TTC   | 481 |
| Gln Glu Arg Phe Phe Leu Ser Gly Phe Arg Leu Leu Leu Phe Ser Phe   |     |
| 145 150 155 160                                                   |     |
| ATG CTG GCT CTT TTA GGG ATT TTA GTG CAA GCG TTA GTT ATC ATT TTT   | 529 |
| Met Leu Ala Leu Leu Gly Ile Leu Val Gln Ala Leu Val Ile Ile Phe   |     |
| 165 170 175                                                       |     |
| TTA ACG ACC GCT GTG GTT TTA ATG TGT GTG GCG CTT GGT TTT TTG GCG   | 577 |
| Leu Thr Thr Ala Val Val Leu Met Cys Val Ala Leu Gly Phe Leu Ala   |     |
| 180 185 190                                                       |     |
| CGC GCG TTT TTG AAT TTT TCA CAA GTC TTT TTG AAA GCA TGAAAGTTTT AA | 628 |
| Arg Ala Phe Leu Asn Phe Ser Gln Val Phe Leu Lys Ala               |     |
| 195 200 205                                                       |     |
| AACTCCTGCC TAATTT                                                 | 644 |

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

```

Arg Tyr Phe Leu Gln Asn Ile Ile His Ile His Gln Asn Lys Glu Leu
1 5 10 15
Gln Phe Ile Lys Lys Cys Leu Leu Gly Tyr Phe Phe Ala Pro Leu Cys
20 25 30
Gly Ala Ile Leu Leu Val Leu Phe Ile Val Ser Ser Gly Ala Lys Ser
35 40 45
Phe Gln Ile Ser Asn Leu Phe Asn Asn Gln Leu Ala Tyr Ile Val Leu
50 55 60
Leu Ser Leu Phe Leu Cys Ala Leu Gly Phe Ile Ala Gly Ala Ile Gly
65 70 75 80
Phe Tyr Arg Leu Ser Lys Ile Thr Arg His Leu Ser Phe Phe Glu Asn
85 90 95
Phe Ala Phe Ser Phe Leu Ala Val Ile Leu Cys Ala Ile Leu Ser Tyr
100 105 110
Leu Val Pro Asn Ala Ser Asn Ala Leu Ser Leu Ile Gly Asn Gly Val
115 120 125
Ser Ile Phe Tyr Leu His Lys Leu Tyr Arg Glu Leu Ser Leu Tyr Thr
130 135 140
Gln Glu Arg Phe Phe Leu Ser Gly Phe Arg Leu Leu Leu Phe Ser Phe
145 150 155 160
Met Leu Ala Leu Leu Gly Ile Leu Val Gln Ala Leu Val Ile Ile Phe
165 170 175
Leu Thr Thr Ala Val Val Leu Met Cys Val Ala Leu Gly Phe Leu Ala
180 185 190
Arg Ala Phe Leu Asn Phe Ser Gln Val Phe Leu Lys Ala
195 200 205

```

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 62...598
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

```

GTGTGGCGCT TGGTTTTTTG GCGCGCGCGT TTTTGAATTT TTCACAAGTC TTTTGTAAAG 60
C ATG AAA GTT TTA AAA CTC CTG CCT AAT TTT TTA ACA ATT TTA CGC ATT 109
Met Lys Val Leu Lys Leu Leu Pro Asn Phe Leu Thr Ile Leu Arg Ile
1 5 10 15

GTC TTA TCC TTA TTT TTA TTA TTT TTA TTG TTA AAC ACG CGC ACT TAT 157
Val Leu Ser Leu Phe Leu Leu Phe Leu Leu Asn Thr Arg Thr Tyr
20 25 30

TTT AGT TTT TTA ACC CCC TTT CAA ACC AAT ATG ATC TCT TCA TTG GTT 205
Phe Ser Phe Leu Thr Pro Phe Gln Thr Asn Met Ile Ser Ser Leu Val
35 40 45

```



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     | 70  |     | 75  |     | 80  |     |     |     |     |     |     |     |     |     |
| Asp | Lys | Ile | Leu | Ile | Leu | Ser | Ala | Phe | Leu | Gly | Leu | Val | Tyr | Leu | Asp |
|     |     | 85  |     | 90  |     |     |     |     |     |     |     |     |     | 95  |     |
| Arg | Val | Asn | Ala | Trp | Ile | Pro | Phe | Val | Ile | Leu | Gly | Arg | Glu | Phe | Phe |
|     |     | 100 |     | 105 |     |     |     |     |     |     |     |     | 110 |     |     |
| Ile | Ser | Gly | Leu | Arg | Val | Leu | Ala | Ala | Asn | Glu | Lys | Lys | Asp | Ile | Pro |
|     |     | 115 |     | 120 |     |     |     |     |     |     |     |     | 125 |     |     |
| Val | Asn | Ala | Leu | Gly | Lys | Tyr | Lys | Thr | Val | Ser | Gln | Val | Val | Ala | Ile |
|     |     | 130 |     | 135 |     |     |     |     |     |     |     | 140 |     |     |     |
| Gly | Ala | Leu | Leu | Ala | Asp | Val | Thr | Tyr | Ser | Tyr | Ala | Leu | Val | Ala | Ile |
|     |     | 145 |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Val | Phe | Leu | Thr | Leu | Tyr | Ser | Gly | Ile | Asp | Tyr | Thr | Ile | Lys | Tyr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Tyr | Lys | Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 913 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...879
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

|            |          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATAGAAGAAG | AGTGAGAA | ATG | CAA | GAT | TTT | ATT | AAG | ATT | TTT | ATT | CAA | GAG |     | 51  |     |
|            |          | Met | Gln | Asp | Phe | Ile | Lys | Ile | Phe | Ile | Gln | Glu |     |     |     |
|            |          | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |
| GTT        | GTC      | TCT | ACT | TTA | GAA | GGG | TTA | GTG | GGT | AAG | GCT | CCA | AGC | GTG | GGA |
| Val        | Val      | Ser | Thr | Leu | Glu | Gly | Leu | Val | Gly | Lys | Ala | Pro | Ser | Val | Gly |
|            |          | 15  |     |     |     | 20  |     |     |     |     | 25  |     |     |     | 99  |
| TTA        | GAA      | AAA | GAA | ATT | TCT | AGT | AGC | GAC | GAA | TCT | TTT | TTG | AAA | TTA | ATC |
| Leu        | Glu      | Lys | Glu | Ile | Ser | Ser | Ser | Asp | Glu | Ser | Phe | Leu | Lys | Leu | Ile |
|            |          | 30  |     |     |     | 35  |     |     |     |     | 40  |     |     |     | 147 |
| AGC        | ACG      | CCT | TAT | GCA | AGA | GTT | GTG | ATA | AGC | GCG | ATT | GAA | AAA | GAA | GAG |
| Ser        | Thr      | Pro | Tyr | Ala | Arg | Val | Val | Ile | Ser | Ala | Ile | Glu | Lys | Glu | Glu |
|            |          | 45  |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 195 |
| AGC        | TCT      | ATT | GAA | TTA | CTG | GCT | CCG | GTA | GTT | TTA | GTT | ACC | TCT | TTA | AGC |
| Ser        | Ser      | Ile | Glu | Leu | Leu | Ala | Pro | Val | Val | Leu | Val | Thr | Ser | Leu | Ser |
|            |          | 60  |     |     | 65  |     |     |     | 70  |     |     |     |     | 75  | 243 |
| GAT        | TTG      | ATG | CTA | GGA | GGT | GAG | GGA | GCG | AGT | AAG | GAA | GAA | ATG | GAT | AAT |
| Asp        | Leu      | Met | Leu | Gly | Gly | Glu | Gly | Ala | Ser | Lys | Glu | Glu | Met | Asp | Asn |
|            |          |     | 80  |     |     |     |     | 85  |     |     |     |     |     | 90  | 291 |

|                                                                                                                                                       |     |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| GAC GAT TTA GAC GCT TTT AAA GAA ATG GCT TCT AAT ATT TTT GGC GCG<br>Asp Asp Leu Asp Ala Phe Lys Glu Met Ala Ser Asn Ile Phe Gly Ala<br>95 100 105      | 339 |
| ATC GCT ACA AGC TTG AAG TCT CAA GAA TTG CTC CCT AAA CTC AAT TTC<br>Ile Ala Thr Ser Leu Lys Ser Gln Glu Leu Leu Pro Lys Leu Asn Phe<br>110 115 120     | 387 |
| ACC ACT ATA AAC GCT GAA ATC GCT AAA GAG CTT CCT AAA AAA GAA GAT<br>Thr Thr Ile Asn Ala Glu Ile Ala Lys Glu Leu Pro Lys Lys Glu Asp<br>125 130 135     | 435 |
| TAC GCT AAA GCG ATG GTG TTT TCT TTT AAA ATG GAA GCC ATC AAA GAA<br>Tyr Ala Lys Ala Met Val Phe Ser Phe Lys Met Glu Ala Ile Lys Glu<br>140 145 150 155 | 483 |
| AGC CAA ATC ATT TTA TTG ACT ACG GCG GCT TTT GAG GGC CAA TTT GAA<br>Ser Gln Ile Ile Leu Leu Thr Thr Ala Ala Phe Glu Gly Gln Phe Glu<br>160 165 170     | 531 |
| AAA ACG CAT AAA GAA GAA AAA GAA GAA ACG ACA GAG GGC GTT GCT GAA<br>Lys Thr His Lys Glu Glu Lys Glu Glu Thr Thr Glu Gly Val Ala Glu<br>175 180 185     | 579 |
| GAG GTT AAA ACC CAT GAT GCG TCT TTA GAA AAC ATA GAA ATC CGC AAT<br>Glu Val Lys Thr His Asp Ala Ser Leu Glu Asn Ile Glu Ile Arg Asn<br>190 195 200     | 627 |
| ATC AGC ATG CTT TTA GAC GTG AAA TTG AAC GTT AAG GTG CGC ATC GGG<br>Ile Ser Met Leu Leu Asp Val Lys Leu Asn Val Lys Val Arg Ile Gly<br>205 210 215     | 675 |
| CAA AAA AAA ATG ATT TTA AAA GAC GTG GTC TCT ATG GAT ATA GGG AGC<br>Gln Lys Lys Met Ile Leu Lys Asp Val Val Ser Met Asp Ile Gly Ser<br>220 225 230 235 | 723 |
| GTG GTA GAG CTG GAT CAA TTG GTG AAT GAC CCT TTG GAA ATT CTT GTA<br>Val Val Glu Leu Asp Gln Leu Val Asn Asp Pro Leu Glu Ile Leu Val<br>240 245 250     | 771 |
| GAT GAC AAG GTG ATC GCT AAG GGC GAA GTG GTG ATT GTG GAT GGG AAT<br>Asp Asp Lys Val Ile Ala Lys Gly Glu Val Val Ile Val Asp Gly Asn<br>255 260 265     | 819 |
| TTT GGC ATT CAA ATC ACG GAT ATT GGC ACT AAA AAA GAA CGC TTA GAA<br>Phe Gly Ile Gln Ile Thr Asp Ile Gly Thr Lys Lys Glu Arg Leu Glu<br>270 275 280     | 867 |
| CAA TTG AAA CAT TAAATCTTTT TATCATAAAA AGGAAAGGGA TATG<br>Gln Leu Lys His<br>285                                                                       | 913 |

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 287 amino acids
  - (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Asp | Phe | Ile | Lys | Ile | Phe | Ile | Gln | Glu | Val | Val | Ser | Thr | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Gly | Leu | Val | Gly | Lys | Ala | Pro | Ser | Val | Gly | Leu | Glu | Lys | Glu | Ile |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ser | Ser | Ser | Asp | Glu | Ser | Phe | Leu | Lys | Leu | Ile | Ser | Thr | Pro | Tyr | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Val | Val | Ile | Ser | Ala | Ile | Glu | Lys | Glu | Glu | Ser | Ser | Ile | Glu | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ala | Pro | Val | Val | Leu | Val | Thr | Ser | Leu | Ser | Asp | Leu | Met | Leu | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Glu | Gly | Ala | Ser | Lys | Glu | Glu | Met | Asp | Asn | Asp | Asp | Leu | Asp | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Lys | Glu | Met | Ala | Ser | Asn | Ile | Phe | Gly | Ala | Ile | Ala | Thr | Ser | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Ser | Gln | Glu | Leu | Leu | Pro | Lys | Leu | Asn | Phe | Thr | Thr | Ile | Asn | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Glu | Ile | Ala | Lys | Glu | Leu | Pro | Lys | Lys | Glu | Asp | Tyr | Ala | Lys | Ala | Met |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Phe | Ser | Phe | Lys | Met | Glu | Ala | Ile | Lys | Glu | Ser | Gln | Ile | Ile | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |
| Leu | Thr | Thr | Ala | Ala | Phe | Glu | Gly | Gln | Phe | Glu | Lys | Thr | His | Lys | Glu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Lys | Glu | Glu | Thr | Thr | Glu | Gly | Val | Ala | Glu | Glu | Val | Lys | Thr | His |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asp | Ala | Ser | Leu | Glu | Asn | Ile | Glu | Ile | Arg | Asn | Ile | Ser | Met | Leu | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asp | Val | Lys | Leu | Asn | Val | Lys | Val | Arg | Ile | Gly | Gln | Lys | Lys | Met | Ile |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Lys | Asp | Val | Val | Ser | Met | Asp | Ile | Gly | Ser | Val | Val | Glu | Leu | Asp |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gln | Leu | Val | Asn | Asp | Pro | Leu | Glu | Ile | Leu | Val | Asp | Asp | Lys | Val | Ile |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Lys | Gly | Glu | Val | Val | Ile | Val | Asp | Gly | Asn | Phe | Gly | Ile | Gln | Ile |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Thr | Asp | Ile | Gly | Thr | Lys | Lys | Glu | Arg | Leu | Glu | Gln | Leu | Lys | His |     |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1111 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 13...1056  
(D) OTHER INFORMATION:



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

|            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| TAAAAAAGGA | GA  | ATG | ATG | CAA | GTT | TAC | CAC | CTT | TCA | CAC | ATT | GAT | TTA | GAC | 51  |     |
|            | Met | Met | Gln | Val | Tyr | His | Leu | Ser | His | Ile | Asp | Leu | Asp |     |     |     |
|            | 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     |     |
| GGC        | TAT | GCA | TGC | CAG | CTT | GTT | TCA | AAA | CAA | TTT | TTT | AAA | AAT | ATC | CAA | 99  |
| Gly        | Tyr | Ala | Cys | Gln | Leu | Val | Ser | Lys | Gln | Phe | Phe | Lys | Asn | Ile | Gln |     |
|            | 15  |     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |
| TGC        | TAT | AAC | GCT | AAT | TAC | GGG | CGT | GAA | GTC | TCA | GCG | AGA | ATT | TAT | GAG | 147 |
| Cys        | Tyr | Asn | Ala | Asn | Tyr | Gly | Arg | Glu | Val | Ser | Ala | Arg | Ile | Tyr | Glu |     |
|            | 30  |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |
| ATT        | TTA | AAC | GCA | ATC | GCT | CAG | TCT | AAA | GAG | AGT | GAA | TTC | CTT | ATT | TTG | 195 |
| Ile        | Leu | Asn | Ala | Ile | Ala | Gln | Ser | Lys | Glu | Ser | Glu | Phe | Leu | Ile | Leu |     |
|            |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |
| GTT        | AGC | GAT | TTG | AAT | CTG | AAT | TTG | AAT | GAA | GCA | GAG | TAT | TTG | CAG | GAT | 243 |
| Val        | Ser | Asp | Leu | Asn | Leu | Asn | Leu | Asn | Glu | Ala | Glu | Tyr | Leu | Gln | Asp |     |
|            |     |     | 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |
| AAG        | ATC | CAA | GAA | CAC | CGC | TTG | CAA | AAT | AAA | AAC | ATT | CAA | ATC | CAG | CTT | 291 |
| Lys        | Ile | Gln | Glu | His | Arg | Leu | Gln | Asn | Lys | Asn | Ile | Gln | Ile | Gln | Leu |     |
|            |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |
| TTA        | GAT | CAC | CAT | ATC | AGC | GGT | AAG | GAA | GTG | GCT | GAG | AGT | TTC | CAT | TGG | 339 |
| Leu        | Asp | His | His | Ile | Ser | Gly | Lys | Glu | Val | Ala | Glu | Ser | Phe | His | Trp |     |
|            | 95  |     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |
| TAT        | TTT | TTA | GAC | ATT | AAC | CGT | TGC | GCG | ACT | AAA | ATC | GTG | TAT | GAA | TTT | 387 |
| Tyr        | Phe | Leu | Asp | Ile | Asn | Arg | Cys | Ala | Thr | Lys | Ile | Val | Tyr | Glu | Phe |     |
|            | 110 |     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |
| TTG        | AAA | AAG | CAT | TAC | GCT | ATT | TTA | GAG | CCA | AAA | AAC | ACA | ACA | TGG | CTA | 435 |
| Leu        | Lys | Lys | His | Tyr | Ala | Ile | Leu | Glu | Pro | Lys | Asn | Thr | Thr | Trp | Leu |     |
|            |     |     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |
| GAG        | CCT | TTA | GTG | GAA | ATG | GTC | AAT | TCT | GTG | GAT | ATT | TGG | GAC | ACG | CAA | 483 |
| Glu        | Pro | Leu | Val | Glu | Met | Val | Asn | Ser | Val | Asp | Ile | Trp | Asp | Thr | Gln |     |
|            |     |     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |
| GGT        | TAT | GGC | TTT | GAA | TTA | GGC | AAG | GTG | TGC | ATG | CGC | ATG | ATT | AAC | CAA | 531 |
| Gly        | Tyr | Gly | Phe | Glu | Leu | Gly | Lys | Val | Cys | Met | Arg | Met | Ile | Asn | Gln |     |
|            |     | 160 |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |
| AGC        | TCT | GAA | TTG | AAT | CGT | TTC | ATG | TTT | GAT | GAT | GAA | AAC | CGC | AAC | TAT | 579 |
| Ser        | Ser | Glu | Leu | Asn | Arg | Phe | Met | Phe | Asp | Asp | Glu | Asn | Arg | Asn | Tyr |     |
|            | 175 |     |     |     | 180 |     |     |     |     |     | 185 |     |     |     |     |     |
| AAA        | TTA | AAG | CTT | TTA | GAA | GAA | GTT | AAA | AAC | TAT | TTG | TTT | TTA | GAA | AAT | 627 |
| Lys        | Leu | Lys | Leu | Leu | Glu | Glu | Val | Lys | Asn | Tyr | Leu | Phe | Leu | Glu | Asn |     |
|            | 190 |     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |
| GCC        | CCT | GTA | GCC | TAT | GAT | AAC | GAT | TTG | TTC | AAA | CTC | AAA | AAA | ATC | GCT | 675 |
| Ala        | Pro | Val | Ala | Tyr | Asp | Asn | Asp | Leu | Phe | Lys | Leu | Lys | Lys | Ile | Ala |     |

| 210                                                    |     |     |     |     |     |     |     |     |     | 215 |     |     |     |     |       |      |      |  |  | 220 |  |  |  |  |  |  |  |  |  |  |
|--------------------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-------|------|------|--|--|-----|--|--|--|--|--|--|--|--|--|--|
| TTA                                                    | GGG | GGC | GAC | CCT | GAT | GCA | GAA | ACG | ATG | GAC | AAT | ATC | TCT | TCA | AAC   |      | 723  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Leu                                                    | Gly | Gly | Asp | Pro | Asp | Ala | Glu | Thr | Met | Asp | Asn | Ile | Ser | Ser | Asn   |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
|                                                        |     |     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |       |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| GCG                                                    | CAA | ACG | CAT | TTG | CTC | TCT | TTA | AAA | AAG | CAT | GAT | TGC | AGC | GTT | TAT   |      | 771  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Ala                                                    | Gln | Thr | His | Leu | Leu | Ser | Leu | Lys | Lys | His | Asp | Cys | Ser | Val | Tyr   |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
|                                                        |     | 240 |     |     |     |     | 245 |     |     |     |     | 250 |     |     |       |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| TAC                                                    | CAG | GAT | AAA | AAA | GGG | TTT | TTA | AGT | TAT | TCT | ATG | GGG | GGC | ATT | AGC   |      | 819  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Tyr                                                    | Gln | Asp | Lys | Lys | Gly | Phe | Leu | Ser | Tyr | Ser | Met | Gly | Gly | Ile | Ser   |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
|                                                        | 255 |     |     |     |     | 260 |     |     |     |     | 265 |     |     |     |       |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| GTG                                                    | TTG | GCT | AAC | CTT | TTT | TTA | ACG | CAA | AAT | CCG | GAT | TTT | GAT | TTT | TAT   |      | 867  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Val                                                    | Leu | Ala | Asn | Leu | Phe | Leu | Thr | Gln | Asn | Pro | Asp | Phe | Asp | Phe | Tyr   |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| 270                                                    |     |     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285   |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| ATG                                                    | GAT | GTG | AAC | GCT | AAA | GGG | AAT | GTG | AGC | TTA | AGG | GCG | AAT | GGG | AAT   |      | 915  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Met                                                    | Asp | Val | Asn | Ala | Lys | Gly | Asn | Val | Ser | Leu | Arg | Ala | Asn | Gly | Asn   |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
|                                                        |     |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |       |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| TGC                                                    | GAT | GTG | TGC | GAA | CTC | AGT | CAA | ATG | TGT | TTT | AAT | GGG | GGT | GGG | CAT   |      | 963  |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Cys                                                    | Asp | Val | Cys | Glu | Leu | Ser | Gln | Met | Cys | Phe | Asn | Gly | Gly | Gly | His   |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
|                                                        |     |     | 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |       |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| AGG                                                    | AAT | GCG | AGC | GGA | GGC | AAG | ATT | GAT | GGT | TTT | AGG | GAG | AGT | TTC | AAT   |      | 1011 |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Arg                                                    | Asn | Ala | Ser | Gly | Gly | Lys | Ile | Asp | Gly | Phe | Arg | Glu | Ser | Phe | Asn   |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
|                                                        |     | 320 |     |     |     | 325 |     |     |     |     | 330 |     |     |     |       |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| TAT                                                    | AGG | GAT | ATT | AAA | GAA | CAA | ATT | GAA | GAA | ATC | TTC | AAC | AAC | GCT | TAAAA |      | 1061 |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Tyr                                                    | Arg | Asp | Ile | Lys | Glu | Gln | Ile | Glu | Glu | Ile | Phe | Asn | Asn | Ala |       |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
|                                                        | 335 |     |     |     | 340 |     |     |     |     | 345 |     |     |     |     |       |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| CTAAGCTGTT TAGAAAAAAC TAACAAAAAC TGAAAAGAGT TTAAAAGCTC |     |     |     |     |     |     |     |     |     |     |     |     |     |     |       | 1111 |      |  |  |     |  |  |  |  |  |  |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Gln | Val | Tyr | His | Leu | Ser | His | Ile | Asp | Leu | Asp | Gly | Tyr | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Cys | Gln | Leu | Val | Ser | Lys | Gln | Phe | Phe | Lys | Asn | Ile | Gln | Cys | Tyr | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Asn | Tyr | Gly | Arg | Glu | Val | Ser | Ala | Arg | Ile | Tyr | Glu | Ile | Leu | Asn |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ala | Ile | Ala | Gln | Ser | Lys | Glu | Ser | Glu | Phe | Leu | Ile | Leu | Val | Ser | Asp |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Leu | Asn | Leu | Asn | Leu | Asn | Glu | Ala | Glu | Tyr | Leu | Gln | Asp | Lys | Ile | Gln |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Glu | His | Arg | Leu | Gln | Asn | Lys | Asn | Ile | Gln | Ile | Gln | Leu | Leu | Asp | His |  |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| His | Ile | Ser | Gly | Lys | Glu | Val | Ala | Glu | Ser | Phe | His | Trp | Tyr | Phe | Leu |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Asp | Ile | Asn | Arg | Cys | Ala | Thr | Lys | Ile | Val | Tyr | Glu | Phe | Leu | Lys | Lys |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| His | Tyr | Ala | Ile | Leu | Glu | Pro | Lys | Asn | Thr | Thr | Trp | Leu | Glu | Pro | Leu |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Val | Glu | Met | Val | Asn | Ser | Val | Asp | Ile | Trp | Asp | Thr | Gln | Gly | Tyr | Gly |  |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |  |  |
| Phe | Glu | Leu | Gly | Lys | Val | Cys | Met | Arg | Met | Ile | Asn | Gln | Ser | Ser | Glu |  |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |  |
| Leu | Asn | Arg | Phe | Met | Phe | Asp | Asp | Glu | Asn | Arg | Asn | Tyr | Lys | Leu | Lys |  |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Leu | Leu | Glu | Glu | Val | Lys | Asn | Tyr | Leu | Phe | Leu | Glu | Asn | Ala | Pro | Val |  |  |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |  |
| Ala | Tyr | Asp | Asn | Asp | Leu | Phe | Lys | Leu | Lys | Lys | Ile | Ala | Leu | Gly | Gly |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |
| Asp | Pro | Asp | Ala | Glu | Thr | Met | Asp | Asn | Ile | Ser | Ser | Asn | Ala | Gln | Thr |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |  |  |
| His | Leu | Leu | Ser | Leu | Lys | Lys | His | Asp | Cys | Ser | Val | Tyr | Tyr | Gln | Asp |  |  |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |  |  |
| Lys | Lys | Gly | Phe | Leu | Ser | Tyr | Ser | Met | Gly | Gly | Ile | Ser | Val | Leu | Ala |  |  |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |
| Asn | Leu | Phe | Leu | Thr | Gln | Asn | Pro | Asp | Phe | Asp | Phe | Tyr | Met | Asp | Val |  |  |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |  |  |
| Asn | Ala | Lys | Gly | Asn | Val | Ser | Leu | Arg | Ala | Asn | Gly | Asn | Cys | Asp | Val |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |
| Cys | Glu | Leu | Ser | Gln | Met | Cys | Phe | Asn | Gly | Gly | Gly | His | Arg | Asn | Ala |  |  |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |  |  |
| Ser | Gly | Gly | Lys | Ile | Asp | Gly | Phe | Arg | Glu | Ser | Phe | Asn | Tyr | Arg | Asp |  |  |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |  |  |
| Ile | Lys | Glu | Gln | Ile | Glu | Glu | Ile | Phe | Asn | Asn | Ala |     |     |     |     |  |  |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2070 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 39...2024
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

|             |                 |                 |                         |                         |     |
|-------------|-----------------|-----------------|-------------------------|-------------------------|-----|
| ATAAAAAATG  | CGCTTAAAAC      | CATGAAAAAG      | GAGATGCG                | ATG CAA TTA GAC GAA GAT | 56  |
|             |                 |                 | Met Gln Leu Asp Glu Asp |                         |     |
|             |                 |                 | 1                       | 5                       |     |
| TTA GAA TTC | GCT AAA AAA ATC | TTT AAC CCT AAC | AGA GCG TTT GCC AAG     |                         | 104 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Glu | Phe | Ala | Lys | Lys | Ile | Phe | Asn | Pro | Asn | Arg | Ala | Phe | Ala | Lys |     |
|     |     |     | 10  |     |     |     | 15  |     |     |     |     |     | 20  |     |     |     |
| CAA | GCC | AGG | ATT | AAA | AAC | ATG | TGC | GAA | TAT | AAA | GAT | TTA | GTG | CAT | GAA | 152 |
| Gln | Ala | Arg | Ile | Lys | Asn | Met | Cys | Glu | Tyr | Lys | Asp | Leu | Val | His | Glu |     |
|     |     |     | 25  |     |     |     | 30  |     |     |     |     |     | 35  |     |     |     |
| GCC | AAT | GAA | GAT | TAT | GAA | CAT | TTT | TGG | GGC | GAT | TTA | GCC | AAG | CAG | AAA | 200 |
| Ala | Asn | Glu | Asp | Tyr | Glu | His | Phe | Trp | Gly | Asp | Leu | Ala | Lys | Gln | Lys |     |
|     |     |     | 40  |     |     |     | 45  |     |     |     |     |     | 50  |     |     |     |
| CTC | ACA | TGG | TTT | AAA | CCT | TTT | GAT | AAG | GTT | TTA | AAC | AGC | GAT | AAC | GCC | 248 |
| Leu | Thr | Trp | Phe | Lys | Pro | Phe | Asp | Lys | Val | Leu | Asn | Ser | Asp | Asn | Ala |     |
|     |     |     | 55  |     |     |     | 60  |     |     |     |     |     | 65  |     |     | 70  |
| CCT | TTT | TTC | AAA | TGG | TTT | GAA | AAC | GGC | AAA | ATC | AAT | GTT | TCT | TAC | AAT | 296 |
| Pro | Phe | Phe | Lys | Trp | Phe | Glu | Asn | Gly | Lys | Ile | Asn | Val | Ser | Tyr | Asn |     |
|     |     |     | 75  |     |     |     | 80  |     |     |     |     |     | 85  |     |     |     |
| TGC | ATA | GAC | AGG | CAT | TTA | AAA | GAC | AAA | AAA | AAT | AAA | GTG | GCG | ATC | ATT | 344 |
| Cys | Ile | Asp | Arg | His | Leu | Lys | Asp | Lys | Lys | Asn | Lys | Val | Ala | Ile | Ile |     |
|     |     |     | 90  |     |     |     | 95  |     |     |     |     |     | 100 |     |     |     |
| TTT | GAA | GGG | GAA | ATG | GGG | GAT | TAT | AAT | GTC | ATC | ACT | TAC | AGA | AAA | CTC | 392 |
| Phe | Glu | Gly | Glu | Met | Gly | Asp | Tyr | Asn | Val | Ile | Thr | Tyr | Arg | Lys | Leu |     |
|     |     |     | 105 |     |     |     | 110 |     |     |     |     |     | 115 |     |     |     |
| CAC | TCT | GAA | GTC | AAT | AAA | ACA | GCC | AAC | CTT | TTA | AAA | AAC | GAA | TTC | AAT | 440 |
| His | Ser | Glu | Val | Asn | Lys | Thr | Ala | Asn | Leu | Leu | Lys | Asn | Glu | Phe | Asn |     |
|     |     |     | 120 |     |     |     | 125 |     |     |     |     |     | 130 |     |     |     |
| GTC | AAA | AAA | GGC | GAT | AGG | GTC | ATT | ATC | TAT | ATG | CCC | ATG | ATT | GTA | GAA | 488 |
| Val | Lys | Lys | Gly | Asp | Arg | Val | Ile | Ile | Tyr | Met | Pro | Met | Ile | Val | Glu |     |
|     |     |     | 135 |     |     |     | 140 |     |     |     |     |     | 145 |     |     | 150 |
| AGC | GTT | TAT | ATG | ATG | CTC | GCA | TGC | ACT | AGG | ATT | GGA | GCG | ATC | CAT | AGC | 536 |
| Ser | Val | Tyr | Met | Met | Leu | Ala | Cys | Thr | Arg | Ile | Gly | Ala | Ile | His | Ser |     |
|     |     |     | 155 |     |     |     | 160 |     |     |     |     |     | 165 |     |     |     |
| ATC | GTT | TTT | GCT | GGG | TTT | AGC | CCT | GAA | GCC | TTA | AGG | GAT | AGG | ATC | AAC | 584 |
| Ile | Val | Phe | Ala | Gly | Phe | Ser | Pro | Glu | Ala | Leu | Arg | Asp | Arg | Ile | Asn |     |
|     |     |     | 170 |     |     |     | 175 |     |     |     |     |     | 180 |     |     |     |
| GAC | GCT | CAA | GCT | AAA | TTA | GTT | ATC | ACA | GCG | GAT | GGG | ACT | TTT | AGA | AAA | 632 |
| Asp | Ala | Gln | Ala | Lys | Leu | Val | Ile | Thr | Ala | Asp | Gly | Thr | Phe | Arg | Lys |     |
|     |     |     | 185 |     |     |     | 190 |     |     |     |     |     | 195 |     |     |     |
| GGC | AAA | CCT | TAC | ATG | CTC | AAG | CCA | GCC | CTT | GAC | AAG | GCT | CTA | GAA | AAT | 680 |
| Gly | Lys | Pro | Tyr | Met | Leu | Lys | Pro | Ala | Leu | Asp | Lys | Ala | Leu | Glu | Asn |     |
|     |     |     | 200 |     |     |     | 205 |     |     |     |     |     | 210 |     |     |     |
| AAC | GCC | TGC | CCT | AGC | GTG | GAA | AAA | GCG | CTC | ATT | GTG | ATA | CGA | AAC | GCC | 728 |
| Asn | Ala | Cys | Pro | Ser | Val | Glu | Lys | Ala | Leu | Ile | Val | Ile | Arg | Asn | Ala |     |
|     |     |     | 215 |     |     |     | 220 |     |     |     |     |     | 225 |     |     | 230 |
| AAA | GAG | ATT | GAC | TAT | GTG | AGA | GGG | CGC | GAT | TTT | GTC | TAT | AAT | GAA | ATG | 776 |
| Lys | Glu | Ile | Asp | Tyr | Val | Arg | Gly | Arg | Asp | Phe | Val | Tyr | Asn | Glu | Met |     |
|     |     |     | 235 |     |     |     | 240 |     |     |     |     |     | 245 |     |     |     |

|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| GTC<br>Val        | AAT<br>Asn        | TAC<br>Tyr        | CAA<br>Gln<br>250 | TCC<br>Ser        | GAC<br>Asp        | AAA<br>Lys        | TGC<br>Cys        | GAA<br>Glu<br>255 | CCT<br>Pro        | GAA<br>Glu        | ATG<br>Met        | ATG<br>Met        | GAC<br>Asp<br>260 | TCT<br>Ser        | GAA<br>Glu        | 824  |
| GAT<br>Asp        | CCT<br>Pro        | TTA<br>Leu<br>265 | TTC<br>Phe        | TTG<br>Leu        | CTC<br>Leu        | TAT<br>Tyr        | ACA<br>Thr<br>270 | AGC<br>Ser        | GGA<br>Gly        | TCA<br>Ser        | ACC<br>Thr        | GGA<br>Gly<br>275 | AAG<br>Lys        | CCT<br>Pro        | AAA<br>Lys        | 872  |
| GGC<br>Gly        | GTT<br>Val<br>280 | CAA<br>Gln        | CAC<br>His        | AGC<br>Ser        | AGT<br>Ser        | GCG<br>Ala<br>285 | GGG<br>Gly        | TAT<br>Tyr        | TTG<br>Leu        | TTA<br>Leu        | TGG<br>Trp<br>290 | GCG<br>Ala        | CAA<br>Gln        | ATG<br>Met        | ACG<br>Thr        | 920  |
| ATG<br>Met<br>295 | GAG<br>Glu        | TGG<br>Trp        | GTT<br>Val        | TTT<br>Phe        | GAT<br>Asp<br>300 | ATT<br>Ile        | AGA<br>Arg        | GAT<br>Asp        | AAC<br>Asn        | GAT<br>Asp<br>305 | AAT<br>Asn        | TTT<br>Phe        | TGG<br>Trp        | TGC<br>Cys        | ACC<br>Thr<br>310 | 968  |
| GCC<br>Ala        | GAT<br>Asp        | ATT<br>Ile        | GGC<br>Gly        | TGG<br>Trp<br>315 | ATC<br>Ile        | ACA<br>Thr        | GGG<br>Gly        | CAC<br>His        | ACT<br>Thr<br>320 | TAT<br>Tyr        | GTG<br>Val        | GTT<br>Val        | TAT<br>Tyr        | GGA<br>Gly<br>325 | CCT<br>Pro        | 1016 |
| TTA<br>Leu        | GCT<br>Ala        | TGT<br>Cys        | GGG<br>Gly<br>330 | GCG<br>Ala        | ACG<br>Thr        | ACT<br>Thr        | TTG<br>Leu        | ATA<br>Ile<br>335 | CTA<br>Leu        | GAA<br>Glu        | GGC<br>Gly        | ACG<br>Thr        | ATG<br>Met<br>340 | TCT<br>Ser        | TAT<br>Tyr        | 1064 |
| CCG<br>Pro        | GAT<br>Asp        | TAT<br>Tyr<br>345 | GGG<br>Gly        | AGA<br>Arg        | TGG<br>Trp        | TGG<br>Trp        | AGG<br>Arg<br>350 | ATG<br>Met        | ATA<br>Ile        | GAA<br>Glu        | GAA<br>Glu        | TAC<br>Tyr<br>355 | CGT<br>Arg        | GTG<br>Val        | GAT<br>Asp        | 1112 |
| AAA<br>Lys        | TTC<br>Phe<br>360 | TAC<br>Tyr        | ACT<br>Thr        | TCC<br>Ser        | CCT<br>Pro        | ACC<br>Thr<br>365 | GCT<br>Ala        | ATA<br>Ile        | AGA<br>Arg        | ATG<br>Met        | TTG<br>Leu<br>370 | CAT<br>His        | GCC<br>Ala        | AAA<br>Lys        | GGT<br>Gly        | 1160 |
| GAA<br>Glu<br>375 | AAC<br>Asn        | GAA<br>Glu        | CCC<br>Pro        | TCA<br>Ser        | AAG<br>Lys<br>380 | TAT<br>Tyr        | AAT<br>Asn        | TTA<br>Leu        | GAG<br>Glu        | TCG<br>Ser<br>385 | CTC<br>Leu        | AAA<br>Lys        | GTT<br>Val        | TTA<br>Leu        | GGA<br>Gly<br>390 | 1208 |
| ACG<br>Thr        | GTG<br>Val        | GGA<br>Gly        | GAG<br>Glu        | CCC<br>Pro<br>395 | ATT<br>Ile        | AAC<br>Asn        | CCT<br>Pro        | ACA<br>Thr        | GCA<br>Ala<br>400 | TGG<br>Trp        | AAA<br>Lys        | TGG<br>Trp        | TTT<br>Phe        | TAT<br>Tyr<br>405 | GAA<br>Glu        | 1256 |
| AAA<br>Lys        | ATC<br>Ile        | GGC<br>Gly        | AAC<br>Asn<br>410 | TCA<br>Ser        | AAA<br>Lys        | TGC<br>Cys        | AGC<br>Ser        | ATC<br>Ile<br>415 | GTG<br>Val        | GAT<br>Asp        | ACT<br>Thr        | TGG<br>Trp        | TGG<br>Trp        | CAG<br>Gln        | ACA<br>Thr        | 1304 |
| GAA<br>Glu        | ACA<br>Thr        | GGC<br>Gly<br>425 | GGG<br>Gly        | CAC<br>His        | ATC<br>Ile        | ATC<br>Ile        | AGC<br>Ser<br>430 | CCT<br>Pro        | TTA<br>Leu        | CCG<br>Pro        | GGA<br>Gly        | GCT<br>Ala<br>435 | ACG<br>Thr        | CCT<br>Pro        | ATA<br>Ile        | 1352 |
| AGG<br>Arg        | GCC<br>Ala<br>440 | AGT<br>Ser        | TGC<br>Cys        | GCG<br>Ala        | ACT<br>Thr        | TTA<br>Leu<br>445 | CCT<br>Pro        | TTG<br>Leu        | CCT<br>Pro        | GGA<br>Gly        | ATC<br>Ile<br>450 | CAT<br>His        | GCG<br>Ala        | GAA<br>Glu        | GTT<br>Val        | 1400 |
| TTA<br>Leu<br>455 | AAC<br>Asn        | GAA<br>Glu        | GAC<br>Asp        | GGC<br>Gly        | ACT<br>Thr<br>460 | AAA<br>Lys        | ACA<br>Thr        | AAG<br>Lys        | CCT<br>Pro        | GGA<br>Gly<br>465 | GAG<br>Glu        | CAA<br>Gln        | GGG<br>Gly        | TTT<br>Phe        | TTA<br>Leu<br>470 | 1448 |
| TGC<br>Cys        | ATC<br>Ile        | ACT<br>Thr        | AAG<br>Lys        | CCA<br>Pro        | TGG<br>Trp        | CCT<br>Pro        | TCT<br>Ser        | ATG<br>Met        | ATA<br>Ile        | AGA<br>Arg        | AAC<br>Asn        | ATT<br>Ile        | TGG<br>Trp        | GGC<br>Gly        | GAT<br>Asp        | 1496 |

| 475                                               |     |     |     |     |     |     |     |     |     | 480 |     |     |     |     |     |   |  |  |  | 485 |  |  |  |  |  |  |  |  |  |      |
|---------------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---|--|--|--|-----|--|--|--|--|--|--|--|--|--|------|
| GAA                                               | AAA | CGA | TAC | ATT | GAT | AGC | TAT | TTT | TCT | CAG | ATC | AAG | TTG | AAT | GGG |   |  |  |  |     |  |  |  |  |  |  |  |  |  | 1544 |
| Glu                                               | Lys | Arg | Tyr | Ile | Asp | Ser | Tyr | Phe | Ser | Gln | Ile | Lys | Leu | Asn | Gly |   |  |  |  |     |  |  |  |  |  |  |  |  |  |      |
|                                                   |     |     | 490 |     |     |     |     | 495 |     |     |     |     | 500 |     |     |   |  |  |  |     |  |  |  |  |  |  |  |  |  |      |
| GAA                                               | TAT | GTC | TAC | CTC | TCT | GGA | GAT | GGC | GCT | ATC | GTG | GAT | GAA | AAC | GGA |   |  |  |  |     |  |  |  |  |  |  |  |  |  | 1592 |
| Glu                                               | Tyr | Val | Tyr | Leu | Ser | Gly | Asp | Gly | Ala | Ile | Val | Asp | Glu | Asn | Gly |   |  |  |  |     |  |  |  |  |  |  |  |  |  |      |
|                                                   |     | 505 |     |     |     |     | 510 |     |     |     |     | 515 |     |     |     |   |  |  |  |     |  |  |  |  |  |  |  |  |  |      |
| TAC                                               | ATT | ACT | ATT | ATT | GGG | CGC | ACA | GAT | GAT | ATT | GTG | AAT | GTG | AGT | GGG |   |  |  |  |     |  |  |  |  |  |  |  |  |  | 1640 |
| Tyr                                               | Ile | Thr | Ile | Ile | Gly | Arg | Thr | Asp | Asp | Ile | Val | Asn | Val | Ser | Gly |   |  |  |  |     |  |  |  |  |  |  |  |  |  |      |
|                                                   |     | 520 |     |     |     | 525 |     |     |     |     | 530 |     |     |     |     |   |  |  |  |     |  |  |  |  |  |  |  |  |  |      |
| CAT                                               | AGG | ATT | GGC | ACG | GCT | GAA | GTG | GAG | AGC | GCT | ATT | TCC | AAG | CAT | GAA |   |  |  |  |     |  |  |  |  |  |  |  |  |  | 1688 |
| His                                               | Arg | Ile | Gly | Thr | Ala | Glu | Val | Glu | Ser | Ala | Ile | Ser | Lys | His | Glu |   |  |  |  |     |  |  |  |  |  |  |  |  |  |      |
|                                                   |     |     |     |     | 540 |     |     |     |     | 545 |     |     |     |     | 550 |   |  |  |  |     |  |  |  |  |  |  |  |  |  |      |
| ATG                                               | GTG | GCT | GAA | TGC | GCG | GTG | GTG | GGT | ATC | CCT | GAT | GCG | ATT | AAA | GGA |   |  |  |  |     |  |  |  |  |  |  |  |  |  | 1736 |
| Met                                               | Val | Ala | Glu | Cys | Ala | Val | Val | Gly | Ile | Pro | Asp | Ala | Ile | Lys | Gly |   |  |  |  |     |  |  |  |  |  |  |  |  |  |      |
|                                                   |     |     |     | 555 |     |     |     |     | 560 |     |     |     |     | 565 |     |   |  |  |  |     |  |  |  |  |  |  |  |  |  |      |
| GAG                                               | GGC | TTG | TTT | GCG | TTT | GTG | GTG | CTG | TGC | GAT | GGG | GCT | AAA | TGC | AAT |   |  |  |  |     |  |  |  |  |  |  |  |  |  | 1784 |
| Glu                                               | Gly | Leu | Phe | Ala | Phe | Val | Val | Leu | Cys | Asp | Gly | Ala | Lys | Cys | Asn |   |  |  |  |     |  |  |  |  |  |  |  |  |  |      |
|                                                   |     |     | 570 |     |     |     |     | 575 |     |     |     |     | 580 |     |     |   |  |  |  |     |  |  |  |  |  |  |  |  |  |      |
| CTT                                               | GGC | GAG | AGT | TTA | GAA | TTG | CTA | AAA | GAA | ATG | AAC | CAT | ATC | TTA | TCC |   |  |  |  |     |  |  |  |  |  |  |  |  |  | 1832 |
| Leu                                               | Gly | Glu | Ser | Leu | Glu | Leu | Leu | Lys | Glu | Met | Asn | His | Ile | Leu | Ser |   |  |  |  |     |  |  |  |  |  |  |  |  |  |      |
|                                                   |     |     | 585 |     |     |     | 590 |     |     |     |     | 595 |     |     |     |   |  |  |  |     |  |  |  |  |  |  |  |  |  |      |
| ATT                                               | GAG | ATT | GGA | AAG | ATC | GCG | AAA | TTA | GAC | AAT | GTC | ATG | TAT | GTG | CCA |   |  |  |  |     |  |  |  |  |  |  |  |  |  | 1880 |
| Ile                                               | Glu | Ile | Gly | Lys | Ile | Ala | Lys | Leu | Asp | Asn | Val | Met | Tyr | Val | Pro |   |  |  |  |     |  |  |  |  |  |  |  |  |  |      |
|                                                   |     | 600 |     |     |     | 605 |     |     |     |     | 610 |     |     |     |     |   |  |  |  |     |  |  |  |  |  |  |  |  |  |      |
| GGT                                               | TTG | CCT | AAA | ACC | AGG | AGC | GGG | AAA | ATC | ATG | AGA | AGG | CTT | TTG | AAA |   |  |  |  |     |  |  |  |  |  |  |  |  |  | 1928 |
| Gly                                               | Leu | Pro | Lys | Thr | Arg | Ser | Gly | Lys | Ile | Met | Arg | Arg | Leu | Leu | Lys |   |  |  |  |     |  |  |  |  |  |  |  |  |  |      |
|                                                   |     | 615 |     |     | 620 |     |     |     | 625 |     |     |     |     | 630 |     |   |  |  |  |     |  |  |  |  |  |  |  |  |  |      |
| TCC                                               | ATC | GCC | AAA | AAA | GAG | CCT | ATC | ACT | CAA | GAT | TTA | AGC | ACG | CTA | GAA |   |  |  |  |     |  |  |  |  |  |  |  |  |  | 1976 |
| Ser                                               | Ile | Ala | Lys | Lys | Glu | Pro | Ile | Thr | Gln | Asp | Leu | Ser | Thr | Leu | Glu |   |  |  |  |     |  |  |  |  |  |  |  |  |  |      |
|                                                   |     |     |     | 635 |     |     |     |     | 640 |     |     |     |     | 645 |     |   |  |  |  |     |  |  |  |  |  |  |  |  |  |      |
| GAT                                               | GTG | AAT | GTG | GTT | AAA | GAA | ATA | ATG | AGC | ATC | GCT | CAA | ATG | GAG | GAG | T |  |  |  |     |  |  |  |  |  |  |  |  |  | 2025 |
| Asp                                               | Val | Asn | Val | Val | Lys | Glu | Ile | Met | Ser | Ile | Ala | Gln | Met | Glu | Glu |   |  |  |  |     |  |  |  |  |  |  |  |  |  |      |
|                                                   |     |     | 650 |     |     |     | 655 |     |     |     |     |     | 660 |     |     |   |  |  |  |     |  |  |  |  |  |  |  |  |  |      |
| AAAATCTAAA AAATGCTTTT TAGCGTTTTT TAGCCAAATA ATAAG |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |   |  |  |  |     |  |  |  |  |  |  |  |  |  | 2070 |

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

```

Met Gln Leu Asp Glu Asp Leu Glu Phe Ala Lys Lys Ile Phe Asn Pro
 1 5 10 15
Asn Arg Ala Phe Ala Lys Gln Ala Arg Ile Lys Asn Met Cys Glu Tyr
 20 25 30
Lys Asp Leu Val His Glu Ala Asn Glu Asp Tyr Glu His Phe Trp Gly
 35 40 45
Asp Leu Ala Lys Gln Lys Leu Thr Trp Phe Lys Pro Phe Asp Lys Val
 50 55 60
Leu Asn Ser Asp Asn Ala Pro Phe Phe Lys Trp Phe Glu Asn Gly Lys
 65 70 75 80
Ile Asn Val Ser Tyr Asn Cys Ile Asp Arg His Leu Lys Asp Lys Lys
 85 90 95
Asn Lys Val Ala Ile Ile Phe Glu Gly Glu Met Gly Asp Tyr Asn Val
 100 105 110
Ile Thr Tyr Arg Lys Leu His Ser Glu Val Asn Lys Thr Ala Asn Leu
 115 120 125
Leu Lys Asn Glu Phe Asn Val Lys Lys Gly Asp Arg Val Ile Ile Tyr
 130 135 140
Met Pro Met Ile Val Glu Ser Val Tyr Met Met Leu Ala Cys Thr Arg
 145 150 155 160
Ile Gly Ala Ile His Ser Ile Val Phe Ala Gly Phe Ser Pro Glu Ala
 165 170 175
Leu Arg Asp Arg Ile Asn Asp Ala Gln Ala Lys Leu Val Ile Thr Ala
 180 185 190
Asp Gly Thr Phe Arg Lys Gly Lys Pro Tyr Met Leu Lys Pro Ala Leu
 195 200 205
Asp Lys Ala Leu Glu Asn Asn Ala Cys Pro Ser Val Glu Lys Ala Leu
 210 215 220
Ile Val Ile Arg Asn Ala Lys Glu Ile Asp Tyr Val Arg Gly Arg Asp
 225 230 235 240
Phe Val Tyr Asn Glu Met Val Asn Tyr Gln Ser Asp Lys Cys Glu Pro
 245 250 255
Glu Met Met Asp Ser Glu Asp Pro Leu Phe Leu Leu Tyr Thr Ser Gly
 260 265 270
Ser Thr Gly Lys Pro Lys Gly Val Gln His Ser Ser Ala Gly Tyr Leu
 275 280 285
Leu Trp Ala Gln Met Thr Met Glu Trp Val Phe Asp Ile Arg Asp Asn
 290 295 300
Asp Asn Phe Trp Cys Thr Ala Asp Ile Gly Trp Ile Thr Gly His Thr
 305 310 315 320
Tyr Val Val Tyr Gly Pro Leu Ala Cys Gly Ala Thr Thr Leu Ile Leu
 325 330 335
Glu Gly Thr Met Ser Tyr Pro Asp Tyr Gly Arg Trp Trp Arg Met Ile
 340 345 350
Glu Glu Tyr Arg Val Asp Lys Phe Tyr Thr Ser Pro Thr Ala Ile Arg
 355 360 365
Met Leu His Ala Lys Gly Glu Asn Glu Pro Ser Lys Tyr Asn Leu Glu
 370 375 380
Ser Leu Lys Val Leu Gly Thr Val Gly Glu Pro Ile Asn Pro Thr Ala
 385 390 395 400
Trp Lys Trp Phe Tyr Glu Lys Ile Gly Asn Ser Lys Cys Ser Ile Val
 405 410 415
Asp Thr Trp Trp Gln Thr Glu Thr Gly Gly His Ile Ile Ser Pro Leu
 420 425 430
Pro Gly Ala Thr Pro Ile Arg Ala Ser Cys Ala Thr Leu Pro Leu Pro
 435 440 445

```





|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GTC ATA GGG TTT TTA GAA AAA AAC CAT GCC CTT TTG CAA TAT TTT CTT   | 195 |
| Val Ile Gly Phe Leu Glu Lys Asn His Ala Leu Leu Gln Tyr Phe Leu   |     |
| 45 50 55                                                          |     |
| ATT ATT TTT AAA TAC GAT ATT GAA TCA GAA GTC AAA GCC GTT TTG CGC   | 243 |
| Ile Ile Phe Lys Tyr Asp Ile Glu Ser Glu Val Lys Ala Val Leu Arg   |     |
| 60 65 70 75                                                       |     |
| AAA CAC CAG CTT TTG TTT TTA GAA ACG AAT CGC GTT TTA AAC GGA CGC   | 291 |
| Lys His Gln Leu Leu Phe Leu Glu Thr Asn Arg Val Leu Asn Gly Arg   |     |
| 80 85 90                                                          |     |
| CAT ATC AAA ACC ATG CCT TTA AAA GAC GAA ACC GAT CAT CCA AAA CCC   | 339 |
| His Ile Lys Thr Met Pro Leu Lys Asp Glu Thr Asp His Pro Lys Pro   |     |
| 95 100 105                                                        |     |
| AAT CAT TCT AAA ACA GAA CCT AAA ACA ACG ATT TAT GAG CGC CAT ATC   | 387 |
| Asn His Ser Lys Thr Glu Pro Lys Thr Thr Ile Tyr Glu Arg His Ile   |     |
| 110 115 120                                                       |     |
| AGG AGT GGG GAA GAG ATT TAT AGC ACT AAT CAC CTT ATT TTT TTG GGT   | 435 |
| Arg Ser Gly Glu Glu Ile Tyr Ser Thr Asn His Leu Ile Phe Leu Gly   |     |
| 125 130 135                                                       |     |
| AAT ATC CAT AAT GGA GCC AAG ATT ATT TCA GAG GGC TGT GTG TCT GTT   | 483 |
| Asn Ile His Asn Gly Ala Lys Ile Ile Ser Glu Gly Cys Val Ser Val   |     |
| 140 145 150 155                                                   |     |
| TAT GGG GTT TGC GAA GGG GCG ATT GTG TGC TTT GGA GAG TGT TTG ATC   | 531 |
| Tyr Gly Val Cys Glu Gly Ala Ile Val Cys Phe Gly Glu Cys Leu Ile   |     |
| 160 165 170                                                       |     |
| TTA AAA GAA GTC AAG AGC GCT CAA ATC GTT TTT CAA AAC AAA ATT TTG   | 579 |
| Leu Lys Glu Val Lys Ser Ala Gln Ile Val Phe Gln Asn Lys Ile Leu   |     |
| 175 180 185                                                       |     |
| TCT CTA AAA GAG GTT GAA CCG CTT TTG GTA AAT AAA AAT ATT AAA ATA   | 627 |
| Ser Leu Lys Glu Val Glu Pro Leu Leu Val Asn Lys Asn Ile Lys Ile   |     |
| 190 195 200                                                       |     |
| ATC ACT AAA AAT GAC GAT ATA CTA GAC ATA AAG GAA GTA TTA TGAAACAAA | 678 |
| Ile Thr Lys Asn Asp Asp Ile Leu Asp Ile Lys Glu Val Leu           |     |
| 205 210 215                                                       |     |
| CAACCATTA CCACTCTGTG GAATTAGTAG GGATAGGCTT GCACAAG                | 725 |

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Lys | Asn | Gln | Tyr | His | Arg | Pro | His | Arg | Ala | Ser | Gln | Thr | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Asn | Glu | Arg | Ile | Val | Met | Leu | Lys | Thr | Asn | Gln | Lys | Asn | Val | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Phe | Glu | Ile | Glu | Lys | Gln | Glu | Pro | Glu | Ala | Val | Ile | Gly | Phe | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Lys | Asn | His | Ala | Leu | Leu | Gln | Tyr | Phe | Leu | Ile | Ile | Phe | Lys | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Ile | Glu | Ser | Glu | Val | Lys | Ala | Val | Leu | Arg | Lys | His | Gln | Leu | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Phe | Leu | Glu | Thr | Asn | Arg | Val | Leu | Asn | Gly | Arg | His | Ile | Lys | Thr | Met |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Leu | Lys | Asp | Glu | Thr | Asp | His | Pro | Lys | Pro | Asn | His | Ser | Lys | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Pro | Lys | Thr | Thr | Ile | Tyr | Glu | Arg | His | Ile | Arg | Ser | Gly | Glu | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Tyr | Ser | Thr | Asn | His | Leu | Ile | Phe | Leu | Gly | Asn | Ile | His | Asn | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Lys | Ile | Ile | Ser | Glu | Gly | Cys | Val | Ser | Val | Tyr | Gly | Val | Cys | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gly | Ala | Ile | Val | Cys | Phe | Gly | Glu | Cys | Leu | Ile | Leu | Lys | Glu | Val | Lys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Ala | Gln | Ile | Val | Phe | Gln | Asn | Lys | Ile | Leu | Ser | Leu | Lys | Glu | Val |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Pro | Leu | Leu | Val | Asn | Lys | Asn | Ile | Lys | Ile | Ile | Thr | Lys | Asn | Asp |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Asp | Ile | Leu | Asp | Ile | Lys | Glu | Val | Leu |     |     |     |     |     |     |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 64...1068
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

|                                                                 |            |            |            |            |            |    |
|-----------------------------------------------------------------|------------|------------|------------|------------|------------|----|
| AAAGAAAATC                                                      | TGTTATTGGA | TAAACCCAAG | TCTTTAGAAG | TGCCTTTGAC | TAGGCCCGAA | 60 |
| ATC ATG GGG CTA GAA GAC AAG TGC CTT TTA TAT GAA ATT AAA GCT AAT | 108        |            |            |            |            |    |
| Met Gly Leu Glu Asp Lys Cys Leu Leu Tyr Glu Ile Lys Ala Asn     |            |            |            |            |            |    |
| 1                                                               | 5          |            | 10         |            | 15         |    |
| GAT TGG AGT TAT GCT AAT TTT TTC AAT GGC AAT AAA GCG TCT TTC AAA | 156        |            |            |            |            |    |
| Asp Trp Ser Tyr Ala Asn Phe Phe Asn Gly Asn Lys Ala Ser Phe Lys |            |            |            |            |            |    |
|                                                                 | 20         |            | 25         |            | 30         |    |
| CAA GAA GTG TGT GTT GAT ACG ATA AAA CCC TCA ATC ACT ATT TTA TCT | 204        |            |            |            |            |    |
| Gln Glu Val Cys Val Asp Thr Ile Lys Pro Ser Ile Thr Ile Leu Ser |            |            |            |            |            |    |

| 35                |                   |                   |                   |                   |                   |                   | 40                |                   |                   |                   |                   | 45                |                   |                   |                   |     |  |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|--|
| CGA<br>Arg        | TCC<br>Ser        | CCA<br>Pro<br>50  | AGC<br>Ser        | ATC<br>Ile        | GCT<br>Ala        | TAT<br>Tyr        | GGG<br>Gly<br>55  | GGG<br>Gly        | AGC<br>Ser        | GCG<br>Ala        | ATA<br>Ile        | GTC<br>Val<br>60  | GTT<br>Val        | TTT<br>Phe        | GAA<br>Glu        | 252 |  |
| GCT<br>Ala        | TTG<br>Leu<br>65  | GAT<br>Asp        | AAG<br>Lys        | AAT<br>Asn        | TTG<br>Leu        | TCT<br>Ser<br>70  | CAA<br>Gln        | GCG<br>Ala        | TTT<br>Phe        | GTG<br>Val        | CGC<br>Arg<br>75  | GTC<br>Val        | AAA<br>Lys        | AAA<br>Lys        | AAG<br>Lys        | 300 |  |
| GAT<br>Asp<br>80  | TTT<br>Phe        | GAA<br>Glu        | GCT<br>Ala        | TTC<br>Phe        | AGG<br>Arg<br>85  | CTT<br>Leu        | TTA<br>Leu        | GAA<br>Glu        | TTC<br>Phe        | AAA<br>Lys<br>90  | CAG<br>Gln        | CGT<br>Arg        | AAT<br>Asn        | GTT<br>Val        | TTT<br>Phe<br>95  | 348 |  |
| ATC<br>Ile        | GCT<br>Ala        | CTA<br>Leu        | GTG<br>Val        | CCT<br>Pro<br>100 | TGG<br>Trp        | TCT<br>Ser        | TAT<br>Tyr        | AAA<br>Lys        | AAT<br>Asn<br>105 | AAG<br>Lys        | GAT<br>Asp        | TTT<br>Phe        | AAG<br>Lys        | GCG<br>Ala<br>110 | TTC<br>Phe        | 396 |  |
| ATT<br>Ile        | GTC<br>Val        | GCT<br>Ala        | AAA<br>Lys<br>115 | GAT<br>Asp        | AAA<br>Lys        | GCC<br>Ala        | TAT<br>Tyr        | AAC<br>Asn<br>120 | TTT<br>Phe        | AAT<br>Asn        | ACC<br>Thr        | GCC<br>Ala        | CCT<br>Pro<br>125 | TTA<br>Leu        | TTG<br>Leu        | 444 |  |
| TTC<br>Phe        | AAG<br>Lys<br>130 | CGA<br>Arg        | AAA<br>Lys        | ATC<br>Ile        | CAT<br>His        | CGT<br>Arg        | TTG<br>Leu<br>135 | AGG<br>Arg        | GAA<br>Glu        | AAA<br>Lys        | GAT<br>Asp        | ATA<br>Ile<br>140 | GAC<br>Asp        | TTA<br>Leu        | AGC<br>Ser        | 492 |  |
| GCC<br>Ala        | TTA<br>Leu<br>145 | AAA<br>Lys        | GAT<br>Asp        | AAG<br>Lys        | ATT<br>Ile        | GCA<br>Ala<br>150 | AAG<br>Lys        | CAA<br>Gln        | GAA<br>Glu        | AAA<br>Lys        | TTT<br>Phe<br>155 | CAA<br>Gln        | AAC<br>Asn        | GAC<br>Asp        | ACT<br>Thr        | 540 |  |
| GAA<br>Glu<br>160 | CAA<br>Gln        | GCT<br>Ala        | TTA<br>Leu        | TTA<br>Leu        | GAA<br>Glu<br>165 | AGA<br>Arg        | TTT<br>Phe        | TCC<br>Ser        | AAT<br>Asn        | GCG<br>Ala<br>170 | CGC<br>Arg        | CCA<br>Pro        | AAA<br>Lys        | GAT<br>Asp        | TTA<br>Leu<br>175 | 588 |  |
| GAA<br>Glu        | AAA<br>Lys        | ATC<br>Ile        | CAA<br>Gln        | AAG<br>Lys<br>180 | ATC<br>Ile        | GCT<br>Ala        | TTA<br>Leu        | GAG<br>Glu        | CAA<br>Gln<br>185 | GGG<br>Gly        | GAT<br>Asp        | TTT<br>Phe        | TAT<br>Tyr        | AAG<br>Lys<br>190 | GAT<br>Asp        | 636 |  |
| TTT<br>Phe        | TCT<br>Ser        | CAT<br>His        | TTT<br>Phe<br>195 | CAA<br>Gln        | GCG<br>Ala        | CTA<br>Leu        | AAA<br>Lys        | CCC<br>Pro<br>200 | TTG<br>Leu        | AAC<br>Asn        | GGG<br>Gly        | CCT<br>Pro        | TTT<br>Phe<br>205 | AAA<br>Lys        | ATG<br>Met        | 684 |  |
| GCA<br>Ala        | AGC<br>Ser        | AAT<br>Asn<br>210 | TTT<br>Phe        | TTA<br>Leu        | GAA<br>Glu        | AAT<br>Asn        | CGG<br>Arg<br>215 | CGT<br>Arg        | ATC<br>Ile        | TTA<br>Leu        | AAG<br>Lys        | AAT<br>Asn<br>220 | AAT<br>Asn        | CAG<br>Gln        | GTG<br>Val        | 732 |  |
| TTG<br>Leu        | TTT<br>Phe<br>225 | AAA<br>Lys        | TTC<br>Phe        | TTG<br>Leu        | CAT<br>His        | TTA<br>Leu<br>230 | GGG<br>Gly        | GTG<br>Val        | GAT<br>Asp        | TTG<br>Leu        | ATA<br>Ile<br>235 | CCT<br>Pro        | GGC<br>Gly        | AAG<br>Lys        | GAT<br>Asp        | 780 |  |
| TTA<br>Leu<br>240 | TCT<br>Ser        | TTA<br>Leu        | GCG<br>Ala        | TTT<br>Phe        | GAT<br>Asp<br>245 | TTG<br>Leu        | TCT<br>Ser        | GTG<br>Val        | AAG<br>Lys        | AGG<br>Arg<br>250 | GTT<br>Val        | TTT<br>Phe        | AAG<br>Lys        | GGG<br>Gly        | GAG<br>Glu<br>255 | 828 |  |
| TTC<br>Phe        | GAT<br>Asp        | TTT<br>Phe        | TAT<br>Tyr        | GGT<br>Gly<br>260 | AAT<br>Asn        | AGT<br>Ser        | TTA<br>Leu        | ATC<br>Ile        | CAT<br>His<br>265 | TGC<br>Cys        | TAT<br>Tyr        | GGG<br>Gly        | TTA<br>Leu        | GGT<br>Gly<br>270 | TTG<br>Leu        | 876 |  |

|                                                           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |        |
|-----------------------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--------|
| TGC                                                       | GTT | TTT | TTA | GCC | CAT | TTA | AAA | GAT | GAT | AAA | AGC | GTG | GGG | AGT | AGT  | 924    |
| Cys                                                       | Val | Phe | Leu | Ala | His | Leu | Lys | Asp | Asp | Lys | Ser | Val | Gly | Ser | Ser  |        |
|                                                           |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |      |        |
|                                                           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |        |
| GGT                                                       | TTG | AAA | TTA | GGG | AGC | GGG | TTG | CAT | TTA | GGG | ATG | CTT | TTG | CAA | GGG  | 972    |
| Gly                                                       | Leu | Lys | Leu | Gly | Ser | Gly | Leu | His | Leu | Gly | Met | Leu | Leu | Gln | Gly  |        |
|                                                           |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |      |        |
|                                                           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |        |
| GTT                                                       | TTT | GTC | CGG | CCC | AAT | GAA | TGG | CTT | AAT | GAG | CAA | TGG | ATA | AAA | ACC  | 1020   |
| Val                                                       | Phe | Val | Arg | Pro | Asn | Glu | Trp | Leu | Asn | Glu | Gln | Trp | Ile | Lys | Thr  |        |
|                                                           | 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |      |        |
|                                                           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |        |
| AAT                                                       | ATC | ACC | GCC | CCC | ATA | GAG | CAA | GCC | AAA | CGG | CTT | TTA | ATG | AAA | GGA  | T 1069 |
| Asn                                                       | Ile | Thr | Ala | Pro | Ile | Glu | Gln | Ala | Lys | Arg | Leu | Leu | Met | Lys | Gly  |        |
| 320                                                       |     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335  |        |
|                                                           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |        |
| AGTCATGTTA AAAACGAATC AAAAAAATGT GCATGCGTTT GAAATTGAAA AG |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 1121 |        |

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Leu | Glu | Asp | Lys | Cys | Leu | Leu | Tyr | Glu | Ile | Lys | Ala | Asn | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Trp | Ser | Tyr | Ala | Asn | Phe | Phe | Asn | Gly | Asn | Lys | Ala | Ser | Phe | Lys | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Val | Cys | Val | Asp | Thr | Ile | Lys | Pro | Ser | Ile | Thr | Ile | Leu | Ser | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Pro | Ser | Ile | Ala | Tyr | Gly | Gly | Ser | Ala | Ile | Val | Val | Phe | Glu | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Leu | Asp | Lys | Asn | Leu | Ser | Gln | Ala | Phe | Val | Arg | Val | Lys | Lys | Lys | Asp |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Phe | Glu | Ala | Phe | Arg | Leu | Leu | Glu | Phe | Lys | Gln | Arg | Asn | Val | Phe | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Leu | Val | Pro | Trp | Ser | Tyr | Lys | Asn | Lys | Asp | Phe | Lys | Ala | Phe | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Ala | Lys | Asp | Lys | Ala | Tyr | Asn | Phe | Asn | Thr | Ala | Pro | Leu | Leu | Phe |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Arg | Lys | Ile | His | Arg | Leu | Arg | Glu | Lys | Asp | Ile | Asp | Leu | Ser | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Leu | Lys | Asp | Lys | Ile | Ala | Lys | Gln | Glu | Lys | Phe | Gln | Asn | Asp | Thr | Glu |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Gln | Ala | Leu | Leu | Glu | Arg | Phe | Ser | Asn | Ala | Arg | Pro | Lys | Asp | Leu | Glu |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Lys | Ile | Gln | Lys | Ile | Ala | Leu | Glu | Gln | Gly | Asp | Phe | Tyr | Lys | Asp | Phe |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     | 190 |     |     |     |
| Ser | His | Phe | Gln | Ala | Leu | Lys | Pro | Leu | Asn | Gly | Pro | Phe | Lys | Met | Ala |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Asn | Phe | Leu | Glu | Asn | Arg | Arg | Ile | Leu | Lys | Asn | Asn | Gln | Val | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Lys | Phe | Leu | His | Leu | Gly | Val | Asp | Leu | Ile | Pro | Gly | Lys | Asp | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ser | Leu | Ala | Phe | Asp | Leu | Ser | Val | Lys | Arg | Val | Phe | Lys | Gly | Glu | Phe |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asp | Phe | Tyr | Gly | Asn | Ser | Leu | Ile | His | Cys | Tyr | Gly | Leu | Gly | Leu | Cys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Phe | Leu | Ala | His | Leu | Lys | Asp | Asp | Lys | Ser | Val | Gly | Ser | Ser | Gly |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Lys | Leu | Gly | Ser | Gly | Leu | His | Leu | Gly | Met | Leu | Leu | Gln | Gly | Val |
|     | 290 |     |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     |
| Phe | Val | Arg | Pro | Asn | Glu | Trp | Leu | Asn | Glu | Gln | Trp | Ile | Lys | Thr | Asn |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     | 320 |
| Ile | Thr | Ala | Pro | Ile | Glu | Gln | Ala | Lys | Arg | Leu | Leu | Met | Lys | Gly |     |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1004 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 28...969
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

|       |       |       |       |         |     |     |     |     |     |     |     |     |     |     |     |
|-------|-------|-------|-------|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| TTACA | ACTAT | TTATT | GTAAA | GGCTAAA | ATG | TTG | AAA | TTT | AAA | TAT | GGT | TTG | ATT |     | 54  |
|       |       |       |       |         | Met | Leu | Lys | Phe | Lys | Tyr | Gly | Leu | Ile |     |     |
|       |       |       |       |         | 1   |     |     |     |     | 5   |     |     |     |     |     |
| TAT   | ATC   | GCG   | CTC   | ATA     | CTA | GGA | CTT | CAA | GCG | ACA | GAT | TAT | GAC | AAT | TTA |
| Tyr   | Ile   | Ala   | Leu   | Ile     | Leu | Gly | Leu | Gln | Ala | Thr | Asp | Tyr | Asp | Asn | Leu |
| 10    |       |       |       |         | 15  |     |     |     | 20  |     |     |     |     | 25  | 102 |
| GAA   | GAA   | GAA   | AAC   | CAA     | CAA | TTA | GAT | GAA | AAA | ATA | AAC | CAT | TTA | AAG | CAA |
| Glu   | Glu   | Glu   | Asn   | Gln     | Gln | Leu | Asp | Glu | Lys | Ile | Asn | His | Leu | Lys | Gln |
|       |       |       | 30    |         |     |     |     | 35  |     |     |     |     | 40  |     | 150 |
| CAG   | CTC   | ACC   | GAA   | AAA     | GGG | GTT | TCG | CCC | AAA | GAG | ATG | GAT | AAG | GAT | AAG |
| Gln   | Leu   | Thr   | Glu   | Lys     | Gly | Val | Ser | Pro | Lys | Glu | Met | Asp | Lys | Asp | Lys |
|       |       |       | 45    |         |     |     |     | 50  |     |     |     |     | 55  |     | 198 |
| TTT   | GAA   | GAA   | GAA   | TAC     | ATC | AAT | CGA | TCT | TAT | CCT | AAA | ATT | TCT | TCC | AAG |
| Phe   | Glu   | Glu   | Glu   | Tyr     | Ile | Asn | Arg | Ser | Tyr | Pro | Lys | Ile | Ser | Ser | Lys |
|       |       |       | 60    |         |     |     | 65  |     |     |     |     | 70  |     |     | 246 |
| AAA   | AAA   | GAG   | AAA   | TTG     | CTC | AAA | TCT | TTT | TCC | ATA | GCC | GAT | GAT | AAG | AGT |
| Lys   | Lys   | Glu   | Lys   | Leu     | Leu | Lys | Ser | Phe | Ser | Ile | Ala | Asp | Asp | Lys | Ser |
|       |       | 75    |       |         |     | 80  |     |     |     |     | 85  |     |     |     | 294 |
| GGG   | GTT   | TTT   | TTA   | GGG     | GGT | GGG | TAT | GCT | TAT | GGG | GAA | CTT | AAC | TTG | TCT |
|       |       |       |       |         |     |     |     |     |     |     |     |     |     |     | 342 |

|         |            |           |            |         |         |         |         |         |         |         |         |         |         |         |         |      |
|---------|------------|-----------|------------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|------|
| Gly 90  | Val        | Phe       | Leu        | Gly 95  | Gly     | Gly     | Tyr     | Ala     | Tyr     | Gly 100 | Glu     | Leu     | Asn     | Leu     | Ser 105 |      |
| TAT     | CAA        | GGG       | GAA        | ATG     | TTA     | GAC     | AGA     | TAC     | GGC     | GCG     | AAT     | GCC     | CCT     | AGC     | GCG     | 390  |
| Tyr     | Gln        | Gly       | Glu        | Met 110 | Leu     | Asp     | Arg     | Tyr     | Gly 115 | Ala     | Asn     | Ala     | Pro     | Ser 120 | Ala     |      |
| TTT     | AAA        | AAC       | AAT        | ATC     | AAT     | ATT     | AAC     | GCT     | CCT     | GTT     | TCT     | ATG     | ATT     | AGC     | GCT     | 438  |
| Phe     | Lys        | Asn       | Asn        | Ile 125 | Asn     | Ile     | Asn     | Ala 130 | Pro     | Val     | Ser     | Met     | Ile 135 | Ser     | Ala     |      |
| AAA     | TTT        | GGG       | TAT        | CAA     | AAA     | TAC     | TTT     | GTG     | TCT     | TAT     | TTT     | GGG     | ACA     | CGA     | TTT     | 486  |
| Lys     | Phe        | Gly 140   | Tyr        | Gln     | Lys     | Tyr     | Phe 145 | Val     | Ser     | Tyr     | Phe     | Gly 150 | Thr     | Arg     | Phe     |      |
| TAT     | GGG        | GAT       | TTA        | TTG     | CTT     | GGG     | GGT     | GGG     | GCA     | TTA     | AAA     | GAG     | GAT     | GCA     | ATC     | 534  |
| Tyr     | Gly 155    | Asp       | Leu        | Leu     | Leu     | Gly 160 | Gly     | Gly     | Ala     | Leu     | Lys     | Glu     | Asp     | Ala     | Ile     |      |
| AAG     | CAG        | CCT       | GTA        | GGC     | TCG     | TTT     | ATT     | TAT     | GTT     | TTA     | GGG     | GCT     | GTC     | AAT     | ACC     | 582  |
| Lys 170 | Gln        | Pro       | Val        | Gly     | Ser 175 | Phe     | Ile     | Tyr     | Val     | Leu     | Gly 180 | Ala     | Val     | Asn     | Thr 185 |      |
| GAT     | TTA        | TTG       | TTT        | GAT     | ATG     | CCT     | TTA     | GAT     | TTT     | AAA     | ACT     | AAA     | AAG     | CAT     | TTT     | 630  |
| Asp     | Leu        | Leu       | Phe        | Asp 190 | Met     | Pro     | Leu     | Asp     | Phe 195 | Lys     | Thr     | Lys     | Lys     | His     | Phe 200 |      |
| TTA     | GGC        | GTT       | TAT        | GCG     | GGT     | TTT     | GGG     | ATA     | GGG     | CTT     | ATG     | CTC     | TAT     | CAA     | GAC     | 678  |
| Leu     | Gly        | Val       | Tyr        | Ala 205 | Gly     | Phe     | Gly     | Ile 210 | Gly     | Leu     | Met     | Leu     | Tyr     | Gln     | Asp 215 |      |
| AGG     | CCT        | AAT       | CAA        | AAC     | GGG     | AGG     | AAT     | TTA     | GTA     | GTG     | GGG     | GGC     | TAT     | TCA     | AGC     | 726  |
| Arg     | Pro        | Asn 220   | Gln        | Asn     | Gly     | Arg     | Asn 225 | Leu     | Val     | Val     | Gly     | Gly     | Tyr     | Ser     | Ser     |      |
| CCT     | AAT        | TTT       | TTA        | TGG     | AAA     | TCT     | TTG     | ATT     | GAA     | GTG     | GAT     | TAC     | ACT     | TTT     | AAT     | 774  |
| Pro     | Asn        | Phe       | Leu        | Trp     | Lys     | Ser     | Leu     | Ile     | Glu     | Val     | Asp     | Tyr     | Thr     | Phe     | Asn 245 |      |
| GTG     | GGC        | GTG       | AGT        | TTA     | ACG     | CTT     | TAT     | AGG     | AAA     | CAC     | CGT     | TTA     | GAG     | ATT     | GGC     | 822  |
| Val 250 | Gly        | Val       | Ser        | Leu     | Thr 255 | Leu     | Tyr     | Arg     | Lys     | His 260 | Arg     | Leu     | Glu     | Ile     | Gly 265 |      |
| ACA     | AAA        | TTG       | CCG        | ATT     | AGC     | TAT     | TTG     | AGA     | ATG     | GGA     | GTG     | GAA     | GAG     | GGA     | GCG     | 870  |
| Thr     | Lys        | Leu       | Pro        | Ile 270 | Ser     | Tyr     | Leu     | Arg     | Met     | Gly 275 | Val     | Glu     | Glu     | Gly     | Ala 280 |      |
| ATT     | TAT        | CAA       | AAT        | AAA     | GAA     | GAT     | GAT     | GAG     | CGT     | TTG     | TTG     | GTT     | TCG     | GCT     | AAC     | 918  |
| Ile     | Tyr        | Gln       | Asn        | Lys 285 | Glu     | Asp     | Asp     | Glu 290 | Arg     | Leu     | Leu     | Val     | Ser     | Ala     | Asn 295 |      |
| AAC     | CAG        | TTC       | AAG        | CGA     | TCC     | AGT     | TTT     | TTA     | TTA     | GTG     | AAT     | TAT     | GCG     | TTT     | ATT     | 966  |
| Asn     | Gln        | Phe       | Lys        | Arg     | Ser     | Ser     | Phe 305 | Leu     | Leu     | Val     | Asn     | Tyr     | Ala     | Phe     | Ile 310 |      |
| TTT     | TAAGGCTTGA | TCTTGAGTT | AAGGTTTAAA | ATTTT   |         |         |         |         |         |         |         |         |         |         |         | 1004 |
| Phe     |            |           |            |         |         |         |         |         |         |         |         |         |         |         |         |      |

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Met Leu Lys Phe Lys Tyr Gly Leu Ile Tyr Ile Ala Leu Ile Leu Gly  
1 5 10 15  
Leu Gln Ala Thr Asp Tyr Asp Asn Leu Glu Glu Glu Asn Gln Gln Leu  
20 25 30  
Asp Glu Lys Ile Asn His Leu Lys Gln Gln Leu Thr Glu Lys Gly Val  
35 40 45  
Ser Pro Lys Glu Met Asp Lys Asp Lys Phe Glu Glu Glu Tyr Ile Asn  
50 55 60  
Arg Ser Tyr Pro Lys Ile Ser Ser Lys Lys Lys Glu Lys Leu Leu Lys  
65 70 75 80  
Ser Phe Ser Ile Ala Asp Asp Lys Ser Gly Val Phe Leu Gly Gly Gly  
85 90 95  
Tyr Ala Tyr Gly Glu Leu Asn Leu Ser Tyr Gln Gly Glu Met Leu Asp  
100 105 110  
Arg Tyr Gly Ala Asn Ala Pro Ser Ala Phe Lys Asn Asn Ile Asn Ile  
115 120 125  
Asn Ala Pro Val Ser Met Ile Ser Ala Lys Phe Gly Tyr Gln Lys Tyr  
130 135 140  
Phe Val Ser Tyr Phe Gly Thr Arg Phe Tyr Gly Asp Leu Leu Leu Gly  
145 150 155 160  
Gly Gly Ala Leu Lys Glu Asp Ala Ile Lys Gln Pro Val Gly Ser Phe  
165 170 175  
Ile Tyr Val Leu Gly Ala Val Asn Thr Asp Leu Leu Phe Asp Met Pro  
180 185 190  
Leu Asp Phe Lys Thr Lys Lys His Phe Leu Gly Val Tyr Ala Gly Phe  
195 200 205  
Gly Ile Gly Leu Met Leu Tyr Gln Asp Arg Pro Asn Gln Asn Gly Arg  
210 215 220  
Asn Leu Val Val Gly Gly Tyr Ser Ser Pro Asn Phe Leu Trp Lys Ser  
225 230 235 240  
Leu Ile Glu Val Asp Tyr Thr Phe Asn Val Gly Val Ser Leu Thr Leu  
245 250 255  
Tyr Arg Lys His Arg Leu Glu Ile Gly Thr Lys Leu Pro Ile Ser Tyr  
260 265 270  
Leu Arg Met Gly Val Glu Glu Gly Ala Ile Tyr Gln Asn Lys Glu Asp  
275 280 285  
Asp Glu Arg Leu Leu Val Ser Ala Asn Asn Gln Phe Lys Arg Ser Ser  
290 295 300  
Phe Leu Leu Val Asn Tyr Ala Phe Ile Phe  
305 310

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 874 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 18...827  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AACACTTAGG ATTTTATA ATG AGC ATG CAA ACC GCC CCA ATT AAA AAG ATC | 50  |
| Met Ser Met Gln Thr Ala Pro Ile Lys Lys Ile                     |     |
| 1 5 10                                                          |     |
| ACT CTC AAC CAC CTC CAA GCT AAA AAA AAT CAA GAA AAA ATC ATC GCT | 98  |
| Thr Leu Asn His Leu Gln Ala Lys Lys Asn Gln Glu Lys Ile Ile Ala |     |
| 15 20 25                                                        |     |
| ATT ACC GCT TAT GAT GCG CTG TTC GCT CAA ATA TTT GAT CCG CTA GTG | 146 |
| Ile Thr Ala Tyr Asp Ala Leu Phe Ala Gln Ile Phe Asp Pro Leu Val |     |
| 30 35 40                                                        |     |
| GAT GTG ATT TTA GTG GGC GAT AGT TTG AAT ATG AGT TTT TTC AAT CAA | 194 |
| Asp Val Ile Leu Val Gly Asp Ser Leu Asn Met Ser Phe Phe Asn Gln |     |
| 45 50 55                                                        |     |
| AAC GAC ACT TTA AGC GCG AGT GTG GAA ATG ATG CTC TAT CAC ACC AAA | 242 |
| Asn Asp Thr Leu Ser Ala Ser Val Glu Met Met Leu Tyr His Thr Lys |     |
| 60 65 70 75                                                     |     |
| GCC GTG TGC GCG GGC GCT AAG ACT CCT TTT ATC ATC ACA GAC ATG CCT | 290 |
| Ala Val Cys Ala Gly Ala Lys Thr Pro Phe Ile Ile Thr Asp Met Pro |     |
| 80 85 90                                                        |     |
| TTT GGA AGC TAT AAA GAT GAA AAA ACA GCC CTA AAA AAC GCC ATT AGG | 338 |
| Phe Gly Ser Tyr Lys Asp Glu Lys Thr Ala Leu Lys Asn Ala Ile Arg |     |
| 95 100 105                                                      |     |
| GTT TAT AAA GAA ACC CAA GCG AGC GCA ATC AAA TTA GAG GGG GGG AAA | 386 |
| Val Tyr Lys Glu Thr Gln Ala Ser Ala Ile Lys Leu Glu Gly Gly Lys |     |
| 110 115 120                                                     |     |
| GAA AAA GCG AAA CTG GTT AAA ACG CTC ACT AAT GAG GGC GTT ATT GTG | 434 |
| Glu Lys Ala Lys Leu Val Lys Thr Leu Thr Asn Glu Gly Val Ile Val |     |
| 125 130 135                                                     |     |
| GTA GGG CAT ATT GGC TTG ATG CCC CAA TTC GTG CGC CTT GAT GGA GGT | 482 |
| Val Gly His Ile Gly Leu Met Pro Gln Phe Val Arg Leu Asp Gly Gly |     |
| 140 145 150 155                                                 |     |
| TAT AAG ATT AAG GGC AAA AAT GAA GAA CAA CAA AAA AAG CTT TTA GAA | 530 |
| Tyr Lys Ile Lys Gly Lys Asn Glu Glu Gln Gln Lys Lys Leu Leu Glu |     |
| 160 165 170                                                     |     |



|     |     |     |                                                     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----------------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GAC | GCC | TTG | AGT                                                 | TTA | GAA | GAA | GCT | GGG | GTG | GGT | TTG | TTG | GTT | TTA | GAG | 578 |
| Asp | Ala | Leu | Ser                                                 | Leu | Glu | Glu | Ala | Gly | Val | Gly | Leu | Leu | Val | Leu | Glu |     |
|     |     |     | 175                                                 |     |     |     |     | 180 |     |     |     |     | 185 |     |     |     |
|     |     |     |                                                     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GGT | ATA | ACC | ACC                                                 | CCT | ATC | GCT | CAA | AAA | ATC | ACG | CAA | AAA | ATC | AAA | ATC | 626 |
| Gly | Ile | Thr | Thr                                                 | Pro | Ile | Ala | Gln | Lys | Ile | Thr | Gln | Lys | Ile | Lys | Ile |     |
|     |     | 190 |                                                     |     |     |     | 195 |     |     |     |     | 200 |     |     |     |     |
|     |     |     |                                                     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| CCC | ACG | ATC | GGC                                                 | ATA | GGG | AGC | GGT | AAA | GAT | TGC | GAT | GGG | CAG | ATT | TTA | 674 |
| Pro | Thr | Ile | Gly                                                 | Ile | Gly | Ser | Gly | Lys | Asp | Cys | Asp | Gly | Gln | Ile | Leu |     |
|     | 205 |     |                                                     |     |     | 210 |     |     |     |     | 215 |     |     |     |     |     |
|     |     |     |                                                     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GTG | TGG | AGC | GAT                                                 | ATG | TTA | GGC | TTT | TTT | GAT | AGC | TTT | AAG | CCT | AAA | TTC | 722 |
| Val | Trp | Ser | Asp                                                 | Met | Leu | Gly | Phe | Phe | Asp | Ser | Phe | Lys | Pro | Lys | Phe |     |
| 220 |     |     |                                                     |     | 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |
|     |     |     |                                                     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GTG | CGA | GAA | TAC                                                 | CTT | AAG | GGG | AAA | GAA | TTG | ATT | CAA | AAC | GCT | ATC | AAA | 770 |
| Val | Arg | Glu | Tyr                                                 | Leu | Lys | Gly | Lys | Glu | Leu | Ile | Gln | Asn | Ala | Ile | Lys |     |
|     |     |     |                                                     | 240 |     |     |     | 245 |     |     |     |     |     | 250 |     |     |
|     |     |     |                                                     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| CAA | TAC | GCT | GAT                                                 | GAT | GTG | AAA | AAG | GGA | AAC | TTC | CCT | AAC | GAA | TTA | GAA | 818 |
| Gln | Tyr | Ala | Asp                                                 | Asp | Val | Lys | Lys | Gly | Asn | Phe | Pro | Asn | Glu | Leu | Glu |     |
|     |     |     | 255                                                 |     |     |     |     | 260 |     |     |     |     | 265 |     |     |     |
|     |     |     |                                                     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| AGT | TAT | CAT | TAATGAAAGA ACGGATAGTC AATTTAGAAA CTTTGGATTT TGAAATT |     |     |     |     |     |     |     |     |     | 874 |     |     |     |
| Ser | Tyr | His |                                                     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 270 |                                                     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Met | Gln | Thr | Ala | Pro | Ile | Lys | Lys | Ile | Thr | Leu | Asn | His | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Ala | Lys | Lys | Asn | Gln | Glu | Lys | Ile | Ile | Ala | Ile | Thr | Ala | Tyr | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Leu | Phe | Ala | Gln | Ile | Phe | Asp | Pro | Leu | Val | Asp | Val | Ile | Leu | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Asp | Ser | Leu | Asn | Met | Ser | Phe | Phe | Asn | Gln | Asn | Asp | Thr | Leu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Ser | Val | Glu | Met | Met | Leu | Tyr | His | Thr | Lys | Ala | Val | Cys | Ala | Gly |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Lys | Thr | Pro | Phe | Ile | Ile | Thr | Asp | Met | Pro | Phe | Gly | Ser | Tyr | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asp | Glu | Lys | Thr | Ala | Leu | Lys | Asn | Ala | Ile | Arg | Val | Tyr | Lys | Glu | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Ala | Ser | Ala | Ile | Lys | Leu | Glu | Gly | Gly | Lys | Glu | Lys | Ala | Lys | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Lys | Thr | Leu | Thr | Asn | Glu | Gly | Val | Ile | Val | Val | Gly | His | Ile | Gly |

|                                                                 |     |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|-----|
| 130                                                             |     | 135 |     | 140 |     |
| Leu Met Pro Gln Phe Val Arg Leu Asp Gly Gly Tyr Lys Ile Lys Gly |     |     |     |     |     |
| 145                                                             |     | 150 |     | 155 | 160 |
| Lys Asn Glu Glu Gln Lys Lys Leu Leu Glu Asp Ala Leu Ser Leu     |     |     |     |     |     |
|                                                                 | 165 |     | 170 |     | 175 |
| Glu Glu Ala Gly Val Gly Leu Leu Val Leu Glu Gly Ile Thr Thr Pro |     |     |     |     |     |
|                                                                 | 180 |     | 185 |     | 190 |
| Ile Ala Gln Lys Ile Thr Gln Lys Ile Lys Ile Pro Thr Ile Gly Ile |     |     |     |     |     |
|                                                                 | 195 |     | 200 |     | 205 |
| Gly Ser Gly Lys Asp Cys Asp Gly Gln Ile Leu Val Trp Ser Asp Met |     |     |     |     |     |
|                                                                 | 210 |     | 215 |     | 220 |
| Leu Gly Phe Phe Asp Ser Phe Lys Pro Lys Phe Val Arg Glu Tyr Leu |     |     |     |     |     |
| 225                                                             |     | 230 |     | 235 | 240 |
| Lys Gly Lys Glu Leu Ile Gln Asn Ala Ile Lys Gln Tyr Ala Asp Asp |     |     |     |     |     |
|                                                                 | 245 |     | 250 |     | 255 |
| Val Lys Lys Gly Asn Phe Pro Asn Glu Leu Glu Ser Tyr His         |     |     |     |     |     |
|                                                                 | 260 |     | 265 |     | 270 |

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 41...520
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

|                                                                 |                     |     |
|-----------------------------------------------------------------|---------------------|-----|
| AATAACGATA AAATTTTAAA GGGTGTA AAA GTAGATTGTT                    | ATG TTT GGC ATG GGC | 55  |
|                                                                 | Met Phe Gly Met Gly |     |
|                                                                 | 1 5                 |     |
| TTT TTT GAA ATC CTT GTG GTG TTG GTT GTA GCG ATT ATT TTT TTA GGG |                     | 103 |
| Phe Phe Glu Ile Leu Val Val Leu Val Val Ala Ile Ile Phe Leu Gly |                     |     |
|                                                                 | 10 15 20            |     |
| CCA GAA AAA TTC CCC CAG GCT GTC GTG GAT GTG GTG AAG TTT TTT CGC |                     | 151 |
| Pro Glu Lys Phe Pro Gln Ala Val Val Asp Val Val Lys Phe Phe Arg |                     |     |
|                                                                 | 25 30 35            |     |
| GCG GTT AAA AAA ACG CTC AAT GAC GCT AAG GAC ACT TTA GAT AAA GAA |                     | 199 |
| Ala Val Lys Lys Thr Leu Asn Asp Ala Lys Asp Thr Leu Asp Lys Glu |                     |     |
|                                                                 | 40 45 50            |     |
| ATC AAT ATT GAA GAA ATC AAA AAA GAA ACC CTA GAG TAT CAA AAG CTC |                     | 247 |
| Ile Asn Ile Glu Glu Ile Lys Lys Glu Thr Leu Glu Tyr Gln Lys Leu |                     |     |
|                                                                 | 55 60 65            |     |
| TTT GAA AAC AAA GTG GAG AGT CTT AAG GGC GTT AAG ATT GAA GAA TTA |                     | 295 |
| Phe Glu Asn Lys Val Glu Ser Leu Lys Gly Val Lys Ile Glu Glu Leu |                     |     |



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 46...324
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TAAAGGCGAG CAGTTAAAAG ATGAAATCGC TTGTAAAGAC ACTGA ATG CTT TAT GCA | 57  |
| Met Leu Tyr Ala                                                   |     |
| 1                                                                 |     |
| <br>                                                              |     |
| TCA AAA ACG AGT TTA TTT TTA CAA ATC AAA GGA AAG TTT ATG TTA AGA   | 105 |
| Ser Lys Thr Ser Leu Phe Leu Gln Ile Lys Gly Lys Phe Met Leu Arg   |     |
| 5 10 15 20                                                        |     |
| <br>                                                              |     |
| ATT TTA ATC CCC TTG CTC ATT ATT GTG TGG GTT TTA TGG CGT TTG TTT   | 153 |
| Ile Leu Ile Pro Leu Leu Ile Ile Val Trp Val Leu Trp Arg Leu Phe   |     |
| 25 30 35                                                          |     |
| <br>                                                              |     |
| TTG AGG CAA AAA CCC CCT AAA GAC AAC CAC TCT TAC ACG CAA CAA ACC   | 201 |
| Leu Arg Gln Lys Pro Pro Lys Asp Asn His Ser Tyr Thr Gln Gln Thr   |     |
| 40 45 50                                                          |     |
| <br>                                                              |     |
| CCT AAA GAA TTA GAA GAT CAC ATG ATT GTA TGC TCT AAA TGC CAA ACC   | 249 |
| Pro Lys Glu Leu Glu Asp His Met Ile Val Cys Ser Lys Cys Gln Thr   |     |
| 55 60 65                                                          |     |
| <br>                                                              |     |
| TAT GTC TCT AGC AAA GAC GCT ATT TAT AGC GGG GCG GTG GCG TAT TGC   | 297 |
| Tyr Val Ser Ser Lys Asp Ala Ile Tyr Ser Gly Ala Val Ala Tyr Cys   |     |
| 70 75 80                                                          |     |
| <br>                                                              |     |
| AGT GAA ACC TGT TTG AAG GAT AAG AGG TAAATATGCT TATTTTAGGA CACCCTT | 351 |
| Ser Glu Thr Cys Leu Lys Asp Lys Arg                               |     |
| 85 90                                                             |     |
| <br>                                                              |     |
| TAATCCCT                                                          | 359 |

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:





Val Glu Asn Val Ser Ile Gly Gln Thr Leu Ile Lys Ala Ser His Lys  
65 70 75 80  
Glu Gly Asn Asn Arg Val Ile Tyr Ile Ala Lys Arg Val Pro Asp Leu  
85 90 95  
Thr Leu Val Pro Leu Leu Asp Glu Lys Lys Ile Asn Tyr Ser Gly Phe  
100 105 110  
Ser Glu Ser Asn Phe Phe Thr Asp Met Leu Gly Trp Leu Met Pro Ile  
115 120 125  
Leu Val Ile Leu Gly Leu Trp Met Phe Met Ala Asn Arg Met Gln Lys  
130 135 140  
Asn Met Gly Gly Gly Ile Phe Gly Met Gly Ser Ala Lys Lys Leu Ile  
145 150 155 160  
Asn Ala Glu Lys Pro Asn Val Arg Phe Asn Asp Met Ala Gly Asn Glu  
165 170 175  
Glu Ala Lys Glu Glu Val Val Glu Ile Val Asp Phe Leu Lys Tyr Pro  
180 185 190  
Glu Arg Tyr Ala Asn Leu Gly Ala Lys Ile Pro Lys Gly Val Leu Leu  
195 200 205  
Val Gly Pro Pro Gly Thr Gly Lys Thr Leu Leu Ala Lys Ala Val Ala  
210 215 220  
Gly Glu Arg Met Cys Arg Phe Ser Leu Trp Glu Gly Ala Val Ser Leu  
225 230 235 240  
Lys Cys Leu Trp Ala  
245

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 59...1093
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

AAGTGTGTGT ATCGGTTTGA GTGATTCTT GCCCTTGCGC TTTAGGATTG CTACGCCT AT 60  
Met  
1  
GAG CAT TTT AGT AGC GAA CCA GAA AGC GAG TTC TTT AGG GTT ATT TTT 108  
Ser Ile Leu Val Ala Asn Gln Lys Ala Ser Ser Leu Gly Leu Phe Phe  
5 10 15  
TAA AGA CGC TAA AAG TTT AGA AAA AGC AAG GCT AGT CAA TAC GAT CGT 156  
Lys Asp Ala Lys Ser Leu Glu Lys Ala Arg Leu Val Asn Thr Ile Val  
20 25 30  
TTT TGA TAA AAC CGG CAC GCT CAC TAA CGG CAA GCC TGT CGT TAA AAG 204  
Phe Asp Lys Thr Gly Thr Leu Thr Asn Gly Lys Pro Val Val Lys Ser  
35 40 45

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CGT TCA TTC TAA GAT AGA ATT ATT AGA GTT ATT GAG TTT AGC GCT CAG | 252 |
| Val His Ser Lys Ile Glu Leu Leu Glu Leu Ser Leu Ala Leu Ser     |     |
| 50 55 60 65                                                     |     |
| TAT TGA AAA GAG TAG CGA ACA TGT CAT CGC TAA AGG GAT TGT AGA ATA | 300 |
| Ile Glu Lys Ser Ser Glu His Val Ile Ala Lys Gly Ile Val Glu Tyr |     |
| 70 75 80                                                        |     |
| CGC AAA AGA GCA TAA CGC TCC CTT AAA AGA AAT GAG CGG GGT TAA AGT | 348 |
| Ala Lys Glu His Asn Ala Pro Leu Lys Glu Met Ser Gly Val Lys Val |     |
| 85 90 95                                                        |     |
| GAA AAC GGG TTT TGG CAT TAG TGC TAA AAC AGA TTA TCA AGG CAC TAA | 396 |
| Lys Thr Gly Phe Gly Ile Ser Ala Lys Thr Asp Tyr Gln Gly Thr Lys |     |
| 100 105 110                                                     |     |
| AGA GAT TAT TAA AGT AGG CAA CAG CGA GTT TTT TAA CCC TAT TAA CAC | 444 |
| Glu Ile Ile Lys Val Gly Asn Ser Glu Phe Phe Asn Pro Ile Asn Thr |     |
| 115 120 125                                                     |     |
| GCT AGA AAT TAA AGA AAA CGG GAT TTT AGT GTT TGT TGG TAG AGC GAT | 492 |
| Leu Glu Ile Lys Glu Asn Gly Ile Leu Val Phe Val Gly Arg Ala Ile |     |
| 130 135 140 14                                                  |     |
| CAG TGA AAA AGA AGA CGA GCT TTT AGG GGC GTT TGT TTT AGA AGA TTT | 540 |
| Ser Glu Lys Glu Asp Glu Leu Leu Gly Ala Phe Val Leu Glu Asp Leu |     |
| 5 150 155 160                                                   |     |
| GCC CAA AAA AGG CGT GAA AGA GCA TAT CGC TCA AAT CAA AAA TTT AGG | 588 |
| Pro Lys Lys Gly Val Lys Glu His Ile Ala Gln Ile Lys Asn Leu Gly |     |
| 165 170 175                                                     |     |
| CAT TAA CAC CTT TCT TTT AAG CGG AGA CAA TAG GGA GAA TGT CCA AAA | 636 |
| Ile Asn Thr Phe Leu Leu Ser Gly Asp Asn Arg Glu Asn Val Gln Lys |     |
| 180 185 190                                                     |     |
| ATG CGC GTT TGA ATT AGG GAT TGA TGG TTA TAT CAG CAA CGC TAA ACC | 684 |
| Cys Ala Phe Glu Leu Gly Ile Asp Gly Tyr Ile Ser Asn Ala Lys Pro |     |
| 195 200 205                                                     |     |
| ACA AGA CAA GCT CAA TAA GAT CAA AGA GCT TAA GGA AAA AGG GCA GAT | 732 |
| Gln Asp Lys Leu Asn Lys Ile Lys Glu Leu Lys Glu Lys Gly Gln Ile |     |
| 210 215 220 22                                                  |     |
| CGT TAT GAT GGT GGG CGA TGG CTT GAA TGA CGC TCC TAG TCT TGC TAT | 780 |
| Val Met Met Val Gly Asp Gly Leu Asn Asp Ala Pro Ser Leu Ala Met |     |
| 5 230 235 240                                                   |     |
| GAG CGA TGT GGC GGT GGT GAT GGC TAA AGG GAG CGA TGT GAG CGT GCA | 828 |
| Ser Asp Val Ala Val Val Met Ala Lys Gly Ser Asp Val Ser Val Gln |     |
| 245 250 255                                                     |     |
| AGC AGC GGA CAT TGT GAG TTT TAA TAA CGA TAT TAA ATC GGT TTA TAG | 876 |
| Ala Ala Asp Ile Val Ser Phe Asn Asn Asp Ile Lys Ser Val Tyr Ser |     |
| 260 265 270                                                     |     |
| CGC GAT TAA ATT AAG CCA GGC GAC AAT TAA AAA TAT CAA AGA AAA TTT | 924 |
| Ala Ile Lys Leu Ser Gln Ala Thr Ile Lys Asn Ile Lys Glu Asn Leu |     |



|                                                                   |     |     |      |
|-------------------------------------------------------------------|-----|-----|------|
| 275                                                               | 280 | 285 |      |
| GTT TTG GGC TTT TTG TTA TAA TAG CGT GTT CAT CCC TTT AGC TTG TGG   |     |     | 972  |
| Phe Trp Ala Phe Cys Tyr Asn Ser Val Phe Ile Pro Leu Ala Cys Gly   |     |     |      |
| 290                                                               | 295 | 300 | 30   |
| GGT TCT TTA TAA GGC TAA TCT CAT GTT AAG CCC GGC GAT TGC GGG TTT   |     |     | 1020 |
| Val Leu Tyr Lys Ala Asn Leu Met Leu Ser Pro Ala Ile Ala Gly Leu   |     |     |      |
| 5                                                                 | 310 | 315 | 320  |
| AGC GAT GAG TTT AAG CTC TGT GAG TGT GGT CTT AAA CTC CCA AAG GCT   |     |     | 1068 |
| Ala Met Ser Leu Ser Ser Val Ser Val Val Leu Asn Ser Gln Arg Leu   |     |     |      |
|                                                                   | 325 | 330 | 335  |
| AAG GAA TTT TAA AAT TAA GGA TCA T TGAATGAAAG CAACTTTTCA AGTGCCAAG |     |     | 1122 |
| Arg Asn Phe Lys Ile Lys Asp His                                   |     |     |      |
|                                                                   | 340 | 345 |      |
| CATTACTTGC AACCA                                                  |     |     | 1137 |

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ile | Leu | Val | Ala | Asn | Gln | Lys | Ala | Ser | Ser | Leu | Gly | Leu | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Lys | Asp | Ala | Lys | Ser | Leu | Glu | Lys | Ala | Arg | Leu | Val | Asn | Thr | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Phe | Asp | Lys | Thr | Gly | Thr | Leu | Thr | Asn | Gly | Lys | Pro | Val | Val | Lys |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ser | Val | His | Ser | Lys | Ile | Glu | Leu | Leu | Glu | Leu | Leu | Ser | Leu | Ala | Leu |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ser | Ile | Glu | Lys | Ser | Ser | Glu | His | Val | Ile | Ala | Lys | Gly | Ile | Val | Glu |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Tyr | Ala | Lys | Glu | His | Asn | Ala | Pro | Leu | Lys | Glu | Met | Ser | Gly | Val | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Lys | Thr | Gly | Phe | Gly | Ile | Ser | Ala | Lys | Thr | Asp | Tyr | Gln | Gly | Thr |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Lys | Glu | Ile | Ile | Lys | Val | Gly | Asn | Ser | Glu | Phe | Phe | Asn | Pro | Ile | Asn |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Thr | Leu | Glu | Ile | Lys | Glu | Asn | Gly | Ile | Leu | Val | Phe | Val | Gly | Arg | Ala |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Ile | Ser | Glu | Lys | Glu | Asp | Glu | Leu | Leu | Gly | Ala | Phe | Val | Leu | Glu | Asp |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Leu | Pro | Lys | Lys | Gly | Val | Lys | Glu | His | Ile | Ala | Gln | Ile | Lys | Asn | Leu |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Gly | Ile | Asn | Thr | Phe | Leu | Leu | Ser | Gly | Asp | Asn | Arg | Glu | Asn | Val | Gln |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Cys | Ala | Phe | Glu | Leu | Gly | Ile | Asp | Gly | Tyr | Ile | Ser | Asn | Ala | Lys |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |

```

Pro Gln Asp Lys Leu Asn Lys Ile Lys Glu Leu Lys Glu Lys Gly Gln
 210 215 220
Ile Val Met Met Val Gly Asp Gly Leu Asn Asp Ala Pro Ser Leu Ala
225 230 235
Met Ser Asp Val Ala Val Val Met Ala Lys Gly Ser Asp Val Ser Val
 245 250 255
Gln Ala Ala Asp Ile Val Ser Phe Asn Asn Asp Ile Lys Ser Val Tyr
 260 265 270
Ser Ala Ile Lys Leu Ser Gln Ala Thr Ile Lys Asn Ile Lys Glu Asn
 275 280 285
Leu Phe Trp Ala Phe Cys Tyr Asn Ser Val Phe Ile Pro Leu Ala Cys
 290 295 300
Gly Val Leu Tyr Lys Ala Asn Leu Met Leu Ser Pro Ala Ile Ala Gly
305 310 315
Leu Ala Met Ser Leu Ser Ser Val Ser Val Val Leu Asn Ser Gln Arg
 325 330 335
Leu Arg Asn Phe Lys Ile Lys Asp His
 340 345

```

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 575 base pairs .
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...537
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

```

TCAATTCTAT TTAAAAGGTT TTTT ATG GAT ATT TTA AAA ACT CTT CAA AAA 51
 Met Asp Ile Leu Lys Thr Leu Gln Lys
 1 5

CAT TTG GGC GAT GTT GAA ACA AGC GAT TTT ACA ACC AAT GCG ATA GAA 99
His Leu Gly Asp Val Glu Thr Ser Asp Phe Thr Thr Asn Ala Ile Glu
10 15 20 25

AAA TCC CAA CAA ATC GCT AAA TTC AGT AGG GAC ATG AAA AAT ATA AAC 147
Lys Ser Gln Gln Ile Ala Lys Phe Ser Arg Asp Met Lys Asn Ile Asn
 30 35 40

GAG AGC GTT GGA GCG TTA CAA GTC TTG CAA ATC GCT TGC AAA AAG CTT 195
Glu Ser Val Gly Ala Leu Gln Val Leu Gln Ile Ala Cys Lys Lys Leu
 45 50 55

TTC AAT AAG AGC ATG GGT TTA GAA GAT AAA GAC GCT TTG CAA GCT TCT 243
Phe Asn Lys Ser Met Gly Leu Glu Asp Lys Asp Ala Leu Gln Ala Ser
 60 65 70

ATC ATC AAA CAG GAA TTG CGA GAA ATT GTA GAA AAT TGC CAG TTT TTA 291

```



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Ser | Asn | Pro | Lys | Ala | Phe | Met | Pro | Ser | Phe | Ser | Asn | Gln | Ser |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Leu | Lys | Asp | Leu | Leu | Ser | Asp | Asn | Leu | Arg | Ala |     |     |     |     |     |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1025 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...972
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

|                                                                  |             |
|------------------------------------------------------------------|-------------|
| TTTTTAGCGA TTGTGTTCTT GCATGCATTG GGTTTAGCGT TGCTCTTT ATG GCC AAT | 57          |
|                                                                  | Met Ala Asn |
|                                                                  | 1           |
| AAC GCT TCG TTT TAT GCG GCG GCG TCT ATG GCC TAC ATG CTA GGG GCA  | 105         |
| Asn Ala Ser Phe Tyr Ala Ala Ala Ser Met Ala Tyr Met Leu Gly Ala  |             |
| 5 10 15                                                          |             |
| AAG CAT GCG TTT GAT GCG GAT CAC ATC GCT TGC ATA GAT AAC ACC ATT  | 153         |
| Lys His Ala Phe Asp Ala Asp His Ile Ala Cys Ile Asp Asn Thr Ile  |             |
| 20 25 30 35                                                      |             |
| AGA AAG CTC ACC CAA CAA GGC AAA AAC GCC TAT GGT GTG GGG TTT TAC  | 201         |
| Arg Lys Leu Thr Gln Gln Gly Lys Asn Ala Tyr Gly Val Gly Phe Tyr  |             |
| 40 45 50                                                         |             |
| TTT TCT ATG GGG CAT TCA AGC GTG GTG ATT TTA ATG ACC ATC ATC AGC  | 249         |
| Phe Ser Met Gly His Ser Ser Val Val Ile Leu Met Thr Ile Ile Ser  |             |
| 55 60 65                                                         |             |
| GCG TTT GCG ATC GCT TGG GCT AAA GAA CAC ACG CCG ATG CTA GAA GAA  | 297         |
| Ala Phe Ala Ile Ala Trp Ala Lys Glu His Thr Pro Met Leu Glu Glu  |             |
| 70 75 80                                                         |             |
| ATA GGG GGG GTA GTG GGG ACT TTA GTT TCT GGG CTT TTT TTG CTC ATT  | 345         |
| Ile Gly Gly Val Val Gly Thr Leu Val Ser Gly Leu Phe Leu Leu Ile  |             |
| 85 90 95                                                         |             |
| ATA GGG CTA TTG AAT GCG ATT ATT CTC TTG GAT TTA TTA AAA ATA TTC  | 393         |
| Ile Gly Leu Leu Asn Ala Ile Ile Leu Leu Asp Leu Leu Lys Ile Phe  |             |
| 100 105 110 115                                                  |             |
| AAA AAA TCG CAC TCT AAT GAA AGC CTA AGC CAG CAA CAA AAT GAA GAG  | 441         |
| Lys Lys Ser His Ser Asn Glu Ser Leu Ser Gln Gln Gln Asn Glu Glu  |             |
| 120 125 130                                                      |             |

|                                                                 |      |
|-----------------------------------------------------------------|------|
| ATC GAG CGG CTC TTA ACG AGT AGG GGC TTG CTC AAC CGC TTT TTT AAA | 489  |
| Ile Glu Arg Leu Leu Thr Ser Arg Gly Leu Leu Asn Arg Phe Phe Lys |      |
| 135 140 145                                                     |      |
| CCC TTG TTT AAT TTT GTC TCC AAG TCG TGG CAT ATT TAT CCT ATC GGT | 537  |
| Pro Leu Phe Asn Phe Val Ser Lys Ser Trp His Ile Tyr Pro Ile Gly |      |
| 150 155 160                                                     |      |
| TTT CTT TTT GGG CTG GGT TTT GAT ACC GCT AGT GAA ATC GCG CTT TTG | 585  |
| Phe Leu Phe Gly Leu Gly Phe Asp Thr Ala Ser Glu Ile Ala Leu Leu |      |
| 165 170 175                                                     |      |
| GCC CTC TCT AGC AGC GCG ATT AAA GTG AGT ATG GTG GGC ATG CTC TCT | 633  |
| Ala Leu Ser Ser Ser Ala Ile Lys Val Ser Met Val Gly Met Leu Ser |      |
| 180 185 190 195                                                 |      |
| TTA CCC ATT CTT TTT GCC GCT GGC ATG AGT TTG TTT GAC ACT TTA GAT | 681  |
| Leu Pro Ile Leu Phe Ala Ala Gly Met Ser Leu Phe Asp Thr Leu Asp |      |
| 200 205 210                                                     |      |
| GGG GCG TTC ATG CTC AAG GCG TAT GAC TGG GCG TTC AAA ACC CCT TTA | 729  |
| Gly Ala Phe Met Leu Lys Ala Tyr Asp Trp Ala Phe Lys Thr Pro Leu |      |
| 215 220 225                                                     |      |
| AGA AAA ATC TAT TAC AAT ATC TCT ATC ACG GCC TTA AGC GTG TTT ATC | 777  |
| Arg Lys Ile Tyr Tyr Asn Ile Ser Ile Thr Ala Leu Ser Val Phe Ile |      |
| 230 235 240                                                     |      |
| GCG CTC TTT ATT GGC TTG ATT GAG CTT TTT CAA GTC GTT AGC GAG AAA | 825  |
| Ala Leu Phe Ile Gly Leu Ile Glu Leu Phe Gln Val Val Ser Glu Lys |      |
| 245 250 255                                                     |      |
| CTC CAT TTA AAA TTT GAA AAC CGC CTT TTA AGA GCC TTA CAA AGC CTG | 873  |
| Leu His Leu Lys Phe Glu Asn Arg Leu Leu Arg Ala Leu Gln Ser Leu |      |
| 260 265 270 275                                                 |      |
| GAA TTT ACA GAC TTG GGC TAT TAC TTG GTG GGC TTA TTT GTA ATA GCG | 921  |
| Glu Phe Thr Asp Leu Gly Tyr Tyr Leu Val Gly Leu Phe Val Ile Ala |      |
| 280 285 290                                                     |      |
| TTT CTA GGA TCG TTC TTT TTA TGG AAA ATC AAA TTT TCT AAA CTA GAG | 969  |
| Phe Leu Gly Ser Phe Phe Leu Trp Lys Ile Lys Phe Ser Lys Leu Glu |      |
| 295 300 305                                                     |      |
| AGC TGAATTCTAA GCCCTCAAAT TATCGCTTAA TAAATCTTTA AGGCTTTGAT TTG  | 1025 |
| Ser                                                             |      |

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

```

Met Ala Asn Asn Ala Ser Phe Tyr Ala Ala Ala Ser Met Ala Tyr Met
 1 5 10 15
Leu Gly Ala Lys His Ala Phe Asp Ala Asp His Ile Ala Cys Ile Asp
 20 25 30
Asn Thr Ile Arg Lys Leu Thr Gln Gln Gly Lys Asn Ala Tyr Gly Val
 35 40 45
Gly Phe Tyr Phe Ser Met Gly His Ser Ser Val Val Ile Leu Met Thr
 50 55 60
Ile Ile Ser Ala Phe Ala Ile Ala Trp Ala Lys Glu His Thr Pro Met
65 70 75 80
Leu Glu Glu Ile Gly Gly Val Val Gly Thr Leu Val Ser Gly Leu Phe
 85 90 95
Leu Leu Ile Ile Gly Leu Leu Asn Ala Ile Ile Leu Leu Asp Leu Leu
 100 105 110
Lys Ile Phe Lys Lys Ser His Ser Asn Glu Ser Leu Ser Gln Gln Gln
 115 120 125
Asn Glu Glu Ile Glu Arg Leu Leu Thr Ser Arg Gly Leu Leu Asn Arg
 130 135 140
Phe Phe Lys Pro Leu Phe Asn Phe Val Ser Lys Ser Trp His Ile Tyr
145 150 155 160
Pro Ile Gly Phe Leu Phe Gly Leu Gly Phe Asp Thr Ala Ser Glu Ile
 165 170 175
Ala Leu Leu Ala Leu Ser Ser Ser Ala Ile Lys Val Ser Met Val Gly
 180 185 190
Met Leu Ser Leu Pro Ile Leu Phe Ala Ala Gly Met Ser Leu Phe Asp
 195 200 205
Thr Leu Asp Gly Ala Phe Met Leu Lys Ala Tyr Asp Trp Ala Phe Lys
210 215 220
Thr Pro Leu Arg Lys Ile Tyr Tyr Asn Ile Ser Ile Thr Ala Leu Ser
225 230 235 240
Val Phe Ile Ala Leu Phe Ile Gly Leu Ile Glu Leu Phe Gln Val Val
 245 250 255
Ser Glu Lys Leu His Leu Lys Phe Glu Asn Arg Leu Leu Arg Ala Leu
 260 265 270
Gln Ser Leu Glu Phe Thr Asp Leu Gly Tyr Tyr Leu Val Gly Leu Phe
 275 280 285
Val Ile Ala Phe Leu Gly Ser Phe Phe Leu Trp Lys Ile Lys Phe Ser
 290 295 300
Lys Leu Glu Ser
305

```

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 75...989
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

|            |            |            |            |            |            |     |     |     |     |     |     |     |     |     |     |     |
|------------|------------|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| TTGTGAAAGA | AAATGAAGCG | TTTTTTAAAA | TCGGTATCAA | AAACATCGCC | GTGGCTGAAA | 60  |     |     |     |     |     |     |     |     |     |     |
| TTTCTTCGCC | TTTA       | ATG        | GAG        | TTT        | TTA        | GGT | TCA | ATC | GCT | ATA | GCG | CTA | GTG | 110 |     |     |
|            | Met        | Glu        | Phe        | Leu        | Gly        | Ser | Ile | Ala | Ile | Ala | Leu | Val |     |     |     |     |
|            | 1          |            |            |            | 5          |     |     |     |     | 10  |     |     |     |     |     |     |
| ATT        | TAT        | TTA        | GGG        | GGG        | AAT        | GAA | GTG | ATT | AGA | GGC | CAT | ATT | AGC | GTG | GGG | 158 |
| Ile        | Tyr        | Leu        | Gly        | Gly        | Asn        | Glu | Val | Ile | Arg | Gly | His | Ile | Ser | Val | Gly |     |
|            | 15         |            |            |            |            | 20  |     |     |     |     | 25  |     |     |     |     |     |
| GCG        | TTT        | TTT        | TCT        | TTC        | ATT        | ACG | GCC | CTT | TTT | ATG | CTC | TAT | ACG | CCG | ATT | 206 |
| Ala        | Phe        | Phe        | Ser        | Phe        | Ile        | Thr | Ala | Leu | Phe | Met | Leu | Tyr | Thr | Pro | Ile |     |
|            | 30         |            |            |            |            | 35  |     |     |     |     | 40  |     |     |     |     |     |
| AAA        | CGC        | TTA        | ACT        | AGG        | ATT        | GTT | TCT | AAT | TTT | CAA | GAA | GCC | TTA | GTC | GCT | 254 |
| Lys        | Arg        | Leu        | Thr        | Arg        | Ile        | Val | Ser | Asn | Phe | Gln | Glu | Ala | Leu | Val | Ala |     |
|            | 45         |            |            |            | 50         |     |     |     | 55  |     |     |     |     | 60  |     |     |
| AGC        | GAC        | AGG        | ATC        | CAT        | GAG        | ATT | TTA | GAA | AGA | GAG | CCG | GCT | ATT | GTT | GAT | 302 |
| Ser        | Asp        | Arg        | Ile        | His        | Glu        | Ile | Leu | Glu | Arg | Glu | Pro | Ala | Ile | Val | Asp |     |
|            |            |            |            | 65         |            |     |     | 70  |     |     |     |     |     | 75  |     |     |
| GGG        | GAA        | TTG        | ACG        | CTA        | AAT        | AAC | GCC | ATA | CAC | ACC | ATA | GAA | TTT | AAA | AAG | 350 |
| Gly        | Glu        | Leu        | Thr        | Leu        | Asn        | Asn | Ala | Ile | His | Thr | Ile | Glu | Phe | Lys | Lys |     |
|            |            |            | 80         |            |            |     | 85  |     |     |     |     |     | 90  |     |     |     |
| GTA        | TGG        | CTG        | GCT        | TAT        | ACG        | CTA | GAC | AAT | CAA | GAG | CGT | TAT | GTT | TTA | AAC | 398 |
| Val        | Trp        | Leu        | Ala        | Tyr        | Thr        | Leu | Asp | Asn | Gln | Glu | Arg | Tyr | Val | Leu | Asn |     |
|            | 95         |            |            |            |            | 100 |     |     |     |     |     | 105 |     |     |     |     |
| GAT        | ATT        | AGT        | TTG        | AAG        | TTC        | CAA | CAA | AAT | GAA | ATC | ATC | GCT | TTA | AAG | GGC | 446 |
| Asp        | Ile        | Ser        | Leu        | Lys        | Phe        | Gln | Gln | Asn | Glu | Ile | Ile | Ala | Leu | Lys | Gly |     |
|            | 110        |            |            |            |            | 115 |     |     |     |     | 120 |     |     |     |     |     |
| GAA        | AGC        | GGG        | AGC        | GGT        | AAA        | AGC | TCA | TTA | GTG | AAT | CTG | ATC | TTA | CGC | CTT | 494 |
| Glu        | Ser        | Gly        | Ser        | Gly        | Lys        | Ser | Ser | Leu | Val | Asn | Leu | Ile | Leu | Arg | Leu |     |
|            | 125        |            |            |            | 130        |     |     |     |     | 135 |     |     |     |     | 140 |     |
| TAT        | GAG        | CCA        | AGC        | AAA        | GGC        | GAA | ATT | TTC | ATC | AAC | GAT | CAA | AAA | ATA | GAG | 542 |
| Tyr        | Glu        | Pro        | Ser        | Lys        | Gly        | Glu | Ile | Phe | Ile | Asn | Asp | Gln | Lys | Ile | Glu |     |
|            |            |            |            | 145        |            |     |     | 150 |     |     |     |     |     | 155 |     |     |
| AGC        | ATC        | ACT        | CAA        | AAA        | TCC        | TTA | AGA | GAA | AAG | ATT | AGC | GTT | GTC | ACT | CAA | 590 |
| Ser        | Ile        | Thr        | Gln        | Lys        | Ser        | Leu | Arg | Glu | Lys | Ile | Ser | Val | Val | Thr | Gln |     |
|            |            |            | 160        |            |            |     | 165 |     |     |     |     |     | 170 |     |     |     |
| AGG        | GTG        | TTT        | ATT        | TTT        | AAC        | GGG | AGC | GTG | GCT | GAA | AAT | GTG | GCG | TAT | GGT | 638 |
| Arg        | Val        | Phe        | Ile        | Phe        | Asn        | Gly | Ser | Val | Ala | Glu | Asn | Val | Ala | Tyr | Gly |     |
|            | 175        |            |            |            |            | 180 |     |     |     |     |     | 185 |     |     |     |     |
| TTA        | GAA        | ATT        | GAT        | GAG        | GTA        | AAA | ATC | AAA | GAA | TGC | CTA | AAA | AAA | GCT | CAA | 686 |
| Leu        | Glu        | Ile        | Asp        | Glu        | Val        | Lys | Ile | Lys | Glu | Cys | Leu | Lys | Lys | Ala | Gln |     |
|            | 190        |            |            |            |            | 195 |     |     |     |     | 200 |     |     |     |     |     |
| GCC        | TTA        | GAT        | TTT        | GTT        | GAA        | AAA | ATG | CCT | CAT | GGG | ATA | GAG | AGC | GTT | TTA | 734 |











|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CCA GAA ACA ATT GAT TTA GCG CTT TGC GAT GTG AGC TTT ATT TCT TTA   | 486 |
| Pro Glu Thr Ile Asp Leu Ala Leu Cys Asp Val Ser Phe Ile Ser Leu   |     |
| 140 145 150                                                       |     |
| TAT TAT ATT TTA GAA GCG ATT TTG CCT TTA AGC GAT GAA TTT TTA ACA   | 534 |
| Tyr Tyr Ile Leu Glu Ala Ile Leu Pro Leu Ser Asp Glu Phe Leu Thr   |     |
| 155 160 165                                                       |     |
| CTT TTC AAA CCG CAA TTT GAA GTG GGC AGA GGA ATA AAA CGC AAT AAA   | 582 |
| Leu Phe Lys Pro Gln Phe Glu Val Gly Arg Gly Ile Lys Arg Asn Lys   |     |
| 170 175 180                                                       |     |
| AAA GGG GTG GTG GTG GAT AAA GAA GCC ATT TTG AAC GCT TTA GAA AAC   | 630 |
| Lys Gly Val Val Val Asp Lys Glu Ala Ile Leu Asn Ala Leu Glu Asn   |     |
| 185 190 195                                                       |     |
| TTT AAA AAC CAT TTA AAA ACA AAG GAT TTT CAA ATC TTA AAG ATC CAA   | 678 |
| Phe Lys Asn His Leu Lys Thr Lys Asp Phe Gln Ile Leu Lys Ile Gln   |     |
| 200 205 210 215                                                   |     |
| GAA AGC TTA GTG AAA GGG AAA AAC GGG AAT GTT GAA TTT TTT ATC CAT   | 726 |
| Glu Ser Leu Val Lys Gly Lys Asn Gly Asn Val Glu Phe Phe Ile His   |     |
| 220 225 230                                                       |     |
| TTC AAG CGA GCC TAAAATTAAA AGCCTAGCTA TCGGTAAATT TGACGGCTTG CATTT | 783 |
| Phe Lys Arg Ala                                                   |     |
| 235                                                               |     |
| AGGGCA                                                            | 789 |

## (2) INFORMATION FOR SEQ ID NO:246:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Arg Leu Asp Tyr Ala Leu Phe Ser Gln His Leu Val Asn Ser Arg |  |
| 1 5 10 15                                                       |  |
| Glu Lys Ala Lys Ala Leu Val Leu Lys Asn Gln Val Leu Val Asn Lys |  |
| 20 25 30                                                        |  |
| Met Val Val Ser Lys Pro Ser Phe Ile Val Lys Glu Asn Asp Lys Ile |  |
| 35 40 45                                                        |  |
| Glu Leu Ile Ala Glu Lys Leu Phe Val Ser Arg Ala Gly Glu Lys Leu |  |
| 50 55 60                                                        |  |
| Gly Ala Phe Leu Glu Thr His Phe Val Asp Phe Lys Gly Lys Val Val |  |
| 65 70 75 80                                                     |  |
| Leu Asp Val Gly Ala Ser Lys Gly Gly Phe Ser Gln Val Ala Leu Leu |  |
| 85 90 95                                                        |  |
| Lys Gly Ala Lys Arg Val Leu Cys Val Asp Val Gly Lys Met Gln Leu |  |
| 100 105 110                                                     |  |
| Asp Glu Ser Leu Lys Gln Asp Lys Arg Ile Glu Cys Tyr Glu Glu Cys |  |
| 115 120 125                                                     |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Arg | Gly | Phe | Lys | Thr | Pro | Glu | Thr | Ile | Asp | Leu | Ala | Leu | Cys |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Val | Ser | Phe | Ile | Ser | Leu | Tyr | Tyr | Ile | Leu | Glu | Ala | Ile | Leu | Pro |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Ser | Asp | Glu | Phe | Leu | Thr | Leu | Phe | Lys | Pro | Gln | Phe | Glu | Val | Gly |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Arg | Gly | Ile | Lys | Arg | Asn | Lys | Lys | Gly | Val | Val | Val | Asp | Lys | Glu | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Leu | Asn | Ala | Leu | Glu | Asn | Phe | Lys | Asn | His | Leu | Lys | Thr | Lys | Asp |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Phe | Gln | Ile | Leu | Lys | Ile | Gln | Glu | Ser | Leu | Val | Lys | Gly | Lys | Asn | Gly |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Asn | Val | Glu | Phe | Phe | Ile | His | Phe | Lys | Arg | Ala |     |     |     |     |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...858
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

|             |          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-------------|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| TGAAAGGGGAA | AAACGGGA | ATG | TTG | AAT | TTT | TTA | TCC | ATT | TCA | AGC | GAG | CCT |     |     | 51  |
|             |          | Met | Leu | Asn | Phe | Leu | Ser | Ile | Ser | Ser | Glu | Pro |     |     |     |
|             |          | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |
| AAA         | ATT      | AAA | AGC | CTA | GCT | ATC | GGT | AAA | TTT | GAC | GGC | TTG | CAT | TTA | GGG |
| Lys         | Ile      | Lys | Ser | Leu | Ala | Ile | Gly | Lys | Phe | Asp | Gly | Leu | His | Leu | Gly |
|             |          | 15  |     |     |     |     | 20  |     |     |     |     | 25  |     |     | 99  |
| CAT         | CAA      | GCC | CTT | TTT | AAA | GAG | TTA | AAA | GAT | CCC | AAA | GCC | CTT | TTA | ATC |
| His         | Gln      | Ala | Leu | Phe | Lys | Glu | Leu | Lys | Asp | Pro | Lys | Ala | Leu | Leu | Ile |
|             |          | 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |     | 147 |
| ATA         | GAA      | AAA | AAA | CAT | TAC | ACT | AAA | GGC | TAT | TTA | ACC | CCC | CTA | AAA | TAC |
| Ile         | Glu      | Lys | Lys | His | Tyr | Thr | Lys | Gly | Tyr | Leu | Thr | Pro | Leu | Lys | Tyr |
|             | 45       |     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 195 |
| CGC         | GCT      | AAA | CTC | GTG | GGC | ATG | CCT | TTA | TTT | TTT | GTG | TAT | TTA | GAA | GAG |
| Arg         | Ala      | Lys | Leu | Val | Gly | Met | Pro | Leu | Phe | Phe | Val | Tyr | Leu | Glu | Glu |
| 60          |          |     |     |     | 65  |     |     |     |     | 70  |     |     |     | 75  | 243 |
| ATT         | TCA      | CAA | TTA | AAC | GCC | CTA | GAT | TTT | TTA | GAT | CTT | TTA | AAA | AAG | AAA |
| Ile         | Ser      | Gln | Leu | Asn | Ala | Leu | Asp | Phe | Leu | Asp | Leu | Leu | Lys | Lys | Lys |
|             |          |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  | 291 |
| TTT         | CCC      | CAT | TTA | GAA | CGC | CTG | GTC | GTG | GGC | TAT | GAT | TTC | AGG | TTT | GGG |
|             |          |     |     |     |     |     |     |     |     |     |     |     |     |     | 339 |

|            |            |            |        |     |     |     |     |     |     |     |     |     |            |     |     |     |  |
|------------|------------|------------|--------|-----|-----|-----|-----|-----|-----|-----|-----|-----|------------|-----|-----|-----|--|
| Phe        | Pro        | His        | Leu    | Glu | Arg | Leu | Val | Val | Gly | Tyr | Asp | Phe | Arg        | Phe | Gly |     |  |
|            |            |            | 95     |     |     |     |     | 100 |     |     |     |     | 105        |     |     |     |  |
| CAT        | GAG        | AGG        | CAA    | AAT | GAC | GCT | TTA | TTT | TTA | AAA | GAG | CGT | TTT        | GAA | AAA | 387 |  |
| His        | Glu        | Arg        | Gln    | Asn | Asp | Ala | Leu | Phe | Leu | Lys | Glu | Arg | Phe        | Glu | Lys |     |  |
|            |            | 110        |        |     |     |     | 115 |     |     |     |     | 120 |            |     |     |     |  |
| ACC        | ATT        | ATT        | GTG    | CCT | GAA | GTG | AAA | GTC | CAA | GAG | ATT | AGC | GTG        | CAT | TCT | 435 |  |
| Thr        | Ile        | Ile        | Val    | Pro | Glu | Val | Lys | Val | Gln | Glu | Ile | Ser | Val        | His | Ser |     |  |
|            | 125        |            |        |     |     | 130 |     |     |     |     | 135 |     |            |     |     |     |  |
| AAG        | ATG        | ATC        | AAA    | CTA | GCC | CTA | AGT | CAT | GGC | GAC | TTA | TCT | TTA        | GCT | AAC | 483 |  |
| Lys        | Met        | Ile        | Lys    | Leu | Ala | Leu | Ser | His | Gly | Asp | Leu | Ser | Leu        | Ala | Asn |     |  |
| 140        |            |            |        |     | 145 |     |     |     |     | 150 |     |     |            |     | 155 |     |  |
| AAG        | CTC        | TTA        | GGC    | AGA | CCT | TAT | GAA | GTG | TGT | GGG | GAA | GTC | ATT        | AGT | GAT | 531 |  |
| Lys        | Leu        | Leu        | Gly    | Arg | Pro | Tyr | Glu | Val | Cys | Gly | Glu | Val | Ile        | Ser | Asp |     |  |
|            |            |            |        | 160 |     |     |     |     | 165 |     |     |     |            | 170 |     |     |  |
| CAA        | GGT        | TTG        | GGG    | CAT | AAA | GAA | TTA | GCA | CCC | ACT | TTA | AAT | ATA        | AAA | ACT | 579 |  |
| Gln        | Gly        | Leu        | Gly    | His | Lys | Glu | Leu | Ala | Pro | Thr | Leu | Asn | Ile        | Lys | Thr |     |  |
|            |            |            | 175    |     |     |     |     | 180 |     |     |     |     | 185        |     |     |     |  |
| AAA        | GAT        | TTT        | ATC    | CTC | CCT | AGT | TTT | GGG | GTG | TAT | GCG | AGT | TTA        | GTG | AAA | 627 |  |
| Lys        | Asp        | Phe        | Ile    | Leu | Pro | Ser | Phe | Gly | Val | Tyr | Ala | Ser | Leu        | Val | Lys |     |  |
|            |            | 190        |        |     |     |     | 195 |     |     |     |     | 200 |            |     |     |     |  |
| ATA        | AAA        | GAT        | CCA    | ATT | TAT | CAA | AAA | AGC | GTG | AGT | TTT | ATA | GGC        | AAT | CGC | 675 |  |
| Ile        | Lys        | Asp        | Pro    | Ile | Tyr | Gln | Lys | Ser | Val | Ser | Phe | Ile | Gly        | Asn | Arg |     |  |
|            | 205        |            |        |     |     | 210 |     |     |     |     | 215 |     |            |     |     |     |  |
| TTA        | AGC        | ACG        | GAT    | CAA | AAT | TTC | GCC | ATA | GAA | TGC | CAT | GTC | CTT        | GAT | ACC | 723 |  |
| Leu        | Ser        | Thr        | Asp    | Gln | Asn | Phe | Ala | Ile | Glu | Cys | His | Val | Leu        | Asp | Thr |     |  |
| 220        |            |            |        |     | 225 |     |     |     |     | 230 |     |     |            |     | 235 |     |  |
| ATC        | ATA        | GAA        | AAC    | CCG | CCC | CAA | GAA | ATC | GCT | TTG | CGT | TGG | GTT        | CAA | AAA | 771 |  |
| Ile        | Ile        | Glu        | Asn    | Pro | Pro | Gln | Glu | Ile | Ala | Leu | Arg | Trp | Val        | Gln | Lys |     |  |
|            |            |            |        | 240 |     |     |     |     | 245 |     |     |     |            | 250 |     |     |  |
| ATA        | CGA        | GAC        | AAC    | ATG | CGT | TTT | TCT | TCT | TTA | AAA | GAG | CTT | AAA        | AAT | CAG | 819 |  |
| Ile        | Arg        | Asp        | Asn    | Met | Arg | Phe | Ser | Ser | Leu | Lys | Glu | Leu | Lys        | Asn | Gln |     |  |
|            |            |            | 255    |     |     |     |     | 260 |     |     |     |     | 265        |     |     |     |  |
| ATC        | CAA        | CAA        | GAC    | ATC | TTA | AGA | GCC | AAA | GAG | ATT | TTG | AGA | TAATTTGTGT | TA  |     | 870 |  |
| Ile        | Gln        | Gln        | Asp    | Ile | Leu | Arg | Ala | Lys | Glu | Ile | Leu | Arg |            |     |     |     |  |
|            |            | 270        |        |     |     |     | 275 |     |     |     |     | 280 |            |     |     |     |  |
| AAATGACTCT | CAAAAACCTT | AAAAATGGAA | AAATTT |     |     |     |     |     |     |     |     |     |            |     |     | 906 |  |

(2) INFORMATION FOR SEQ ID NO:248:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 280 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Asn | Phe | Leu | Ser | Ile | Ser | Ser | Glu | Pro | Lys | Ile | Lys | Ser | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ile | Gly | Lys | Phe | Asp | Gly | Leu | His | Leu | Gly | His | Gln | Ala | Leu | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Glu | Leu | Lys | Asp | Pro | Lys | Ala | Leu | Leu | Ile | Ile | Glu | Lys | Lys | His |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Thr | Lys | Gly | Tyr | Leu | Thr | Pro | Leu | Lys | Tyr | Arg | Ala | Lys | Leu | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Met | Pro | Leu | Phe | Phe | Val | Tyr | Leu | Glu | Glu | Ile | Ser | Gln | Leu | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Leu | Asp | Phe | Leu | Asp | Leu | Leu | Lys | Lys | Lys | Phe | Pro | His | Leu | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Arg | Leu | Val | Val | Gly | Tyr | Asp | Phe | Arg | Phe | Gly | His | Glu | Arg | Gln | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Asp | Ala | Leu | Phe | Leu | Lys | Glu | Arg | Phe | Glu | Lys | Thr | Ile | Ile | Val | Pro |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |
| Glu | Val | Lys | Val | Gln | Glu | Ile | Ser | Val | His | Ser | Lys | Met | Ile | Lys | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Ala | Leu | Ser | His | Gly | Asp | Leu | Ser | Leu | Ala | Asn | Lys | Leu | Leu | Gly | Arg |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Tyr | Glu | Val | Cys | Gly | Glu | Val | Ile | Ser | Asp | Gln | Gly | Leu | Gly | His |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Glu | Leu | Ala | Pro | Thr | Leu | Asn | Ile | Lys | Thr | Lys | Asp | Phe | Ile | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Pro | Ser | Phe | Gly | Val | Tyr | Ala | Ser | Leu | Val | Lys | Ile | Lys | Asp | Pro | Ile |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |
| Tyr | Gln | Lys | Ser | Val | Ser | Phe | Ile | Gly | Asn | Arg | Leu | Ser | Thr | Asp | Gln |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asn | Phe | Ala | Ile | Glu | Cys | His | Val | Leu | Asp | Thr | Ile | Ile | Glu | Asn | Pro |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Pro | Gln | Glu | Ile | Ala | Leu | Arg | Trp | Val | Gln | Lys | Ile | Arg | Asp | Asn | Met |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Arg | Phe | Ser | Ser | Leu | Lys | Glu | Leu | Lys | Asn | Gln | Ile | Gln | Gln | Asp | Ile |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |
| Leu | Arg | Ala | Lys | Glu | Ile | Leu | Arg |     |     |     |     |     |     |     |     |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 18...2582
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

|            |         |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|------------|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| AAAGACATGT | GCAACCG | ATG | AAA | TCT | AAA | AAA | CTT | TAT | TTG | GCT | TTA | ATC |     |     |     |     | 50 |
|            |         | Met | Lys | Ser | Lys | Lys | Leu | Tyr | Leu | Ala | Leu | Ile |     |     |     |     |    |
|            |         | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     |    |
| ATA        | GGG     | GTT | TTA | TTA | GCG | TTT | TTA | ACC | CTA | TCT | TCA | TGG | CTG | GGT | AAT | 98  |    |
| Ile        | Gly     | Val | Leu | Leu | Ala | Phe | Leu | Thr | Leu | Ser | Ser | Trp | Leu | Gly | Asn |     |    |
|            |         |     | 15  |     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |    |
| AGC        | GGT     | TTA | GTG | GGG | CGT | TTT | GGG | GTG | TGG | TTT | GCC | GCA | CTC | AAT | AAA | 146 |    |
| Ser        | Gly     | Leu | Val | Gly | Arg | Phe | Gly | Val | Trp | Phe | Ala | Ala | Leu | Asn | Lys |     |    |
|            |         | 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |    |
| AAA        | TAT     | TTT | GGG | CAT | CTT | TCA | TTC | ATT | AAT | TTA | CCC | TAT | TTA | GCA | TGG | 194 |    |
| Lys        | Tyr     | Phe | Gly | His | Leu | Ser | Phe | Ile | Asn | Leu | Pro | Tyr | Leu | Ala | Trp |     |    |
|            | 45      |     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |     |    |
| GTT        | TTA     | TTC | CTT | TTA | TAC | AAG | ACT | AAA | AAC | CCT | TTT | ACA | GAA | ATC | GTT | 242 |    |
| Val        | Leu     | Phe | Leu | Leu | Tyr | Lys | Thr | Lys | Asn | Pro | Phe | Thr | Glu | Ile | Val |     |    |
| 60         |         |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |    |
| TTA        | GAA     | AAA | ACT | TTA | GGG | CAT | CTA | TTA | GGC | ATT | TTA | TCT | TTG | CTC | TTT | 290 |    |
| Leu        | Glu     | Lys | Thr | Leu | Gly | His | Leu | Leu | Gly | Ile | Leu | Ser | Leu | Leu | Phe |     |    |
|            |         |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |     |     |    |
| TTA        | CAA     | TCT | AGC | CTA | TTA | AAT | CAA | GGG | GAA | ATC | GGC | AAC | AGC | GCG | CGT | 338 |    |
| Leu        | Gln     | Ser | Ser | Leu | Leu | Asn | Gln | Gly | Glu | Ile | Gly | Asn | Ser | Ala | Arg |     |    |
|            |         |     | 95  |     |     |     | 100 |     |     |     |     |     | 105 |     |     |     |    |
| TTG        | TTT     | TTA | CGC | CCT | TTT | ATA | GGG | GAT | TTT | GGG | CTT | TAT | GCG | CTG | ATA | 386 |    |
| Leu        | Phe     | Leu | Arg | Pro | Phe | Ile | Gly | Asp | Phe | Gly | Leu | Tyr | Ala | Leu | Ile |     |    |
|            |         | 110 |     |     |     |     | 115 |     |     |     |     | 120 |     |     |     |     |    |
| ACG        | CTT     | ATG | GTA | GTT | ATT | TCT | TAT | TTG | ATT | CTA | TTC | AAA | CTA | CCC | CCT | 434 |    |
| Thr        | Leu     | Met | Val | Val | Ile | Ser | Tyr | Leu | Ile | Leu | Phe | Lys | Leu | Pro | Pro |     |    |
|            |         | 125 |     |     |     | 130 |     |     |     |     | 135 |     |     |     |     |     |    |
| AAA        | AGC     | GTT | TTT | TAT | CCT | TAT | ATG | AAC | AAA | ACA | CAA | AAC | CTT | TTA | AAA | 482 |    |
| Lys        | Ser     | Val | Phe | Tyr | Pro | Tyr | Met | Asn | Lys | Thr | Gln | Asn | Leu | Leu | Lys |     |    |
| 140        |         |     |     |     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |    |
| GAG        | ATT     | TAC | AAA | CAA | TGC | TTA | CAA | GCC | TTT | AGC | CCT | AAT | TTT | AGC | CCA | 530 |    |
| Glu        | Ile     | Tyr | Lys | Gln | Cys | Leu | Gln | Ala | Phe | Ser | Pro | Asn | Phe | Ser | Pro |     |    |
|            |         |     |     | 160 |     |     |     | 165 |     |     |     |     |     | 170 |     |     |    |
| AAA        | AAA     | GAG | GGT | TTT | GAA | AAC | ACC | CCA | TCA | GAT | ATT | CAA | AAA | AAA | GAA | 578 |    |
| Lys        | Lys     | Glu | Gly | Phe | Glu | Asn | Thr | Pro | Ser | Asp | Ile | Gln | Lys | Lys | Glu |     |    |
|            |         |     | 175 |     |     |     |     | 180 |     |     |     |     | 185 |     |     |     |    |
| ACC        | AAA     | AAC | GAC | AAA | GAA | AAA | GAA | AAC | CGC | AAA | GAA | AAC | CCT | ATT | AAT | 626 |    |
| Thr        | Lys     | Asn | Asp | Lys | Glu | Lys | Glu | Asn | Arg | Lys | Glu | Asn | Pro | Ile | Asn |     |    |
|            |         | 190 |     |     |     |     | 195 |     |     |     |     | 200 |     |     |     |     |    |
| GAA        | AAC     | CAC | AAA | ACC | CCT | AAC | GAA | GAA | CCG | TTT | TTA | GCG | ATC | CCT | ACC | 674 |    |
| Glu        | Asn     | His | Lys | Thr | Pro | Asn | Glu | Glu | Pro | Phe | Leu | Ala | Ile | Pro | Thr |     |    |
|            | 205     |     |     |     |     | 210 |     |     |     |     | 215 |     |     |     |     |     |    |
| CCC        | TAT     | AAC | ACG | ACT | TTA | AAT | GAT | TCA | GAG | CCG | CAA | GAA | GGC | TTA | GTC | 722 |    |
| Pro        | Tyr     | Asn | Thr | Thr | Leu | Asn | Asp | Ser | Glu | Pro | Gln | Glu | Gly | Leu | Val |     |    |



|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| 220               |                   |                   |                   | 225               |                   |                   |                   | 230               |                   |                   |                   | 235               |                   |                   |                   |      |
| CAA<br>Gln        | ATT<br>Ile        | TCC<br>Ser        | TCC<br>Ser        | CAC<br>His<br>240 | CCC<br>Pro        | CCT<br>Pro        | ACC<br>Thr        | CAT<br>His        | TAC<br>Tyr<br>245 | ACC<br>Thr        | ATT<br>Ile        | TAC<br>Tyr        | CCT<br>Pro        | AAA<br>Lys<br>250 | AGA<br>Arg        | 770  |
| AAC<br>Asn        | CGA<br>Arg        | TTT<br>Phe        | GAT<br>Asp<br>255 | GAT<br>Asp        | TTG<br>Leu        | ACT<br>Thr        | AAC<br>Asn        | CCC<br>Pro<br>260 | ACT<br>Thr        | AAC<br>Asn        | CCC<br>Pro        | CCT<br>Pro        | TTA<br>Leu<br>265 | AAA<br>Lys        | GAA<br>Glu        | 818  |
| ATT<br>Ile        | AAA<br>Lys        | CAA<br>Gln<br>270 | GAA<br>Glu        | ACT<br>Thr        | AAA<br>Lys        | GAA<br>Glu        | AGA<br>Arg<br>275 | GAA<br>Glu        | CCC<br>Pro        | ACG<br>Thr        | CCT<br>Pro        | ACA<br>Thr<br>280 | AAA<br>Lys        | GAA<br>Glu        | ACT<br>Thr        | 866  |
| CTT<br>Leu        | ACG<br>Thr<br>285 | CCC<br>Pro        | ACC<br>Thr        | ACG<br>Thr        | CCC<br>Pro        | AAA<br>Lys<br>290 | CCT<br>Pro        | ATC<br>Ile        | ATG<br>Met        | CCC<br>Pro        | ACA<br>Thr<br>295 | CTT<br>Leu        | GCA<br>Ala        | CCC<br>Pro        | ATA<br>Ile        | 914  |
| ATA<br>Ile<br>300 | GAA<br>Glu        | AAT<br>Asn        | GAC<br>Asp        | AAC<br>Asn        | AAA<br>Lys<br>305 | ACA<br>Thr        | GAA<br>Glu        | AAC<br>Asn        | CAA<br>Gln<br>310 | AAA<br>Lys        | ACC<br>Thr        | CCC<br>Pro        | AAC<br>Asn        | CAC<br>His        | CCT<br>Pro<br>315 | 962  |
| AAA<br>Lys        | AAA<br>Lys        | GAA<br>Glu        | GAA<br>Glu        | AAC<br>Asn<br>320 | CCA<br>Pro        | CAA<br>Gln        | GAA<br>Glu        | AAC<br>Asn        | ACG<br>Thr<br>325 | CAA<br>Gln        | GAA<br>Glu        | GAA<br>Glu        | ATG<br>Met        | ATA<br>Ile<br>330 | GAA<br>Glu        | 1010 |
| GGA<br>Gly        | AGG<br>Arg        | ATA<br>Ile        | GAA<br>Glu<br>335 | GAA<br>Glu        | ATG<br>Met        | ATA<br>Ile        | AAG<br>Lys        | GAA<br>Glu<br>340 | AAT<br>Asn        | CTA<br>Leu        | AAA<br>Lys        | AAA<br>Lys        | GAA<br>Glu<br>345 | GAA<br>Glu        | AAA<br>Lys        | 1058 |
| GAA<br>Glu        | GTG<br>Val<br>350 | CAA<br>Gln        | AAC<br>Asn        | GCT<br>Ala        | CCA<br>Pro        | AAC<br>Asn        | TTT<br>Phe<br>355 | AGC<br>Ser        | CCA<br>Pro        | GTA<br>Val        | ACC<br>Thr        | CCC<br>Pro<br>360 | ACA<br>Thr        | AGC<br>Ser        | GCT<br>Ala        | 1106 |
| AAA<br>Lys        | AAA<br>Lys<br>365 | CCC<br>Pro        | GTT<br>Val        | ATG<br>Met        | GTT<br>Val        | AAA<br>Lys<br>370 | GAA<br>Glu        | TTG<br>Leu        | AGC<br>Ser        | GAA<br>Glu        | AAT<br>Asn<br>375 | AAA<br>Lys        | GAG<br>Glu        | ATA<br>Ile        | TTA<br>Leu        | 1154 |
| GAC<br>Asp<br>380 | GGA<br>Gly        | TTG<br>Leu        | GAT<br>Asp        | TAT<br>Tyr<br>385 | GGC<br>Gly        | GAA<br>Glu        | GTG<br>Val        | CAA<br>Gln        | AAA<br>Lys        | CCC<br>Pro<br>390 | AAA<br>Lys        | GAT<br>Asp        | TAT<br>Tyr        | GAG<br>Glu        | CTT<br>Leu<br>395 | 1202 |
| CCC<br>Pro        | ACC<br>Thr        | ACG<br>Thr        | CAA<br>Gln        | TTA<br>Leu<br>400 | TTG<br>Leu        | AAT<br>Asn        | GCG<br>Ala        | GTT<br>Val        | TGT<br>Cys<br>405 | TTG<br>Leu        | AAA<br>Lys        | GAC<br>Asp        | ACT<br>Thr        | TCT<br>Ser<br>410 | TTA<br>Leu        | 1250 |
| GAC<br>Asp        | GAA<br>Glu        | AAC<br>Asn        | GAG<br>Glu<br>415 | ATT<br>Ile        | GAC<br>Asp        | CAA<br>Gln        | AAA<br>Lys        | ATC<br>Ile<br>420 | CAG<br>Gln        | GAT<br>Asp        | CTA<br>Leu        | TTG<br>Leu        | AGC<br>Ser<br>425 | AAA<br>Lys        | CTG<br>Leu        | 1298 |
| CGC<br>Arg        | ACC<br>Thr        | TTT<br>Phe<br>430 | AAA<br>Lys        | ATT<br>Ile        | GAT<br>Asp        | GGC<br>Gly        | GAT<br>Asp<br>435 | ATT<br>Ile        | ATC<br>Ile        | CGC<br>Arg        | ACT<br>Thr<br>440 | TAT<br>Tyr        | TCA<br>Ser        | GGC<br>Gly        | CCT<br>Pro        | 1346 |
| ATT<br>Ile        | GTA<br>Val<br>445 | ACC<br>Thr        | ACT<br>Thr        | TTT<br>Phe        | GAA<br>Glu<br>450 | TTC<br>Phe        | CGC<br>Arg        | CCA<br>Pro        | GCC<br>Ala        | CCT<br>Pro        | AAC<br>Asn<br>455 | GTT<br>Val        | AAG<br>Lys        | GTG<br>Val        | AGT<br>Ser        | 1394 |

|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| CGT<br>Arg<br>460 | ATT<br>Ile        | TTA<br>Leu        | GGC<br>Gly        | TTG<br>Leu        | AGC<br>Ser<br>465 | GAT<br>Asp        | GAT<br>Asp        | TTA<br>Leu        | GCG<br>Ala        | ATG<br>Met<br>470 | ACT<br>Thr        | TTA<br>Leu        | TGC<br>Cys        | GCT<br>Ala        | GAA<br>Glu<br>475 | 1442 |
| TCC<br>Ser        | ATC<br>Ile        | CGC<br>Arg        | ATT<br>Ile        | CAA<br>Gln<br>480 | GCC<br>Ala        | CCT<br>Pro        | ATT<br>Ile        | AAG<br>Lys        | GGT<br>Gly<br>485 | AAA<br>Lys        | GAT<br>Asp        | GTC<br>Val        | GTT<br>Val        | GGC<br>Gly<br>490 | ATT<br>Ile        | 1490 |
| GAA<br>Glu        | ATC<br>Ile        | CCT<br>Pro        | AAC<br>Asn<br>495 | AGC<br>Ser        | CAA<br>Gln        | AGC<br>Ser        | CAA<br>Gln        | ATT<br>Ile<br>500 | ATT<br>Ile        | TAT<br>Tyr        | TTA<br>Leu        | AGA<br>Arg        | GAA<br>Glu<br>505 | ATT<br>Ile        | CTA<br>Leu        | 1538 |
| GAG<br>Glu        | AGC<br>Ser        | GAA<br>Glu<br>510 | TTG<br>Leu        | TTT<br>Phe        | CAA<br>Gln        | AAA<br>Lys        | TCC<br>Ser<br>515 | AGC<br>Ser        | TCG<br>Ser        | CCC<br>Pro        | TTA<br>Leu<br>520 | ACT<br>Thr        | CTA<br>Leu        | GCT<br>Ala        | TTA<br>Leu        | 1586 |
| GGC<br>Gly        | AAA<br>Lys<br>525 | GAC<br>Asp        | ATT<br>Ile        | GTG<br>Val        | GGT<br>Gly        | AAC<br>Asn<br>530 | CCT<br>Pro        | TTC<br>Phe        | ATC<br>Ile        | ACG<br>Thr        | GAT<br>Asp<br>535 | TTA<br>Leu        | AAA<br>Lys        | AAG<br>Lys        | CTC<br>Leu        | 1634 |
| CCC<br>Pro<br>540 | CAT<br>His        | TTG<br>Leu        | CTC<br>Leu        | ATC<br>Ile        | GCT<br>Ala<br>545 | GGC<br>Gly        | ACG<br>Thr        | ACA<br>Thr        | GGA<br>Gly        | AGC<br>Ser<br>550 | GGT<br>Gly        | AAG<br>Lys        | AGC<br>Ser        | GTG<br>Val        | GGC<br>Gly<br>555 | 1682 |
| GTG<br>Val        | AAT<br>Asn        | GCG<br>Ala        | ATG<br>Met        | ATT<br>Ile<br>560 | TTA<br>Leu        | TCC<br>Ser        | TTA<br>Leu        | CTT<br>Leu        | TAT<br>Tyr<br>565 | AAA<br>Lys        | AAC<br>Asn        | CCT<br>Pro        | CCC<br>Pro        | GAT<br>Asp<br>570 | CAA<br>Gln        | 1730 |
| CTC<br>Leu        | AAA<br>Lys        | TTA<br>Leu        | GTG<br>Val<br>575 | ATG<br>Met        | ATC<br>Ile        | GAT<br>Asp        | CCC<br>Pro        | AAA<br>Lys<br>580 | ATG<br>Met        | GTA<br>Val        | GAA<br>Glu        | TTT<br>Phe        | AGT<br>Ser<br>585 | ATT<br>Ile        | TAT<br>Tyr        | 1778 |
| GCG<br>Ala        | GAT<br>Asp        | ATC<br>Ile<br>590 | CCT<br>Pro        | CAT<br>His        | TTG<br>Leu        | CTC<br>Leu        | ACG<br>Thr<br>595 | CCC<br>Pro        | ATT<br>Ile        | ATC<br>Ile        | ACC<br>Thr        | GAC<br>Asp<br>600 | CCT<br>Pro        | AAA<br>Lys        | AAA<br>Lys        | 1826 |
| GCT<br>Ala        | ATT<br>Ile<br>605 | GGG<br>Gly        | GCT<br>Ala        | TTG<br>Leu        | CAA<br>Gln        | AGC<br>Ser<br>610 | GTG<br>Val        | GCT<br>Ala        | AAA<br>Lys        | GAA<br>Glu        | ATG<br>Met<br>615 | GAA<br>Glu        | CGC<br>Arg        | CGG<br>Arg        | TAT<br>Tyr        | 1874 |
| TCT<br>Ser<br>620 | TTA<br>Leu        | ATG<br>Met        | AGC<br>Ser        | GAA<br>Glu        | TAC<br>Tyr<br>625 | AAG<br>Lys        | GTT<br>Val        | AAA<br>Lys        | ACC<br>Thr        | ATT<br>Ile<br>630 | GAT<br>Asp        | TCT<br>Ser        | TAT<br>Tyr        | AAT<br>Asn        | GAA<br>Glu<br>635 | 1922 |
| CAA<br>Gln        | GCC<br>Ala        | CCA<br>Pro        | AGT<br>Ser        | AAC<br>Asn<br>640 | GGC<br>Gly        | GTT<br>Val        | GAA<br>Glu        | GCG<br>Ala        | TTC<br>Phe<br>645 | CCC<br>Pro        | TAT<br>Tyr        | TTG<br>Leu        | ATT<br>Ile        | GTG<br>Val<br>650 | GTG<br>Val        | 1970 |
| ATT<br>Ile        | GAT<br>Asp        | GAA<br>Glu        | TTA<br>Leu<br>655 | GCG<br>Ala        | GAT<br>Asp        | TTA<br>Leu        | ATG<br>Met        | ATG<br>Met<br>660 | ACA<br>Thr        | GGG<br>Gly        | GGC<br>Gly        | AAA<br>Lys        | GAA<br>Glu<br>665 | GCG<br>Ala        | GAG<br>Glu        | 2018 |
| TTT<br>Phe        | CCT<br>Pro        | ATC<br>Ile<br>670 | GCT<br>Ala        | AGA<br>Arg        | ATC<br>Ile        | GCT<br>Ala        | CAA<br>Gln<br>675 | ATG<br>Met        | GGG<br>Gly        | CGC<br>Arg        | GCG<br>Ala        | AGC<br>Ser<br>680 | GGC<br>Gly        | TTA<br>Leu        | CAC<br>His        | 2066 |
| CTC<br>Leu        | ATT<br>Ile        | GTA<br>Val        | GCG<br>Ala        | ACC<br>Thr        | CAA<br>Gln        | CGC<br>Arg        | CCA<br>Pro        | AGC<br>Ser        | GTG<br>Val        | GAT<br>Asp        | GTC<br>Val        | GTA<br>Val        | ACC<br>Thr        | GGC<br>Gly        | TTG<br>Leu        | 2114 |

| 685                                                                                                                                                   | 690 | 695 |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----|------|
| ATT AAA ACC AAC TTG CCT TCA AGG GTG AGT TTT AGG GTA GGC ACT AAG<br>Ile Lys Thr Asn Leu Pro Ser Arg Val Ser Phe Arg Val Gly Thr Lys<br>700 705 710 715 |     |     | 2162 |
| ATT GAT TCT AAA GTG ATT TTA GAC ACT GAT GGG GCG CAA AGC TTG TTA<br>Ile Asp Ser Lys Val Ile Leu Asp Thr Asp Gly Ala Gln Ser Leu Leu<br>720 725 730     |     |     | 2210 |
| GGA AGA GGC GAT ATG CTC TTT ACC CCC CCA GGA GCG AAC GGG TTA GTG<br>Gly Arg Gly Asp Met Leu Phe Thr Pro Pro Gly Ala Asn Gly Leu Val<br>735 740 745     |     |     | 2258 |
| CGC TTG CAT GCC CCC TTT GCC ACT GAA GAT GAA ATC AAA AAA ATC GTG<br>Arg Leu His Ala Pro Phe Ala Thr Glu Asp Glu Ile Lys Lys Ile Val<br>750 755 760     |     |     | 2306 |
| GAT TTT ATT AAA GCC CAA AAA GAA GTA CAA TAC GAT AAA GAT TTC TTG<br>Asp Phe Ile Lys Ala Gln Lys Glu Val Gln Tyr Asp Lys Asp Phe Leu<br>765 770 775     |     |     | 2354 |
| CTA GAA GAA TCA CGC ATG CCT TTA GAC ACC CCT AAT TAT CAA GGC GAT<br>Leu Glu Glu Ser Arg Met Pro Leu Asp Thr Pro Asn Tyr Gln Gly Asp<br>780 785 790 795 |     |     | 2402 |
| GAC ATT TTA GAA AGG GCT AAA GCG GTG ATT TTA GAA AAA AAG ATC ACT<br>Asp Ile Leu Glu Arg Ala Lys Ala Val Ile Leu Glu Lys Lys Ile Thr<br>800 805 810     |     |     | 2450 |
| TCT ACG AGT TTT TTA CAA CGC CAA TTA AAA ATC GGC TAC AAC CAA GCC<br>Ser Thr Ser Phe Leu Gln Arg Gln Leu Lys Ile Gly Tyr Asn Gln Ala<br>815 820 825     |     |     | 2498 |
| GCT ACC ATT ACT GAC GAA TTA GAA GCT CAA GGC TTT TTA TCC CCA AGA<br>Ala Thr Ile Thr Asp Glu Leu Glu Ala Gln Gly Phe Leu Ser Pro Arg<br>830 835 840     |     |     | 2546 |
| AAC GCT AAA GGC AAC AGA GAG ATT TTG CAA AAC TTT TAGGCTTTGT TTTCAT<br>Asn Ala Lys Gly Asn Arg Glu Ile Leu Gln Asn Phe<br>845 850 855                   |     |     | 2598 |
| TGGATATTGG CAAACATTAT TTTTGATT                                                                                                                        |     |     | 2627 |

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 855 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ser | Lys | Lys | Leu | Tyr | Leu | Ala | Leu | Ile | Ile | Gly | Val | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Ala        | Phe        | Leu        | Thr<br>20  | Leu        | Ser        | Ser        | Trp        | Leu<br>25  | Gly        | Asn        | Ser        | Gly        | Leu<br>30  | Val        | Gly        |
| Arg        | Phe        | Gly<br>35  | Val        | Trp        | Phe        | Ala        | Ala<br>40  | Leu        | Asn        | Lys        | Lys        | Tyr<br>45  | Phe        | Gly        | His        |
| Leu        | Ser<br>50  | Phe        | Ile        | Asn        | Leu        | Pro<br>55  | Tyr        | Leu        | Ala        | Trp        | Val<br>60  | Leu        | Phe        | Leu        | Leu        |
| Tyr<br>65  | Lys        | Thr        | Lys        | Asn<br>70  | Pro        | Phe        | Thr        | Glu        | Ile        | Val<br>75  | Leu        | Glu        | Lys        | Thr        | Leu<br>80  |
| Gly        | His        | Leu        | Leu        | Gly<br>85  | Ile        | Leu        | Ser        | Leu        | Leu        | Phe        | Leu        | Gln        | Ser        | Ser        | Leu        |
| Leu        | Asn        | Gln        | Gly<br>100 | Glu        | Ile        | Gly        | Asn<br>105 | Ser        | Ala        | Arg        | Leu        | Phe        | Leu<br>110 | Arg        | Pro        |
| Phe        | Ile        | Gly<br>115 | Asp        | Phe        | Gly        | Leu        | Tyr<br>120 | Ala        | Leu        | Ile        | Thr        | Leu<br>125 | Met        | Val        | Val        |
| Ile        | Ser<br>130 | Tyr        | Leu        | Ile        | Leu        | Phe<br>135 | Lys        | Leu        | Pro        | Pro        | Lys<br>140 | Ser        | Val        | Phe        | Tyr        |
| Pro<br>145 | Tyr        | Met        | Asn        | Lys        | Thr<br>150 | Gln        | Asn        | Leu        | Leu        | Lys<br>155 | Glu        | Ile        | Tyr        | Lys        | Gln<br>160 |
| Cys        | Leu        | Gln        | Ala        | Phe<br>165 | Ser        | Pro        | Asn        | Phe        | Ser        | Pro        | Lys        | Lys        | Glu        | Gly        | Phe        |
| Glu        | Asn        | Thr        | Pro<br>180 | Ser        | Asp        | Ile        | Gln<br>185 | Lys        | Lys        | Glu        | Thr        | Lys        | Asn<br>190 | Asp        | Lys        |
| Glu        | Lys        | Glu        | Asn<br>195 | Arg        | Lys        | Glu        | Asn<br>200 | Pro        | Ile        | Asn        | Glu        | Asn<br>205 | His        | Lys        | Thr        |
| Pro        | Asn<br>210 | Glu        | Glu        | Pro        | Phe<br>215 | Leu        | Ala        | Ile        | Pro        | Thr        | Pro<br>220 | Tyr        | Asn        | Thr        | Thr        |
| Leu<br>225 | Asn        | Asp        | Ser        | Glu        | Pro<br>230 | Gln        | Glu        | Gly        | Leu        | Val<br>235 | Gln        | Ile        | Ser        | Ser        | His<br>240 |
| Pro        | Pro        | Thr        | His<br>245 | Tyr        | Thr        | Ile        | Tyr        | Pro        | Lys<br>250 | Arg        | Asn        | Arg        | Phe        | Asp        | Asp        |
| Leu        | Thr        | Asn        | Pro<br>260 | Thr        | Asn        | Pro        | Pro        | Leu<br>265 | Lys        | Glu        | Ile        | Lys        | Gln<br>270 | Glu        | Thr        |
| Lys        | Glu        | Arg        | Glu        | Pro        | Thr        | Pro        | Thr<br>280 | Lys        | Glu        | Thr        | Leu<br>285 | Thr        | Pro        | Thr        | Thr        |
| Pro        | Lys<br>290 | Pro        | Ile        | Met        | Pro        | Thr<br>295 | Leu        | Ala        | Pro        | Ile        | Ile<br>300 | Glu        | Asn        | Asp        | Asn        |
| Lys<br>305 | Thr        | Glu        | Asn        | Gln<br>310 | Lys        | Thr        | Pro        | Asn        | His<br>315 | Pro        | Lys        | Lys        | Glu        | Glu        | Asn<br>320 |
| Pro        | Gln        | Glu        | Asn<br>325 | Thr        | Gln        | Glu        | Glu        | Met<br>330 | Ile        | Glu        | Gly        | Arg        | Ile        | Glu<br>335 | Glu        |
| Met        | Ile        | Lys        | Glu<br>340 | Asn        | Leu        | Lys        | Lys        | Glu<br>345 | Glu        | Lys        | Glu        | Val        | Gln<br>350 | Asn        | Ala        |
| Pro        | Asn<br>355 | Phe        | Ser        | Pro        | Val        | Thr        | Pro<br>360 | Thr        | Ser        | Ala        | Lys<br>365 | Lys        | Pro        | Val        | Met        |
| Val        | Lys<br>370 | Glu        | Leu        | Ser        | Glu        | Asn<br>375 | Lys        | Glu        | Ile        | Leu        | Asp<br>380 | Gly        | Leu        | Asp        | Tyr        |
| Gly<br>385 | Glu        | Val        | Gln        | Lys        | Pro<br>390 | Lys        | Asp        | Tyr        | Glu        | Leu<br>395 | Pro        | Thr        | Thr        | Gln        | Leu<br>400 |
| Leu        | Asn        | Ala        | Val        | Cys<br>405 | Leu        | Lys        | Asp        | Thr        | Ser<br>410 | Leu        | Asp        | Glu        | Asn<br>415 | Glu        | Ile        |
| Asp        | Gln        | Lys        | Ile<br>420 | Gln        | Asp        | Leu        | Leu        | Ser<br>425 | Lys        | Leu        | Arg        | Thr        | Phe<br>430 | Lys        | Ile        |
| Asp        | Gly<br>435 | Asp        | Ile        | Ile        | Arg        | Thr        | Tyr<br>440 | Ser        | Gly        | Pro        | Ile<br>445 | Val        | Thr        | Thr        | Phe        |
| Glu        | Phe<br>450 | Arg        | Pro        | Ala        | Pro        | Asn<br>455 | Val        | Lys        | Val        | Ser<br>460 | Arg        | Ile        | Leu        | Gly        | Leu        |
| Ser<br>465 | Asp        | Asp        | Leu        | Ala<br>470 | Met        | Thr        | Leu        | Cys        | Ala<br>475 | Glu        | Ser        | Ile        | Arg        | Ile        | Gln<br>480 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Pro | Ile | Lys | Gly | Lys | Asp | Val | Val | Gly | Ile | Glu | Ile | Pro | Asn | Ser | 485 | 490 | 495 |
| Gln | Ser | Gln | Ile | Ile | Tyr | Leu | Arg | Glu | Ile | Leu | Glu | Ser | Glu | Leu | Phe | 500 | 505 | 510 |
| Gln | Lys | Ser | Ser | Ser | Pro | Leu | Thr | Leu | Ala | Leu | Gly | Lys | Asp | Ile | Val | 515 | 520 | 525 |
| Gly | Asn | Pro | Phe | Ile | Thr | Asp | Leu | Lys | Lys | Leu | Pro | His | Leu | Leu | Ile | 530 | 535 | 540 |
| Ala | Gly | Thr | Thr | Gly | Ser | Gly | Lys | Ser | Val | Gly | Val | Asn | Ala | Met | Ile | 545 | 550 | 555 |
| Leu | Ser | Leu | Leu | Tyr | Lys | Asn | Pro | Pro | Asp | Gln | Leu | Lys | Leu | Val | Met | 565 | 570 | 575 |
| Ile | Asp | Pro | Lys | Met | Val | Glu | Phe | Ser | Ile | Tyr | Ala | Asp | Ile | Pro | His | 580 | 585 | 590 |
| Leu | Leu | Thr | Pro | Ile | Ile | Thr | Asp | Pro | Lys | Lys | Ala | Ile | Gly | Ala | Leu | 595 | 600 | 605 |
| Gln | Ser | Val | Ala | Lys | Glu | Met | Glu | Arg | Arg | Tyr | Ser | Leu | Met | Ser | Glu | 610 | 615 | 620 |
| Tyr | Lys | Val | Lys | Thr | Ile | Asp | Ser | Tyr | Asn | Glu | Gln | Ala | Pro | Ser | Asn | 625 | 630 | 635 |
| Gly | Val | Glu | Ala | Phe | Pro | Tyr | Leu | Ile | Val | Val | Ile | Asp | Glu | Leu | Ala | 645 | 650 | 655 |
| Asp | Leu | Met | Met | Thr | Gly | Gly | Lys | Glu | Ala | Glu | Phe | Pro | Ile | Ala | Arg | 660 | 665 | 670 |
| Ile | Ala | Gln | Met | Gly | Arg | Ala | Ser | Gly | Leu | His | Leu | Ile | Val | Ala | Thr | 675 | 680 | 685 |
| Gln | Arg | Pro | Ser | Val | Asp | Val | Val | Thr | Gly | Leu | Ile | Lys | Thr | Asn | Leu | 690 | 695 | 700 |
| Pro | Ser | Arg | Val | Ser | Phe | Arg | Val | Gly | Thr | Lys | Ile | Asp | Ser | Lys | Val | 705 | 710 | 715 |
| Ile | Leu | Asp | Thr | Asp | Gly | Ala | Gln | Ser | Leu | Leu | Gly | Arg | Gly | Asp | Met | 725 | 730 | 735 |
| Leu | Phe | Thr | Pro | Gly | Ala | Asn | Gly | Leu | Val | Arg | Leu | His | Ala | Pro |     | 740 | 745 | 750 |
| Phe | Ala | Thr | Glu | Asp | Glu | Ile | Lys | Lys | Ile | Val | Asp | Phe | Ile | Lys | Ala | 755 | 760 | 765 |
| Gln | Lys | Glu | Val | Gln | Tyr | Asp | Lys | Asp | Phe | Leu | Leu | Glu | Glu | Ser | Arg | 770 | 775 | 780 |
| Met | Pro | Leu | Asp | Thr | Pro | Asn | Tyr | Gln | Gly | Asp | Asp | Ile | Leu | Glu | Arg | 785 | 790 | 795 |
| Ala | Lys | Ala | Val | Ile | Leu | Glu | Lys | Lys | Ile | Thr | Ser | Thr | Ser | Phe | Leu | 805 | 810 | 815 |
| Gln | Arg | Gln | Leu | Lys | Ile | Gly | Tyr | Asn | Gln | Ala | Ala | Thr | Ile | Thr | Asp | 820 | 825 | 830 |
| Glu | Leu | Glu | Ala | Gln | Gly | Phe | Leu | Ser | Pro | Arg | Asn | Ala | Lys | Gly | Asn | 835 | 840 | 845 |
| Arg | Glu | Ile | Leu | Gln | Asn | Phe |     |     |     |     |     |     |     |     |     | 850 | 855 |     |

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1136 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1094
- (D) OTHER INFORMATION:

1094...51

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

|                                                                 |            |            |            |            |     |     |    |
|-----------------------------------------------------------------|------------|------------|------------|------------|-----|-----|----|
| AACCATAAAA                                                      | ACGATACAAT | AGCGGTATTT | TAATAAAACA | AGGAGTTTTA | ATG | AGA | 56 |
|                                                                 |            |            |            |            | Met | Arg |    |
|                                                                 |            |            |            |            | 1   |     |    |
| GTT CAA TCT AAA GGT TTT GCT ATT TTT TCT AAA GAC GGG CAT TTC AAA | 104        |            |            |            |     |     |    |
| Val Gln Ser Lys Gly Phe Ala Ile Phe Ser Lys Asp Gly His Phe Lys |            |            |            |            |     |     |    |
| 5 10 15                                                         |            |            |            |            |     |     |    |
| CCC CAT GAT TTT AGC CGC CAT GCT GTA GGC CCT AAA GAT GTG TTG ATT | 152        |            |            |            |     |     |    |
| Pro His Asp Phe Ser Arg His Ala Val Gly Pro Lys Asp Val Leu Ile |            |            |            |            |     |     |    |
| 20 25 30                                                        |            |            |            |            |     |     |    |
| GAC ATT CTT TAT GCA GGG ATT TGT CAT AGC GAT ATT CAT AGC GCT TAT | 200        |            |            |            |     |     |    |
| Asp Ile Leu Tyr Ala Gly Ile Cys His Ser Asp Ile His Ser Ala Tyr |            |            |            |            |     |     |    |
| 35 40 45 50                                                     |            |            |            |            |     |     |    |
| AGC GAA TGG AAA GAA GGC ATT TAC CCT ATG GTT CCT GGG CAT GAA ATT | 248        |            |            |            |     |     |    |
| Ser Glu Trp Lys Glu Gly Ile Tyr Pro Met Val Pro Gly His Glu Ile |            |            |            |            |     |     |    |
| 55 60 65                                                        |            |            |            |            |     |     |    |
| GCT GGG GCC ATC AAA GAA GTG GGT AAG GAA GTT AAG AAA TTT AAG GTT | 296        |            |            |            |     |     |    |
| Ala Gly Ala Ile Lys Glu Val Gly Lys Glu Val Lys Lys Phe Lys Val |            |            |            |            |     |     |    |
| 70 75 80                                                        |            |            |            |            |     |     |    |
| GGC GAT GTG GTG GGC GTG GGC TGT TTT GTC AAT TCA TGC AAA GCG TGT | 344        |            |            |            |     |     |    |
| Gly Asp Val Val Gly Val Gly Cys Phe Val Asn Ser Cys Lys Ala Cys |            |            |            |            |     |     |    |
| 85 90 95                                                        |            |            |            |            |     |     |    |
| AAG CCC TGT AAA GAA CAC CAA GAG CAA TTT TGC GCC AAA GTG GTA TTC | 392        |            |            |            |     |     |    |
| Lys Pro Cys Lys Glu His Gln Glu Phe Cys Ala Lys Val Val Phe     |            |            |            |            |     |     |    |
| 100 105 110                                                     |            |            |            |            |     |     |    |
| ACT TAC GAT TGT TTG GAT TAT TTC CAT GAC AAC GAA CCC CAC ATG GGC | 440        |            |            |            |     |     |    |
| Thr Tyr Asp Cys Leu Asp Tyr Phe His Asp Asn Glu Pro His Met Gly |            |            |            |            |     |     |    |
| 115 120 125 130                                                 |            |            |            |            |     |     |    |
| GGA TAC TCT AAT AAT ATT GTA GTG GAT GAA AAC TAT GTG ATT AGC GTG | 488        |            |            |            |     |     |    |
| Gly Tyr Ser Asn Asn Ile Val Val Asp Glu Asn Tyr Val Ile Ser Val |            |            |            |            |     |     |    |
| 135 140 145                                                     |            |            |            |            |     |     |    |
| GAT AAA AAC GCT CCT TTA GAA AAA GTA GCC CCC TTG CTT TGT GCG GGC | 536        |            |            |            |     |     |    |
| Asp Lys Asn Ala Pro Leu Glu Lys Val Ala Pro Leu Leu Cys Ala Gly |            |            |            |            |     |     |    |
| 150 155 160                                                     |            |            |            |            |     |     |    |
| ATC ACC ACT TAT TCG CCC TTA AAA TTT TCT AAG GTT ACT AAA GGC ACA | 584        |            |            |            |     |     |    |
| Ile Thr Thr Tyr Ser Pro Leu Lys Phe Ser Lys Val Thr Lys Gly Thr |            |            |            |            |     |     |    |
| 165 170 175                                                     |            |            |            |            |     |     |    |
| AAA GTT GGC GTC GCT GGG TTT GGC GGG CTA GGA AGC ATG GCG GTT AAA | 632        |            |            |            |     |     |    |
| Lys Val Gly Val Ala Gly Phe Gly Gly Leu Gly Ser Met Ala Val Lys |            |            |            |            |     |     |    |
| 180 185 190                                                     |            |            |            |            |     |     |    |
| TAC GCT GTG GCT ATG GGG GCT GAA GTG AGC GTT TTT GCA AGA AAC GAA | 680        |            |            |            |     |     |    |
| Tyr Ala Val Ala Met Gly Ala Glu Val Ser Val Phe Ala Arg Asn Glu |            |            |            |            |     |     |    |
| 195 200 205 210                                                 |            |            |            |            |     |     |    |





|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ile | Ala | Gly | Ala | Ile | Lys | Glu | Val | Gly | Lys | Glu | Val | Lys | Lys | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Val | Gly | Asp | Val | Val | Gly | Val | Gly | Cys | Phe | Val | Asn | Ser | Cys | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Cys | Lys | Pro | Cys | Lys | Glu | His | Gln | Glu | Gln | Phe | Cys | Ala | Lys | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Phe | Thr | Tyr | Asp | Cys | Leu | Asp | Tyr | Phe | His | Asp | Asn | Glu | Pro | His |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Met | Gly | Gly | Tyr | Ser | Asn | Asn | Ile | Val | Val | Asp | Glu | Asn | Tyr | Val | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Val | Asp | Lys | Asn | Ala | Pro | Leu | Glu | Lys | Val | Ala | Pro | Leu | Leu | Cys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Gly | Ile | Thr | Thr | Tyr | Ser | Pro | Leu | Lys | Phe | Ser | Lys | Val | Thr | Lys |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Thr | Lys | Val | Gly | Val | Ala | Gly | Phe | Gly | Gly | Leu | Gly | Ser | Met | Ala |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Val | Lys | Tyr | Ala | Val | Ala | Met | Gly | Ala | Glu | Val | Ser | Val | Phe | Ala | Arg |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asn | Glu | His | Lys | Lys | Gln | Asp | Ala | Leu | Ser | Met | Gly | Val | Lys | His | Phe |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Tyr | Thr | Asp | Pro | Lys | Gln | Cys | Lys | Glu | Glu | Leu | Asp | Phe | Ile | Ile | Ser |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Thr | Ile | Pro | Thr | His | Tyr | Asp | Leu | Lys | Asp | Tyr | Leu | Lys | Leu | Leu | Thr |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Tyr | Asn | Gly | Asp | Leu | Ala | Leu | Val | Gly | Leu | Pro | Pro | Val | Glu | Ile | Ala |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Pro | Ala | Leu | Ser | Val | Phe | Asp | Phe | Ile | His | Leu | Gly | Asn | Arg | Lys | Val |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Tyr | Gly | Ser | Leu | Ile | Gly | Gly | Ile | Lys | Glu | Thr | Gln | Glu | Met | Met | Asp |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Phe | Ser | Ile | Lys | His | Asn | Ile | Tyr | Pro | Glu | Ile | Asp | Leu | Ile | Leu | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Lys | Asp | Ile | Asp | Thr | Ala | Tyr | His | Asn | Leu | Thr | His | Gly | Lys | Ala | Lys |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Phe | Arg | Tyr | Val | Ile | Asp | Met | Lys | Lys | Ser | Phe | Asp |     |     |     |     |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...1317
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

TTAAAAAAGG GTGTTTAATT TTTT ATG ACT TCA GCT TCA AGC CAT TCT TTT  
Met Thr Ser Ala Ser Ser His Ser Phe  
1 5

|                   |                   |                   |                   |                   |                   |                  |                   |                   |                   |                   |                   |                   |                   |                   |                   |     |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| AAA<br>Lys<br>10  | GAA<br>Glu        | CAA<br>Gln        | GAT<br>Asp        | TTT<br>Phe<br>30  | CAT<br>His<br>15  | ATT<br>Ile       | CCT<br>Pro        | ATC<br>Ile        | GCT<br>Ala        | TTT<br>Phe<br>20  | GCT<br>Ala        | TTT<br>Phe        | GAT<br>Asp        | AAG<br>Lys        | AAT<br>Asn<br>25  | 99  |
| TAC<br>Tyr        | CTC<br>Leu        | ATT<br>Ile        | CCT<br>Pro        | GCG<br>Ala<br>30  | GGC<br>Gly        | GCG<br>Ala       | TGT<br>Cys        | CTT<br>Leu        | TAT<br>Tyr<br>35  | TCC<br>Ser        | TTG<br>Leu        | CTA<br>Leu        | GAA<br>Glu<br>40  | AGC<br>Ser        | ATC<br>Ile        | 147 |
| GCT<br>Ala        | AAA<br>Lys        | GCC<br>Ala        | AAT<br>Asn<br>45  | AAA<br>Lys        | AAA<br>Lys        | ATC<br>Ile       | CGT<br>Arg        | TAC<br>Tyr<br>50  | ACC<br>Thr        | CTA<br>Leu        | CAC<br>His        | GCT<br>Ala        | TTA<br>Leu<br>55  | GTG<br>Val        | GTA<br>Val        | 195 |
| GGC<br>Gly        | TTG<br>Leu        | AAT<br>Asn<br>60  | GAA<br>Glu        | GAA<br>Glu        | GAT<br>Asp        | AAA<br>Lys       | GCA<br>Ala<br>65  | AAG<br>Lys        | CTT<br>Leu        | AAT<br>Asn        | CAA<br>Gln        | ATC<br>Ile<br>70  | ACA<br>Thr        | GAG<br>Glu        | CCT<br>Pro        | 243 |
| TTT<br>Phe<br>75  | AAA<br>Lys        | GAA<br>Glu        | TTT<br>Phe        | GCC<br>Ala        | GCT<br>Ala        | TTG<br>Leu<br>80 | GAA<br>Glu        | GTG<br>Val        | AGA<br>Arg        | GAT<br>Asp<br>85  | ATT<br>Ile        | GAG<br>Glu        | TCT<br>Ser        | TTT<br>Phe        | TTA<br>Leu        | 291 |
| GAC<br>Asp<br>90  | ACT<br>Thr        | ATC<br>Ile        | CCT<br>Pro        | AAC<br>Asn        | CCT<br>Pro<br>95  | TTT<br>Phe       | GAT<br>Asp        | GAG<br>Glu        | GAT<br>Asp<br>100 | TTC<br>Phe        | ACT<br>Thr        | AAG<br>Lys        | CGT<br>Arg        | TTT<br>Phe        | TCT<br>Ser<br>105 | 339 |
| AAA<br>Lys        | ATG<br>Met        | GTG<br>Val        | TTA<br>Leu        | GTG<br>Val<br>110 | AAG<br>Lys        | TAT<br>Tyr       | TTT<br>Phe        | TTG<br>Leu        | GCG<br>Ala<br>115 | GAT<br>Asp        | TTG<br>Leu        | TTC<br>Phe        | CCC<br>Pro<br>120 | AAA<br>Lys        | TAT<br>Tyr        | 387 |
| TCC<br>Ser        | AAA<br>Lys        | ATG<br>Met        | GTG<br>Val<br>125 | TGG<br>Trp        | AGC<br>Ser        | GAT<br>Asp       | GTG<br>Val        | GAT<br>Asp<br>130 | GTC<br>Val        | ATC<br>Ile        | TTT<br>Phe        | TGC<br>Cys        | AAT<br>Asn<br>135 | GAA<br>Glu        | TTT<br>Phe        | 435 |
| AGC<br>Ser        | GCT<br>Ala        | GAT<br>Asp<br>140 | TTC<br>Phe        | TTA<br>Leu        | AAC<br>Asn        | CTT<br>Leu       | GAA<br>Glu<br>145 | GAA<br>Glu        | AAT<br>Asn        | GAT<br>Asp        | GAG<br>Glu        | AAT<br>Asn<br>150 | TAT<br>Tyr        | TTT<br>Phe        | TAT<br>Tyr        | 483 |
| GGA<br>Gly        | GTT<br>Val<br>155 | TTA<br>Leu        | GAA<br>Glu        | GTT<br>Val        | GAA<br>Glu<br>160 | AAG<br>Lys       | CAC<br>His        | CAC<br>His        | ATG<br>Met        | ATG<br>Met        | GAA<br>Glu<br>165 | GGG<br>Gly        | TTT<br>Phe        | TTG<br>Leu        | TTT<br>Phe        | 531 |
| TGC<br>Cys<br>170 | AAT<br>Asn        | TTA<br>Leu        | GAT<br>Asp        | TAC<br>Tyr        | CAG<br>Gln<br>175 | CGC<br>Arg       | AAG<br>Lys        | AAA<br>Lys        | AAT<br>Asn        | TTC<br>Phe<br>180 | ACC<br>Thr        | TTA<br>Leu        | AGA<br>Arg        | ATG<br>Met        | CAT<br>His<br>185 | 579 |
| GAG<br>Glu        | CTT<br>Leu        | TTA<br>Leu        | AGG<br>Arg        | GGG<br>Gly<br>190 | AAT<br>Asn        | GAG<br>Glu       | GCT<br>Ala        | AAA<br>Lys        | GGG<br>Gly<br>195 | GAG<br>Glu        | TTG<br>Leu        | GAT<br>Asp        | TTC<br>Phe        | ACG<br>Thr<br>200 | AAA<br>Lys        | 627 |
| TGG<br>Trp        | TGT<br>Cys        | TGG<br>Trp        | CCT<br>Pro<br>205 | AAC<br>Asn        | ATG<br>Met        | AAA<br>Lys       | GCT<br>Ala        | TTA<br>Leu<br>210 | GGG<br>Gly        | ATT<br>Ile        | GAA<br>Glu        | TAT<br>Tyr        | TGC<br>Cys<br>215 | GTT<br>Val        | TTC<br>Phe        | 675 |
| CCT<br>Pro        | TAT<br>Tyr        | TAT<br>Tyr<br>220 | TAC<br>Tyr        | ACC<br>Thr        | ATT<br>Ile        | AAA<br>Lys       | GAT<br>Asp<br>225 | TTT<br>Phe        | TCT<br>Ser        | AAC<br>Asn        | GCG<br>Ala        | TAT<br>Tyr<br>230 | TTA<br>Leu        | AAC<br>Asn        | GAG<br>Glu        | 723 |
| AAT<br>Asn        | TAC<br>Tyr        | AAG<br>Lys        | AAA<br>Lys        | ACC<br>Thr        | ATT<br>Ile        | TTA<br>Leu       | GAG<br>Glu        | GCA<br>Ala        | CGA<br>Arg        | GAA<br>Glu        | AAC<br>Asn        | CCT<br>Pro        | ACC<br>Thr        | ATT<br>Ile        | ATC<br>Ile        | 771 |

| 235                                                               | 240 | 245 |      |
|-------------------------------------------------------------------|-----|-----|------|
| CAC TAT GAC GCT TGG TGG GGA GCG GTG AAG CCT TGG GAC TAT CCT TTT   |     |     | 819  |
| His Tyr Asp Ala Trp Trp Gly Ala Val Lys Pro Trp Asp Tyr Pro Phe   |     |     |      |
| 250                                                               | 255 | 260 | 265  |
| GGT TTA AAA GCG GAT TTA TGG CTG AAC GCT TTG GCT AAA ACC CCT TTT   |     |     | 867  |
| Gly Leu Lys Ala Asp Leu Trp Leu Asn Ala Leu Ala Lys Thr Pro Phe   |     |     |      |
|                                                                   | 270 | 275 | 280  |
| ATG AGC GAT TGG ATT GAT TCG ATC GCT AGG GTG GAA ATA GGC AGC GAA   |     |     | 915  |
| Met Ser Asp Trp Ile Asp Ser Ile Ala Arg Val Glu Ile Gly Ser Glu   |     |     |      |
|                                                                   | 285 | 290 | 295  |
| AAA TGG CAT CGT TAC CAC AGC ATC GTT GCC TAT CAC TAC TAC TTT CCC   |     |     | 963  |
| Lys Trp His Arg Tyr His Ser Ile Val Ala Tyr His Tyr Tyr Phe Pro   |     |     |      |
|                                                                   | 300 | 305 | 310  |
| CTA TGG AAG ACT GAA GAG CAG ATC GCC CAT GAC GCA CTC AAG ACC TTT   |     |     | 1011 |
| Leu Trp Lys Thr Glu Glu Gln Ile Ala His Asp Ala Leu Lys Thr Phe   |     |     |      |
|                                                                   | 315 | 320 | 325  |
| TTA GAC CAT TAT TTT TCG TGC ATC CAT GCC GCA ATC AAG CAA GAA AAT   |     |     | 1059 |
| Leu Asp His Tyr Phe Ser Cys Ile His Ala Ala Ile Lys Gln Glu Asn   |     |     |      |
|                                                                   | 330 | 335 | 340  |
| CTC GGA ATG TTC TTG AAC CAC TAC TTC TCG CAT GCC CAT GCA GAG ATC   |     |     | 1107 |
| Leu Gly Met Phe Leu Asn His Tyr Phe Ser His Ala His Ala Glu Ile   |     |     |      |
|                                                                   | 350 | 355 | 360  |
| AAA GAA AAC TCC CTT GAA ATG TTC TTG AAC CAC TAC TTC TCG CAT GTT   |     |     | 1155 |
| Lys Glu Asn Ser Leu Glu Met Phe Leu Asn His Tyr Phe Ser His Val   |     |     |      |
|                                                                   | 365 | 370 | 375  |
| TAT AGG CTC CCT AAA AAA GCA CGG AAG AGA CTC TTT AGG GTG TTT GTC   |     |     | 1203 |
| Tyr Arg Leu Pro Lys Lys Ala Arg Lys Arg Leu Phe Arg Val Phe Val   |     |     |      |
|                                                                   | 380 | 385 | 390  |
| AAA CAC TGC ATC CTC ATA CCA CTC AAG AGC CTT GTG GGT AAG ACT CTA   |     |     | 1251 |
| Lys His Cys Ile Leu Ile Pro Leu Lys Ser Leu Val Gly Lys Thr Leu   |     |     |      |
|                                                                   | 395 | 400 | 405  |
| CGA CTC TTA AAA CTC CAT GCG CTA GCT AAA AAA ATC CTA ATC CAA CTC   |     |     | 1299 |
| Arg Leu Leu Lys Leu His Ala Leu Ala Lys Lys Ile Leu Ile Gln Leu   |     |     |      |
|                                                                   | 410 | 415 | 420  |
| AAG CTC TTA AAA AAG AGC TAGAGCCAAA ACTTTTAATC AAACGATTTT TTCATATC |     |     | 1355 |
| Lys Leu Leu Lys Lys Ser                                           |     |     |      |
|                                                                   | 430 |     |      |
| AATCACATAG CGGAATTTTCG CTT                                        |     |     | 1378 |

(2) INFORMATION FOR SEQ ID NO:254:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 431 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Thr | Ser | Ala | Ser | Ser | His | Ser | Phe | Lys | Glu | Gln | Asp | Phe | His | Ile |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Pro | Ile | Ala | Phe | Ala | Phe | Asp | Lys | Asn | Tyr | Leu | Ile | Pro | Ala | Gly | Ala |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Cys | Leu | Tyr | Ser | Leu | Leu | Glu | Ser | Ile | Ala | Lys | Ala | Asn | Lys | Lys | Ile |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg | Tyr | Thr | Leu | His | Ala | Leu | Val | Val | Gly | Leu | Asn | Glu | Glu | Asp | Lys |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ala | Lys | Leu | Asn | Gln | Ile | Thr | Glu | Pro | Phe | Lys | Glu | Phe | Ala | Ala | Leu |  |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Glu | Val | Arg | Asp | Ile | Glu | Ser | Phe | Leu | Asp | Thr | Ile | Pro | Asn | Pro | Phe |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Asp | Glu | Asp | Phe | Thr | Lys | Arg | Phe | Ser | Lys | Met | Val | Leu | Val | Lys | Tyr |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Phe | Leu | Ala | Asp | Leu | Phe | Pro | Lys | Tyr | Ser | Lys | Met | Val | Trp | Ser | Asp |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Val | Asp | Val | Ile | Phe | Cys | Asn | Glu | Phe | Ser | Ala | Asp | Phe | Leu | Asn | Leu |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Glu | Glu | Asn | Asp | Glu | Asn | Tyr | Phe | Tyr | Gly | Val | Leu | Glu | Val | Glu | Lys |  |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |  |
| His | His | Met | Met | Glu | Gly | Phe | Leu | Phe | Cys | Asn | Leu | Asp | Tyr | Gln | Arg |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Lys | Lys | Asn | Phe | Thr | Leu | Arg | Met | His | Glu | Leu | Leu | Arg | Gly | Asn | Glu |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Ala | Lys | Gly | Glu | Leu | Asp | Phe | Thr | Lys | Trp | Cys | Trp | Pro | Asn | Met | Lys |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Ala | Leu | Gly | Ile | Glu | Tyr | Cys | Val | Phe | Pro | Tyr | Tyr | Tyr | Thr | Ile | Lys |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Asp | Phe | Ser | Asn | Ala | Tyr | Leu | Asn | Glu | Asn | Tyr | Lys | Lys | Thr | Ile | Leu |  |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Glu | Ala | Arg | Glu | Asn | Pro | Thr | Ile | Ile | His | Tyr | Asp | Ala | Trp | Trp | Gly |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Ala | Val | Lys | Pro | Trp | Asp | Tyr | Pro | Phe | Gly | Leu | Lys | Ala | Asp | Leu | Trp |  |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Leu | Asn | Ala | Leu | Ala | Lys | Thr | Pro | Phe | Met | Ser | Asp | Trp | Ile | Asp | Ser |  |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Ile | Ala | Arg | Val | Glu | Ile | Gly | Ser | Glu | Lys | Trp | His | Arg | Tyr | His | Ser |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Ile | Val | Ala | Tyr | His | Tyr | Tyr | Phe | Pro | Leu | Trp | Lys | Thr | Glu | Glu | Gln |  |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Ile | Ala | His | Asp | Ala | Leu | Lys | Thr | Phe | Leu | Asp | His | Tyr | Phe | Ser | Cys |  |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |  |
| Ile | His | Ala | Ala | Ile | Lys | Gln | Glu | Asn | Leu | Gly | Met | Phe | Leu | Asn | His |  |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |
| Tyr | Phe | Ser | His | Ala | His | Ala | Glu | Ile | Lys | Glu | Asn | Ser | Leu | Glu | Met |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |
| Phe | Leu | Asn | His | Tyr | Phe | Ser | His | Val | Tyr | Arg | Leu | Pro | Lys | Lys | Ala |  |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |
| Arg | Lys | Arg | Leu | Phe | Arg | Val | Phe | Val | Lys | His | Cys | Ile | Leu | Ile | Pro |  |
| 385 |     |     |     | 390 |     |     |     |     |     | 395 |     |     |     |     | 400 |  |
| Leu | Lys | Ser | Leu | Val | Gly | Lys | Thr | Leu | Arg | Leu | Leu | Lys | Leu | His | Ala |  |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |  |

Leu Ala Lys Lys Ile Leu Ile Gln Leu Lys Leu Leu Lys Lys Ser  
 420 425 430

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 650 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 46...603
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GCTGAATTCA ATTTATTTTA TACGATATTA AGGAGACATA TTACC ATG TTT CAA ATT | 57  |
| Met Phe Gln Ile                                                   |     |
| 1                                                                 |     |
| AGA TGG CAT GCA CGA GCG GGT CAA GGT GCA ATC ACT GGC GCT AAA GGG   | 105 |
| Arg Trp His Ala Arg Ala Gly Gln Gly Ala Ile Thr Gly Ala Lys Gly   |     |
| 5 10 15 20                                                        |     |
| TTG GCT GAT GTG ATT TCA AAA ACA GGC AAA GAA GTG CAA GCG TTC GCT   | 153 |
| Leu Ala Asp Val Ile Ser Lys Thr Gly Lys Glu Val Gln Ala Phe Ala   |     |
| 25 30 35                                                          |     |
| TCT TAT GGT TCA GCT AAA AGG GGG GCT GCT ATG ATG GCT TAT AAC CGC   | 201 |
| Ser Tyr Gly Ser Ala Lys Arg Gly Ala Ala Met Met Ala Tyr Asn Arg   |     |
| 40 45 50                                                          |     |
| GTT GAT GAT GAA CCT ATC TTA AAC CAT GAA CGC TTC ATG CAG CCT GAT   | 249 |
| Val Asp Asp Glu Pro Ile Leu Asn His Glu Arg Phe Met Gln Pro Asp   |     |
| 55 60 65                                                          |     |
| TAT GTG CTG GTG ATT GAC CCT GGT TTG GTT TTC ATT GAA AAC ATC TTC   | 297 |
| Tyr Val Leu Val Ile Asp Pro Gly Leu Val Phe Ile Glu Asn Ile Phe   |     |
| 70 75 80                                                          |     |
| GCC AAT GAA AAA GAA GAC ACG ACT TAT ATT ATC ACT AGC TAC CTT AAC   | 345 |
| Ala Asn Glu Lys Glu Asp Thr Thr Tyr Ile Ile Thr Ser Tyr Leu Asn   |     |
| 85 90 95 100                                                      |     |
| AAA GAA GAA TTG TTT GAA AAA AAA CCT GAA TTA AAA ACC CGT AAG GTG   | 393 |
| Lys Glu Glu Leu Phe Glu Lys Lys Pro Glu Leu Lys Thr Arg Lys Val   |     |
| 105 110 115                                                       |     |
| TTT TTA GTG GAT TGT TTA AAA ATC TCT ATG GAA ACC TTA AAA CGC CCC   | 441 |
| Phe Leu Val Asp Cys Leu Lys Ile Ser Met Glu Thr Leu Lys Arg Pro   |     |
| 120 125 130                                                       |     |
| ATC CCT AAC ACG CCC ATG TTA GGG GCG TTA ATG AAA GTG TCT GGC ATG   | 489 |

Ile Pro Asn Thr Pro Met Leu Gly Ala Leu Met Lys Val Ser Gly Met  
135 140 145

CTT GAA ATT GGG GCT TTT AAA GAA GCT TTT AAG AAA GTT TTA GGC AAA 537  
Leu Glu Ile Gly Ala Phe Lys Glu Ala Phe Lys Lys Val Leu Gly Lys  
150 155 160

AAA CTC ACG CAA GAA GTC ATT GAC GCT AAC ATG CTC GCT ATC CAA AGA 585  
Lys Leu Thr Gln Glu Val Ile Asp Ala Asn Met Leu Ala Ile Gln Arg  
165 170 175 180

GCT TAT GAA GAA GTT CAA TAACATTAAG GAACAAAGAT GAAAGATTGG AACGAATT 641  
Ala Tyr Glu Glu Val Gln  
185

TGAAATGGG 650

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Met Phe Gln Ile Arg Trp His Ala Arg Ala Gly Gln Gly Ala Ile Thr  
1 5 10 15  
Gly Ala Lys Gly Leu Ala Asp Val Ile Ser Lys Thr Gly Lys Glu Val  
20 25 30  
Gln Ala Phe Ala Ser Tyr Gly Ser Ala Lys Arg Gly Ala Ala Met Met  
35 40 45  
Ala Tyr Asn Arg Val Asp Asp Glu Pro Ile Leu Asn His Glu Arg Phe  
50 55 60  
Met Gln Pro Asp Tyr Val Leu Val Ile Asp Pro Gly Leu Val Phe Ile  
65 70 75 80  
Glu Asn Ile Phe Ala Asn Glu Lys Glu Asp Thr Thr Tyr Ile Ile Thr  
85 90 95  
Ser Tyr Leu Asn Lys Glu Glu Leu Phe Glu Lys Lys Pro Glu Leu Lys  
100 105 110  
Thr Arg Lys Val Phe Leu Val Asp Cys Leu Lys Ile Ser Met Glu Thr  
115 120 125  
Leu Lys Arg Pro Ile Pro Asn Thr Pro Met Leu Gly Ala Leu Met Lys  
130 135 140  
Val Ser Gly Met Leu Glu Ile Gly Ala Phe Lys Glu Ala Phe Lys Lys  
145 150 155 160  
Val Leu Gly Lys Lys Leu Thr Gln Glu Val Ile Asp Ala Asn Met Leu  
165 170 175  
Ala Ile Gln Arg Ala Tyr Glu Glu Val Gln  
180 185

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1008 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 19...954  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TTGGGGATTT TAACTTTT ATG GAT TTT TGC TCT GGC ATT GGT GGA GGC CGT | 51  |
| Met Asp Phe Cys Ser Gly Ile Gly Gly Gly Arg                     |     |
| 1 5 10                                                          |     |
| TTG GGC TTG GAG CAA TGC CAT TTA AAA TGC GTA GGG CAT GCA GAA ATC | 99  |
| Leu Gly Leu Glu Gln Cys His Leu Lys Cys Val Gly His Ala Glu Ile |     |
| 15 20 25                                                        |     |
| AAT CAT GAA GCC CTT AGG ACT TAT GAA TTA TTT TTT AAA GAT ACC CAT | 147 |
| Asn His Glu Ala Leu Arg Thr Tyr Glu Leu Phe Phe Lys Asp Thr His |     |
| 30 35 40                                                        |     |
| AAT TTT GGG GAT TTG ATG CGA ATC AAC CCT AAT GAT TTA CCC GAT TTT | 195 |
| Asn Phe Gly Asp Leu Met Arg Ile Asn Pro Asn Asp Leu Pro Asp Phe |     |
| 45 50 55                                                        |     |
| GAT GCA CTC ATT AGC GGG TTT CCT TGT CAA GCT TTT TCT ATC AAT GGC | 243 |
| Asp Ala Leu Ile Ser Gly Phe Pro Cys Gln Ala Phe Ser Ile Asn Gly |     |
| 60 65 70 75                                                     |     |
| AAA AGG AAG GGG CTT GAA GAT GAA AGA GGG ACG ATT ATT TAC GGG CTT | 291 |
| Lys Arg Lys Gly Leu Glu Asp Glu Arg Gly Thr Ile Ile Tyr Gly Leu |     |
| 80 85 90                                                        |     |
| ATT CGC ATT TTA AAA GTT AAA CAG CCT GAA TGT TTC TTG CTT GAA AAT | 339 |
| Ile Arg Ile Leu Lys Val Lys Gln Pro Glu Cys Phe Leu Leu Glu Asn |     |
| 95 100 105                                                      |     |
| GTT AAG GGC TTG ATC AAT CAT AAT AAA AAG GCA ACT TTT AAT ATT ATT | 387 |
| Val Lys Gly Leu Ile Asn His Asn Lys Lys Ala Thr Phe Asn Ile Ile |     |
| 110 115 120                                                     |     |
| ATC AAA GCC CTA CAA GAA GTG GGT TAT ACA ACT TAT TAT AAA ATT TTA | 435 |
| Ile Lys Ala Leu Gln Glu Val Gly Tyr Thr Thr Tyr Tyr Lys Ile Leu |     |
| 125 130 135                                                     |     |
| AAC AGC GCT GAT TTT CAA TTA GCC CAA AAT AGA GAA CGC CTT TAT ATC | 483 |
| Asn Ser Ala Asp Phe Gln Leu Ala Gln Asn Arg Glu Arg Leu Tyr Ile |     |
| 140 145 150 155                                                 |     |
| GTA GGG TTT AGG AAG GAT TTA AAA CAC CCA TTT AAT TTC CCT TTA GGT | 531 |
| Val Gly Phe Arg Lys Asp Leu Lys His Pro Phe Asn Phe Pro Leu Gly |     |
| 160 165 170                                                     |     |

|                                                |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |
|------------------------------------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| TTA<br>Leu                                     | GCC<br>Ala        | AAT<br>Asn        | GAT<br>Asp<br>175 | TAT<br>Tyr        | TAT<br>Tyr        | TTC<br>Phe        | AAG<br>Lys        | GAT<br>Asp<br>180 | TTT<br>Phe        | TTA<br>Leu        | GAC<br>Asp        | GCT<br>Ala        | GAT<br>Asp<br>185 | AAT<br>Asn        | GAA<br>Glu        | 579  |
| TGT<br>Cys                                     | TAT<br>Tyr        | TTG<br>Leu<br>190 | GAT<br>Asp        | GTG<br>Val        | AGT<br>Ser        | AAC<br>Asn        | GCT<br>Ala<br>195 | GCA<br>Ala        | TTT<br>Phe        | CAA<br>Gln        | AGA<br>Arg        | TAC<br>Tyr<br>200 | TTG<br>Leu        | CAC<br>His        | AAC<br>Asn        | 627  |
| CGA<br>Arg                                     | TAC<br>Tyr<br>205 | AAC<br>Asn        | CAT<br>His        | AAC<br>Asn        | CGG<br>Arg        | GTT<br>Val<br>210 | TCT<br>Ser        | TTA<br>Leu        | GAG<br>Glu        | GAT<br>Asp<br>215 | CTC<br>Leu        | TTA<br>Leu        | ACT<br>Thr        | TTA<br>Leu        | GAA<br>Glu        | 675  |
| AAC<br>Asn<br>220                              | GCT<br>Ala        | GTT<br>Val        | TTA<br>Leu        | GAC<br>Asp        | ACA<br>Thr<br>225 | AGA<br>Arg        | CAA<br>Gln        | TCT<br>Ser        | GAT<br>Asp        | TTA<br>Leu<br>230 | AGG<br>Arg        | TTG<br>Leu        | TAT<br>Tyr        | TCT<br>Ser        | AAT<br>Asn<br>235 | 723  |
| GTT<br>Val                                     | TTT<br>Phe        | CCT<br>Pro        | ACT<br>Thr        | TTA<br>Leu<br>240 | AGG<br>Arg        | ACT<br>Thr        | TCT<br>Ser        | CGG<br>Arg        | CAT<br>His<br>245 | GGC<br>Gly        | CTG<br>Leu        | TTT<br>Phe        | TAT<br>Tyr        | ACC<br>Thr<br>250 | CAA<br>Gln        | 771  |
| AAA<br>Lys                                     | GGC<br>Gly        | AAA<br>Lys        | ATC<br>Ile<br>255 | AAA<br>Lys        | AGA<br>Arg        | TTA<br>Leu        | AAC<br>Asn        | GCT<br>Ala<br>260 | ATT<br>Ile        | GAA<br>Glu        | AGC<br>Ser        | TTG<br>Leu        | CTT<br>Leu        | TTG<br>Leu        | CAA<br>Gln        | 819  |
| GGA<br>Gly                                     | TTT<br>Phe        | CCT<br>Pro<br>270 | AGG<br>Arg        | GAT<br>Asp        | TTG<br>Leu        | ATC<br>Ile        | GCT<br>Ala<br>275 | AAG<br>Lys        | ATT<br>Ile        | AAA<br>Lys        | GAT<br>Asp        | AAT<br>Asn<br>280 | CCT<br>Pro        | AAC<br>Asn        | TTT<br>Phe        | 867  |
| AAA<br>Lys                                     | GCA<br>Ala<br>285 | AGC<br>Ser        | CAT<br>His        | TTG<br>Leu        | CTA<br>Leu        | TCC<br>Ser<br>290 | CAA<br>Gln        | GCG<br>Ala        | GGG<br>Gly        | AAT<br>Asn        | GCG<br>Ala<br>295 | ATG<br>Met        | AGC<br>Ser        | GTG<br>Val        | AAT<br>Asn        | 915  |
| GTG<br>Val<br>300                              | ATT<br>Ile        | GCT<br>Ala        | GCA<br>Ala        | ATC<br>Ile        | GCT<br>Ala<br>305 | AAA<br>Lys        | CAA<br>Gln        | ATG<br>Met        | TTA<br>Leu        | AAG<br>Lys<br>310 | GCG<br>Ala        | ATT<br>Ile        | TAATAAGGGA        | GC                |                   | 966  |
| TTTAAGGGGA GAATGATTTC AAAATACCCC CTATCCCCTT AA |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   | 1008 |

(2) INFORMATION FOR SEQ ID NO:258:



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Phe | Pro | Cys | Gln | Ala | Phe | Ser | Ile | Asn | Gly | Lys | Arg | Lys | Gly | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Asp | Glu | Arg | Gly | Thr | Ile | Ile | Tyr | Gly | Leu | Ile | Arg | Ile | Leu | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Lys | Gln | Pro | Glu | Cys | Phe | Leu | Leu | Glu | Asn | Val | Lys | Gly | Leu | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | His | Asn | Lys | Lys | Ala | Thr | Phe | Asn | Ile | Ile | Ile | Lys | Ala | Leu | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Val | Gly | Tyr | Thr | Thr | Tyr | Tyr | Lys | Ile | Leu | Asn | Ser | Ala | Asp | Phe |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Leu | Ala | Gln | Asn | Arg | Glu | Arg | Leu | Tyr | Ile | Val | Gly | Phe | Arg | Lys |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Asp | Leu | Lys | His | Pro | Phe | Asn | Phe | Pro | Leu | Gly | Leu | Ala | Asn | Asp | Tyr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Tyr | Phe | Lys | Asp | Phe | Leu | Asp | Ala | Asp | Asn | Glu | Cys | Tyr | Leu | Asp | Val |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Ser | Asn | Ala | Ala | Phe | Gln | Arg | Tyr | Leu | His | Asn | Arg | Tyr | Asn | His | Asn |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Arg | Val | Ser | Leu | Glu | Asp | Leu | Leu | Thr | Leu | Glu | Asn | Ala | Val | Leu | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Thr | Arg | Gln | Ser | Asp | Leu | Arg | Leu | Tyr | Ser | Asn | Val | Phe | Pro | Thr | Leu |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Arg | Thr | Ser | Arg | His | Gly | Leu | Phe | Tyr | Thr | Gln | Lys | Gly | Lys | Ile | Lys |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Arg | Leu | Asn | Ala | Ile | Glu | Ser | Leu | Leu | Leu | Gln | Gly | Phe | Pro | Arg | Asp |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Leu | Ile | Ala | Lys | Ile | Lys | Asp | Asn | Pro | Asn | Phe | Lys | Ala | Ser | His | Leu |
|     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| Leu | Ser | Gln | Ala | Gly | Asn | Ala | Met | Ser | Val | Asn | Val | Ile | Ala | Ala | Ile |
|     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |
| Ala | Lys | Gln | Met | Leu | Lys | Ala | Ile |     |     |     |     |     |     |     |     |
| 305 |     |     |     |     | 310 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 30...1436
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

|            |            |           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|------------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AAAATAAAAA | TTATATTAAT | CAAGGAGCG | ATG | AAA | GCG | ATG | GAA | GGT | AAA | ATC | 53  |     |     |     |     |     |
|            |            |           | Met | Lys | Ala | Met | Glu | Gly | Lys | Ile |     |     |     |     |     |     |
|            |            |           | 1   |     |     |     | 5   |     |     |     |     |     |     |     |     |     |
| ATT        | CAG        | GTT       | TTA | GGC | CCT | GTG | GTA | GAT | GTG | GAG | TTT | GAA | TCC | TAT | CTG | 101 |
| Ile        | Gln        | Val       | Leu | Gly | Pro | Val | Val | Asp | Val | Glu | Phe | Glu | Ser | Tyr | Leu |     |
|            | 10         |           |     |     |     | 15  |     |     |     | 20  |     |     |     |     |     |     |







Gly Leu Asp Glu Leu Ser Glu Glu Asp Lys Lys Thr Val Glu Arg Ala  
 385 390 395 400  
 Arg Lys Ile Glu Lys Phe Leu Ser Gln Pro Phe Phe Val Ala Glu Val  
 405 410 415  
 Phe Thr Gly Ser Pro Gly Lys Tyr Val Thr Leu Gln Glu Thr Leu Glu  
 420 425 430  
 Gly Phe Gly Gly Ile Leu Glu Gly Lys Tyr Asp His Ile Pro Glu Asn  
 435 440 445  
 Ala Phe Tyr Met Val Gly Ser Ile Gln Glu Val Leu Glu Lys Ala Lys  
 450 455 460  
 Asn Met Lys Asn Ser  
 465

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 28...2649
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TAAGGAACGC TCTATTTTAG GATAATA ATG ATA ATG AAA CAA GAA CCC ACC ACC | 54  |
| Met Ile Met Lys Gln Glu Pro Thr Thr                               |     |
| 1 5                                                               |     |
| TAC CAA CCA GAA GAG ATA GAA AAA AAG ATT TAT GAA ATT TGC TCT CAT   | 102 |
| Tyr Gln Pro Glu Glu Ile Glu Lys Lys Ile Tyr Glu Ile Cys Ser His   |     |
| 10 15 20 25                                                       |     |
| AGG GGG TAT TTT GAA ATT GAT GGC AAT GAA GCG ATC CAA GAA AAA AAC   | 150 |
| Arg Gly Tyr Phe Glu Ile Asp Gly Asn Glu Ala Ile Gln Glu Lys Asn   |     |
| 30 35 40                                                          |     |
| AAA CGA TTT TGC TTG ATG ATG CCC CCT CCT AAT GTG ACC GGT GTG TTG   | 198 |
| Lys Arg Phe Cys Leu Met Met Pro Pro Pro Asn Val Thr Gly Val Leu   |     |
| 45 50 55                                                          |     |
| CAC ATA GGG CAT GCC CTG ACT TTA AGC TTG CAA GAT ATT TTA GCG CGT   | 246 |
| His Ile Gly His Ala Leu Thr Leu Ser Leu Gln Asp Ile Leu Ala Arg   |     |
| 60 65 70                                                          |     |
| TAC AAA CGC ATG GAT GGG TAT AAG ACT TTG TAT CAG CCC GGG TTG GAT   | 294 |
| Tyr Lys Arg Met Asp Gly Tyr Lys Thr Leu Tyr Gln Pro Gly Leu Asp   |     |
| 75 80 85                                                          |     |
| CAC GCT GGC ATT GCA ACG CAA AAT GTC GTG GAA AAG CAG CTT TTA AGT   | 342 |
| His Ala Gly Ile Ala Thr Gln Asn Val Val Glu Lys Gln Leu Leu Ser   |     |
| 90 95 100 105                                                     |     |









| 795                                                               | 800 | 805 |      |
|-------------------------------------------------------------------|-----|-----|------|
| TTA AGC CCG CTT GTT GCG CGT TTG AAA AAG CAG TTG GAA AAA TTG GAA   |     |     | 2502 |
| Leu Ser Pro Leu Val Ala Arg Leu Lys Lys Gln Leu Glu Lys Leu Glu   |     |     |      |
| 810                                                               | 815 | 820 | 825  |
| AAA GAA AAA TTA AAA CTC AAT TTG CAC AAT GAA AAT TTT GTC AAA AAC   |     |     | 2550 |
| Lys Glu Lys Leu Lys Leu Asn Leu His Asn Glu Asn Phe Val Lys Asn   |     |     |      |
|                                                                   | 830 | 835 | 840  |
| GCG CCT AAA AGC GTG CTA GAA AAA GCT AAA GAG AGT TTA AAA ACG CTT   |     |     | 2598 |
| Ala Pro Lys Ser Val Leu Glu Lys Ala Lys Glu Ser Leu Lys Thr Leu   |     |     |      |
|                                                                   | 845 | 850 | 855  |
| TTA GAA AAA GAA AGT AAA ATT AAG CAA GAA TTG GAC TTG TTA GAA CAA   |     |     | 2646 |
| Leu Glu Lys Glu Ser Lys Ile Lys Gln Glu Leu Asp Leu Leu Glu Gln   |     |     |      |
|                                                                   | 860 | 865 | 870  |
| CCA TAATAAAAGG ATAGAAAATG TTTCAAGCGT TAAGCGATGG GTTTAAAAAC GCGCTC |     |     | 2705 |
| Pro                                                               |     |     |      |
| AATAAAATCC G                                                      |     |     | 2716 |

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 874 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Met | Lys | Gln | Glu | Pro | Thr | Thr | Tyr | Gln | Pro | Glu | Glu | Ile | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Lys | Ile | Tyr | Glu | Ile | Cys | Ser | His | Arg | Gly | Tyr | Phe | Glu | Ile | Asp |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Asn | Glu | Ala | Ile | Gln | Glu | Lys | Asn | Lys | Arg | Phe | Cys | Leu | Met | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Pro | Pro | Asn | Val | Thr | Gly | Val | Leu | His | Ile | Gly | His | Ala | Leu | Thr |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ser | Leu | Gln | Asp | Ile | Leu | Ala | Arg | Tyr | Lys | Arg | Met | Asp | Gly | Tyr |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Thr | Leu | Tyr | Gln | Pro | Gly | Leu | Asp | His | Ala | Gly | Ile | Ala | Thr | Gln |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Val | Val | Glu | Lys | Gln | Leu | Leu | Ser | Gln | Gly | Ile | Lys | Lys | Glu | Asp |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Gly | Arg | Glu | Glu | Phe | Ile | Lys | Lys | Val | Trp | Glu | Trp | Lys | Glu | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Gly | Gly | Ala | Ile | Leu | Glu | Gln | Met | Lys | Arg | Leu | Gly | Val | Ser | Ala |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Phe | Ser | Arg | Thr | Arg | Phe | Thr | Met | Asp | Lys | Gly | Leu | Gln | Arg | Ala |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Val | Lys | Leu | Ala | Phe | Leu | Lys | Trp | Tyr | Glu | Lys | Gly | Leu | Ile | Ile | Gln |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |











(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Met Asn Gln Glu Ile Leu Asp Val Leu Ile Val Gly Ala Gly Pro Gly  
1 5 10 15  
Gly Ile Ala Thr Ala Val Glu Cys Glu Ile Ala Gly Val Lys Lys Val  
20 25 30  
Leu Leu Cys Glu Lys Thr Glu Ser His Ser Gly Met Leu Glu Lys Phe  
35 40 45  
Tyr Lys Ala Gly Lys Arg Ile Asp Lys Asp Tyr Lys Lys Gln Val Val  
50 55 60  
Glu Leu Lys Gly His Ile Pro Phe Lys Asp Ser Phe Lys Glu Glu Thr  
65 70 75 80  
Leu Glu Asn Phe Thr Asn Leu Leu Lys Glu His His Ile Thr Pro Ser  
85 90 95  
Tyr Lys Thr Asp Ile Glu Ser Val Lys Lys Glu Gly Glu Tyr Phe Lys  
100 105 110  
Ile Thr Thr Thr Ser Asn Thr Thr Tyr His Ala Lys Phe Val Val Val  
115 120 125  
Ala Ile Gly Lys Met Gly Gln Pro Asn Arg Pro Thr Ala Tyr Lys Ile  
130 135 140  
Pro Val Ala Leu Ser Lys Gln Val Val Phe Ser Ile Asn Asp Cys Lys  
145 150 155 160  
Glu Asn Glu Lys Thr Leu Val Ile Gly Gly Gly Asn Ser Ala Val Glu  
165 170 175  
Tyr Ala Ile Ala Leu Cys Lys Thr Thr Pro Thr Thr Leu Asn Tyr Arg  
180 185 190  
Lys Lys Glu Phe Ser Arg Ile Asn Glu Asp Asn Ala Lys Asn Leu Gln  
195 200 205  
Glu Val Leu Asn Asn Asn Thr Leu Lys Ser Lys Leu Gly Val Asp Ile  
210 215 220  
Glu Ser Leu Glu Glu Asp Asn Thr Gln Ile Lys Val Asn Phe Thr Asp  
225 230 235 240  
Asn Thr Ser Glu Ser Phe Asp Arg Leu Leu Tyr Ala Ile Gly Gly Ser  
245 250 255  
Thr Pro Leu Glu Phe Phe Lys Arg Cys Ser Leu Glu Leu Asp Pro Ser  
260 265 270  
Thr Asn Ile Pro Val Val Lys Glu Asn Leu Glu Ser Asn Asn Ile Pro  
275 280 285  
Asn Leu Phe Ile Val Gly Asp Ile Leu Phe Lys Ser Gly Ala Ser Ile  
290 295 300  
Ala Thr Ala Leu Asn His Gly Tyr Asp Val Ala Ile Glu Ile Ala Lys  
305 310 315 320  
Arg Leu His Ser

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 704 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 20...670
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATTTTTTAAGG TATAGCGTT ATG GCA TTA GAT TGG GAT TTT ATG TTT CAC TCC | 52  |
| Met Ala Leu Asp Trp Asp Phe Met Phe His Ser                       |     |
| 1 5 10                                                            |     |
| ATC CCT GCG TTT TTT AAG GGG TTA GAA CTC ACG CTT TAT ATT TCT TTC   | 100 |
| Ile Pro Ala Phe Phe Lys Gly Leu Glu Leu Thr Leu Tyr Ile Ser Phe   |     |
| 15 20 25                                                          |     |
| TTT GGG ATT TTG CTC TCT CTT TTG GTG GGG TTT TTG TGC GCG ATC GTT   | 148 |
| Phe Gly Ile Leu Leu Ser Leu Leu Val Gly Phe Leu Cys Ala Ile Val   |     |
| 30 35 40                                                          |     |
| TTG TAT TTT AAA ACG CGC TTT CTC TCT CCT GTT GTC TAT ATC TAT GGC   | 196 |
| Leu Tyr Phe Lys Thr Arg Phe Leu Ser Pro Val Tyr Ile Tyr Gly       |     |
| 45 50 55                                                          |     |
| GAA ATC GCT AGG AAC ACG CCC CTG CTC ATC CAG CTT TTC TTT TTG TAT   | 244 |
| Glu Ile Ala Arg Asn Thr Pro Leu Leu Ile Gln Leu Phe Phe Leu Tyr   |     |
| 60 65 70 75                                                       |     |
| TAC GGG TTG AAT GAA ATC GGT TTG AGC GCT TTA GAG TGC GCG ATT TTA   | 292 |
| Tyr Gly Leu Asn Glu Ile Gly Leu Ser Ala Leu Glu Cys Ala Ile Leu   |     |
| 80 85 90                                                          |     |
| GCG TTA GGG TTT TTG GGT GGG GGG TAT ATG AGT CAA AGT TTT TTG CTT   | 340 |
| Ala Leu Gly Phe Leu Gly Gly Gly Tyr Met Ser Gln Ser Phe Leu Leu   |     |
| 95 100 105                                                        |     |
| GGG TTT AAG AGC CTA GCT TCC ATT CAA AGA GAA AGC GCT TTG AGT TTG   | 388 |
| Gly Phe Lys Ser Leu Ala Ser Ile Gln Arg Glu Ser Ala Leu Ser Leu   |     |
| 110 115 120                                                       |     |
| GGG TTT AGC CCT TTG AAA ATG ATG TAT TAT ATT ATT CTG CCT CAA AGT   | 436 |
| Gly Phe Ser Pro Leu Lys Met Met Tyr Tyr Ile Ile Leu Pro Gln Ser   |     |
| 125 130 135                                                       |     |
| TTA AGC GTT TCT ATG CCT TCC ATA GGG GCG AAT GTG ATT TTT TTA CTC   | 484 |
| Leu Ser Val Ser Met Pro Ser Ile Gly Ala Asn Val Ile Phe Leu Leu   |     |
| 140 145 150 155                                                   |     |
| AAA GAA ACT TCG GTG GTG GGC GCG ATA GCC CTA ACC GAT ATT ATG TTT   | 532 |
| Lys Glu Thr Ser Val Val Gly Ala Ile Ala Leu Thr Asp Ile Met Phe   |     |
| 160 165 170                                                       |     |
| GTG GCG AAA GAT TTT ATT GGC ATT TAT TAT AAA ACG ACT GAA AGC CTT   | 580 |
| Val Ala Lys Asp Phe Ile Gly Ile Tyr Tyr Lys Thr Thr Glu Ser Leu   |     |
| 175 180 185                                                       |     |
| TTG ATG TTA AGC CTC ACT TAT TTG ATC GCT TTA CTC CCT TTA AGC GTT   | 628 |



Leu Met Leu Ser Leu Thr Tyr Leu Ile Ala Leu Leu Pro Leu Ser Val  
 190 195 200

TTG TTT GTG ATC TTA GAG CGT TTC TTT AAA AAG AAA GTG GCT TAAAATGGG 679  
 Leu Phe Val Ile Leu Glu Arg Phe Phe Lys Lys Lys Val Ala  
 205 210 215

AGTTTTACTA GAATTAGACA ACCTT 704

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Asp | Trp | Asp | Phe | Met | Phe | His | Ser | Ile | Pro | Ala | Phe | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Gly | Leu | Glu | Leu | Thr | Leu | Tyr | Ile | Ser | Phe | Phe | Gly | Ile | Leu | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Leu | Leu | Val | Gly | Phe | Leu | Cys | Ala | Ile | Val | Leu | Tyr | Phe | Lys | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Phe | Leu | Ser | Pro | Val | Val | Tyr | Ile | Tyr | Gly | Glu | Ile | Ala | Arg | Asn |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Thr | Pro | Leu | Leu | Ile | Gln | Leu | Phe | Phe | Leu | Tyr | Tyr | Gly | Leu | Asn | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Gly | Leu | Ser | Ala | Leu | Glu | Cys | Ala | Ile | Leu | Ala | Leu | Gly | Phe | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Gly | Gly | Tyr | Met | Ser | Gln | Ser | Phe | Leu | Leu | Gly | Phe | Lys | Ser | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Ser | Ile | Gln | Arg | Glu | Ser | Ala | Leu | Ser | Leu | Gly | Phe | Ser | Pro | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Met | Met | Tyr | Tyr | Ile | Ile | Leu | Pro | Gln | Ser | Leu | Ser | Val | Ser | Met |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Ser | Ile | Gly | Ala | Asn | Val | Ile | Phe | Leu | Leu | Lys | Glu | Thr | Ser | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Val | Gly | Ala | Ile | Ala | Leu | Thr | Asp | Ile | Met | Phe | Val | Ala | Lys | Asp | Phe |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Gly | Ile | Tyr | Tyr | Lys | Thr | Thr | Glu | Ser | Leu | Leu | Met | Leu | Ser | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Tyr | Leu | Ile | Ala | Leu | Leu | Pro | Leu | Ser | Val | Leu | Phe | Val | Ile | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | Arg | Phe | Phe | Lys | Lys | Lys | Val | Ala |     |     |     |     |     |     |     |
|     |     | 210 |     |     |     | 215 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 737 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 31...699  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

|                                                                 |                                 |    |
|-----------------------------------------------------------------|---------------------------------|----|
| AGCGTTTCTT TAAAAAGAAA GTGGCTTAAA                                | ATG GGA GTT TTA CTA GAA TTA GAC | 54 |
|                                                                 | Met Gly Val Leu Leu Glu Leu Asp |    |
|                                                                 | 1 5                             |    |
| AAC CTT AAG CGT TTG TTA GAA GGG TTT GAA ACC ACT CTT TTG ATC GCT | 102                             |    |
| Asn Leu Lys Arg Leu Leu Glu Gly Phe Glu Thr Thr Leu Leu Ile Ala |                                 |    |
| 10 15 20                                                        |                                 |    |
| CTT AGC TCT GCA ATG ATT TCA ATC ATT GTT GGA ATG CTT TTG GGG AGC | 150                             |    |
| Leu Ser Ser Ala Met Ile Ser Ile Ile Val Gly Met Leu Leu Gly Ser |                                 |    |
| 25 30 35 40                                                     |                                 |    |
| TTG ATG GCG TTT GGT TCT CAA ATA GTG GTT TTG GCG TGT CGT GTG TAT | 198                             |    |
| Leu Met Ala Phe Gly Ser Gln Ile Val Val Leu Ala Cys Arg Val Tyr |                                 |    |
| 45 50 55                                                        |                                 |    |
| TTA GAA AGC ATT CGC ATC ATC CCG CTT TTA GCA TGG CTT TTT ATT GTG | 246                             |    |
| Leu Glu Ser Ile Arg Ile Ile Pro Leu Leu Ala Trp Leu Phe Ile Val |                                 |    |
| 60 65 70                                                        |                                 |    |
| TAT TTC GGG TTA GCG AGC TGG TTT GAT TTG CAT ATT AGC GCG GTT TTG | 294                             |    |
| Tyr Phe Gly Leu Ala Ser Trp Phe Asp Leu His Ile Ser Ala Val Leu |                                 |    |
| 75 80 85                                                        |                                 |    |
| GCA AGC GTT ATT GTT TTT AGC TTG TGG GGT GGC GCT GAA ATG ATG GAT | 342                             |    |
| Ala Ser Val Ile Val Phe Ser Leu Trp Gly Gly Ala Glu Met Met Asp |                                 |    |
| 90 95 100                                                       |                                 |    |
| TTA ACT AGG GGG GTT TTA ACT TCC GTG AGC AAA CAC CAA ATA GAA AGC | 390                             |    |
| Leu Thr Arg Gly Val Leu Thr Ser Val Ser Lys His Gln Ile Glu Ser |                                 |    |
| 105 110 115 120                                                 |                                 |    |
| GCT CTG GCT TTA GGC TTA GAT TCA AAA AAG GTG ATT TTT AAT ATT ATT | 438                             |    |
| Ala Leu Ala Leu Gly Leu Asp Ser Lys Lys Val Ile Phe Asn Ile Ile |                                 |    |
| 125 130 135                                                     |                                 |    |
| TTC CCT CAA AGC TTT TTG TCT TTA TTG CCC TCA AGC CTT AAT TTG TTC | 486                             |    |
| Phe Pro Gln Ser Phe Leu Ser Leu Leu Pro Ser Ser Leu Asn Leu Phe |                                 |    |
| 140 145 150                                                     |                                 |    |
| ACG CGC ATG ATC AAA ACC ACG GCT TTA GTT TCT CTC ATT GGA GCG ATT | 534                             |    |
| Thr Arg Met Ile Lys Thr Thr Ala Leu Val Ser Leu Ile Gly Ala Ile |                                 |    |
| 155 160 165                                                     |                                 |    |
| GAT TTG CTA AAA GTG GGC CAG CAA ATC ATA GAG CTT AAC CTC TTA CGC | 582                             |    |
| Asp Leu Leu Lys Val Gly Gln Gln Ile Ile Glu Leu Asn Leu Leu Arg |                                 |    |
| 170 175 180                                                     |                                 |    |

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATG CCT AAT GCG AGC TTT GTG GTT TAT GGC GTT ATC TTA ATG TTT TAT   | 630 |
| Met Pro Asn Ala Ser Phe Val Val Tyr Gly Val Ile Leu Met Phe Tyr   |     |
| 185 190 195 200                                                   |     |
| TTT AGT TTA TGC TAT AGT TTG AGC CTG TAT AGT TCC TAT TTA GAA AAA   | 678 |
| Phe Ser Leu Cys Tyr Ser Leu Ser Leu Tyr Ser Ser Tyr Leu Glu Lys   |     |
| 205 210 215                                                       |     |
| AAA TTC CAA CAC ATT AGA GGG TAAAATGAGC GTGATTTTAG AAACCAAAGG GTTA | 733 |
| Lys Phe Gln His Ile Arg Gly                                       |     |
| 220                                                               |     |
| AAAA                                                              | 737 |

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Gly Val Leu Leu Glu Leu Asp Asn Leu Lys Arg Leu Leu Glu Gly |  |
| 1 5 10 15                                                       |  |
| Phe Glu Thr Thr Leu Leu Ile Ala Leu Ser Ser Ala Met Ile Ser Ile |  |
| 20 25 30                                                        |  |
| Ile Val Gly Met Leu Leu Gly Ser Leu Met Ala Phe Gly Ser Gln Ile |  |
| 35 40 45                                                        |  |
| Val Val Leu Ala Cys Arg Val Tyr Leu Glu Ser Ile Arg Ile Ile Pro |  |
| 50 55 60                                                        |  |
| Leu Leu Ala Trp Leu Phe Ile Val Tyr Phe Gly Leu Ala Ser Trp Phe |  |
| 65 70 75 80                                                     |  |
| Asp Leu His Ile Ser Ala Val Leu Ala Ser Val Ile Val Phe Ser Leu |  |
| 85 90 95                                                        |  |
| Trp Gly Gly Ala Glu Met Met Asp Leu Thr Arg Gly Val Leu Thr Ser |  |
| 100 105 110                                                     |  |
| Val Ser Lys His Gln Ile Glu Ser Ala Leu Ala Leu Gly Leu Asp Ser |  |
| 115 120 125                                                     |  |
| Lys Lys Val Ile Phe Asn Ile Ile Phe Pro Gln Ser Phe Leu Ser Leu |  |
| 130 135 140                                                     |  |
| Leu Pro Ser Ser Leu Asn Leu Phe Thr Arg Met Ile Lys Thr Thr Ala |  |
| 145 150 155 160                                                 |  |
| Leu Val Ser Leu Ile Gly Ala Ile Asp Leu Leu Lys Val Gly Gln Gln |  |
| 165 170 175                                                     |  |
| Ile Ile Glu Leu Asn Leu Leu Arg Met Pro Asn Ala Ser Phe Val Val |  |
| 180 185 190                                                     |  |
| Tyr Gly Val Ile Leu Met Phe Tyr Phe Ser Leu Cys Tyr Ser Leu Ser |  |
| 195 200 205                                                     |  |
| Leu Tyr Ser Ser Tyr Leu Glu Lys Lys Phe Gln His Ile Arg Gly     |  |
| 210 215 220                                                     |  |

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 807 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 31...774  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

|                                                                 |                                 |     |
|-----------------------------------------------------------------|---------------------------------|-----|
| AAAAAAATT CCAACACATT AGAGGGTAAA                                 | ATG AGC GTG ATT TTA GAA ACC AAA | 54  |
|                                                                 | Met Ser Val Ile Leu Glu Thr Lys |     |
|                                                                 | 1 5                             |     |
| GGG TTA AAA AAA ACC TAT CAA AAC CAT TTG GTT TTA GAC GGC ATC AAT |                                 | 102 |
| Gly Leu Lys Lys Thr Tyr Gln Asn His Leu Val Leu Asp Gly Ile Asn |                                 |     |
| 10 15 20                                                        |                                 |     |
| TTC ACT TTA AAT AAG GGT GAA GTG GCA GTG ATT TTA GGG CCT AGC GGG |                                 | 150 |
| Phe Thr Leu Asn Lys Gly Glu Val Ala Val Ile Leu Gly Pro Ser Gly |                                 |     |
| 25 30 35 40                                                     |                                 |     |
| TGC GGG AAA AGC ACT TTT TTA AAA TGC CTA AAC GGG CTT GAA AAG ATT |                                 | 198 |
| Cys Gly Lys Ser Thr Phe Leu Lys Cys Leu Asn Gly Leu Glu Lys Ile |                                 |     |
| 45 50 55                                                        |                                 |     |
| AAT GAA GGT GAA ATC CTT TTT GAA AAC ACT AAC CTT AAC AAT AAG GCC |                                 | 246 |
| Asn Glu Gly Glu Ile Leu Phe Glu Asn Thr Asn Leu Asn Asn Lys Ala |                                 |     |
| 60 65 70                                                        |                                 |     |
| ACT AAC TGG AAT CAA ATG CGC CAA AAA ATA GGC ATG GTG TTT CAA AAT |                                 | 294 |
| Thr Asn Trp Asn Gln Met Arg Gln Lys Ile Gly Met Val Phe Gln Asn |                                 |     |
| 75 80 85                                                        |                                 |     |
| TAT GAA TTG TTC CCG CAT TTA AAT GTG TTA GAT AAT ATC TTA CTC GCT |                                 | 342 |
| Tyr Glu Leu Phe Pro His Leu Asn Val Leu Asp Asn Ile Leu Leu Ala |                                 |     |
| 90 95 100                                                       |                                 |     |
| CCT ATG AAA GTG CAA AAA CGA TCC AAA GAT GAG GTT ATT TCT CAA GCC |                                 | 390 |
| Pro Met Lys Val Gln Lys Arg Ser Lys Asp Glu Val Ile Ser Gln Ala |                                 |     |
| 105 110 115 120                                                 |                                 |     |
| ATA GAG CTT TTA AAG CGA GTG GGT TTG GAG CAT AAA CAA CAA GCT TAC |                                 | 438 |
| Ile Glu Leu Leu Lys Arg Val Gly Leu Glu His Lys Gln Gln Ala Tyr |                                 |     |
| 125 130 135                                                     |                                 |     |
| CCT AAA GAA TTG AGC GGC GGA CAA AAA CAA CGA GTA GCG ATC GTG CGC |                                 | 486 |
| Pro Lys Glu Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Ile Val Arg |                                 |     |
| 140 145 150                                                     |                                 |     |
| TCT TTA TGC ATG CGA CCA AAA ATC ATG CTT TTT GAT GAA GTA ACC GCC |                                 | 534 |
| Ser Leu Cys Met Arg Pro Lys Ile Met Leu Phe Asp Glu Val Thr Ala |                                 |     |
| 155 160 165                                                     |                                 |     |



```

Val Ile Val Thr His Glu Met Lys Phe Ala Gln Lys Ile Ala His Lys
 195 200 205
Ile Val Phe Phe Asp Ser Gly Lys Ile Ala Glu Glu Asn Asn Ala Lys
 210 215 220
Glu Phe Phe Asn His Pro Lys Ser Gln Arg Ala Gln Lys Phe Leu Glu
 225 230 235 240
Thr Phe His Phe Leu Gly Ser Cys
 245

```

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...561
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

```

AAGGATTTGT TG ATG AGT TAT TTT TAT AAG CAC TGT TTG AAA TTT TCG TTG 51
 Met Ser Tyr Phe Tyr Lys His Cys Leu Lys Phe Ser Leu
 1 5 10

GTT GGG TTG CTA GGG CTT TTG AGC GTT CAG CTT GAC GCT AGG AGT TTT 99
Val Gly Leu Leu Gly Leu Leu Ser Val Gln Leu Asp Ala Arg Ser Phe
 15 20 25

GTT GAT GGG GAT TTA GAC ATT CAG AAA TTC AGC TAT GAA GAT TCT CTA 147
Val Asp Gly Asp Leu Asp Ile Gln Lys Phe Ser Tyr Glu Asp Ser Leu
 30 35 40 45

CTT AAA AAG GGA GAC CCT AAT GGC GTG CAT AAA GTG CAG GTG CGA GAT 195
Leu Lys Lys Gly Asp Pro Asn Gly Val His Lys Val Gln Val Arg Asp
 50 55 60

TAT AAA GGC AAA ATG CAA GAA GCT GAG ATC CAC TCA GAA ATA CGC ATT 243
Tyr Lys Gly Lys Met Gln Glu Ala Glu Ile His Ser Glu Ile Arg Ile
 65 70 75

GCG CTT AAA CCG GGG GTT AAA AAA GAA GTT AAA AAA GGC AAG ATT TAT 291
Ala Leu Lys Pro Gly Val Lys Lys Glu Val Lys Lys Gly Lys Ile Tyr
 80 85 90

AGC GCT CAA ATC AAT GAT GGC ATG TGC TAT GCT TTT AGA ATG CTC CAA 339
Ser Ala Gln Ile Asn Asp Gly Met Cys Tyr Ala Phe Arg Met Leu Gln
 95 100 105

ACC GGC GAT AAT ACC ACA GGC CTT GAT TCT AAA GAG TTC CCC AAG CAA 387
Thr Gly Asp Asn Thr Thr Gly Leu Asp Ser Lys Glu Phe Pro Lys Gln
 110 115 120 125

```

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AGT CGT GAG AAA AAG GGC CGA GTG ATC ACT TTA ATC GGT AAA GGT GAA   | 435 |
| Ser Arg Glu Lys Lys Gly Arg Val Ile Thr Leu Ile Gly Lys Gly Glu   |     |
| 130 135 140                                                       |     |
| GTG CCT TAT CTT ATT TTA GAA ACC GAT TGC CAA GTG GGT GAT ATT GCA   | 483 |
| Val Pro Tyr Leu Ile Leu Glu Thr Asp Cys Gln Val Gly Asp Ile Ala   |     |
| 145 150 155                                                       |     |
| AAG ATC TCT TTG GTG GGT AAT TTT GAT GGC ACT GGG TTT CTT ACG GAA   | 531 |
| Lys Ile Ser Leu Val Gly Asn Phe Asp Gly Thr Gly Phe Leu Thr Glu   |     |
| 160 165 170                                                       |     |
| TAT AAA TTC AAA GAC GCT AAA CCC ATT TAC TAGTCTTTAT TCTTCGCTTC ATT | 584 |
| Tyr Lys Phe Lys Asp Ala Lys Pro Ile Tyr                           |     |
| 175 180                                                           |     |
| CTTAA                                                             | 589 |

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Tyr | Phe | Tyr | Lys | His | Cys | Leu | Lys | Phe | Ser | Leu | Val | Gly | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Gly | Leu | Leu | Ser | Val | Gln | Leu | Asp | Ala | Arg | Ser | Phe | Val | Asp | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Leu | Asp | Ile | Gln | Lys | Phe | Ser | Tyr | Glu | Asp | Ser | Leu | Leu | Lys | Lys |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Gly | Asp | Pro | Asn | Gly | Val | His | Lys | Val | Gln | Val | Arg | Asp | Tyr | Lys | Gly |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Lys | Met | Gln | Glu | Ala | Glu | Ile | His | Ser | Glu | Ile | Arg | Ile | Ala | Leu | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Gly | Val | Lys | Lys | Glu | Val | Lys | Lys | Gly | Lys | Ile | Tyr | Ser | Ala | Gln |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ile | Asn | Asp | Gly | Met | Cys | Tyr | Ala | Phe | Arg | Met | Leu | Gln | Thr | Gly | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Thr | Thr | Gly | Leu | Asp | Ser | Lys | Glu | Phe | Pro | Lys | Gln | Ser | Arg | Glu |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Lys | Lys | Gly | Arg | Val | Ile | Thr | Leu | Ile | Gly | Lys | Gly | Glu | Val | Pro | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Ile | Leu | Glu | Thr | Asp | Cys | Gln | Val | Gly | Asp | Ile | Ala | Lys | Ile | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Leu | Val | Gly | Asn | Phe | Asp | Gly | Thr | Gly | Phe | Leu | Thr | Glu | Tyr | Lys | Phe |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Lys | Asp | Ala | Lys | Pro | Ile | Tyr |     |     |     |     |     |     |     |     |     |
|     |     |     | 180 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 925 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 30...875  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

|          |     |     |      |      |       |     |     |     |     |     |     |     |     |     |     |     |
|----------|-----|-----|------|------|-------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GGAATTTT | GGT | GCT | ACTC | CTTT | CTCGT | ATG | GGT | ATC | GCT | TTT | GCC | CAC | TCT |     | 53  |     |
|          |     |     |      |      |       | Met | Gly | Ile | Ala | Phe | Ala | His | Ser |     |     |     |
|          |     |     |      |      |       | 1   |     |     |     | 5   |     |     |     |     |     |     |
| ATT      | TTT | TGG | TCC  | ATC  | ACG   | GCT | TCT | TTA | GTC | ATT | CGT | GTC | GCG | CCA | AGA | 101 |
| Ile      | Phe | Trp | Ser  | Ile  | Thr   | Ala | Ser | Leu | Val | Ile | Arg | Val | Ala | Pro | Arg |     |
| 10       |     |     |      |      |       | 15  |     |     |     | 20  |     |     |     |     |     |     |
| AAT      | AAA | AAA | CAA  | CAG  | GCC   | TTA | GGG | CTG | TTA | GCG | TTA | GGG | AGT | TCG | TTA | 149 |
| Asn      | Lys | Lys | Gln  | Gln  | Ala   | Leu | Gly | Leu | Leu | Ala | Leu | Gly | Ser | Ser | Leu |     |
| 25       |     |     |      |      | 30    |     |     |     |     | 35  |     |     |     |     | 40  |     |
| GCG      | ATG | ATT | TTA  | GGG  | TTG   | CCG | CTT | GGG | AGG | ATC | ATT | GGG | CAA | ATT | CTA | 197 |
| Ala      | Met | Ile | Leu  | Gly  | Leu   | Pro | Leu | Gly | Arg | Ile | Ile | Gly | Gln | Ile | Leu |     |
|          |     |     |      | 45   |       |     |     | 50  |     |     |     |     |     | 55  |     |     |
| GAT      | TGG | CGT | TCC  | ACT  | TTT   | GGC | GTG | ATC | GGG | GGC | GTT | GCG | ACC | CTT | ATA | 245 |
| Asp      | Trp | Arg | Ser  | Thr  | Phe   | Gly | Val | Ile | Gly | Gly | Val | Ala | Thr | Leu | Ile |     |
|          |     |     | 60   |      |       |     |     | 65  |     |     |     |     | 70  |     |     |     |
| GCG      | TTG | CTT | ATG  | TGG  | AAA   | TTG | CTC | CCG | CAT | CTA | CCC | AGT | AGA | AAC | GCA | 293 |
| Ala      | Leu | Leu | Met  | Trp  | Lys   | Leu | Leu | Pro | His | Leu | Pro | Ser | Arg | Asn | Ala |     |
|          | 75  |     |      |      |       | 80  |     |     |     |     |     | 85  |     |     |     |     |
| GGC      | ACG | CTC | GCA  | AGT  | GTC   | CCT | GTA | TTA | ATG | AAA | CGG | CCG | CTT | TTA | ATG | 341 |
| Gly      | Thr | Leu | Ala  | Ser  | Val   | Pro | Val | Leu | Met | Lys | Arg | Pro | Leu | Leu | Met |     |
|          | 90  |     |      |      |       | 95  |     |     |     | 100 |     |     |     |     |     |     |
| GGG      | ATT | TAT | TTG  | CTT  | GTG   | ATC | ATG | GTC | ATC | TCT | GGG | CAT | TTC | ACC | ACT | 389 |
| Gly      | Ile | Tyr | Leu  | Leu  | Val   | Ile | Met | Val | Ile | Ser | Gly | His | Phe | Thr | Thr |     |
| 105      |     |     |      |      | 110   |     |     |     |     | 115 |     |     |     |     | 120 |     |
| TAT      | AGT | TAT | ATT  | GAG  | CCT   | TTT | ATC | ATT | CAA | ATC | AGC | CAA | TTT | TCT | CCT | 437 |
| Tyr      | Ser | Tyr | Ile  | Glu  | Pro   | Phe | Ile | Ile | Gln | Ile | Ser | Gln | Phe | Ser | Pro |     |
|          |     |     |      | 125  |       |     |     |     | 130 |     |     |     |     | 135 |     |     |
| GAC      | ATT | ACA | ACG  | CTA  | ATG   | TTG | TTT | GTG | TTT | GGG | TTA | GCG | GGC | GTG | GTG | 485 |
| Asp      | Ile | Thr | Thr  | Leu  | Met   | Leu | Phe | Val | Phe | Gly | Leu | Ala | Gly | Val | Val |     |
|          |     |     | 140  |      |       |     |     | 145 |     |     |     |     | 150 |     |     |     |
| GGG      | AGT | TTT | TTG  | TTC  | GGC   | CGT | TTG | TAT | GCA | AAA | AAT | TCA | AGA | AAA | TTT | 533 |
| Gly      | Ser | Phe | Leu  | Phe  | Gly   | Arg | Leu | Tyr | Ala | Lys | Asn | Ser | Arg | Lys | Phe |     |
|          | 155 |     |      |      |       |     | 160 |     |     |     |     | 165 |     |     |     |     |



|                                                                                                                                                       |     |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| ATC GCT TTT GCG ATG GTT TTA GTC ATT TGC CCG CAA CTC TTG CTT TTT<br>Ile Ala Phe Ala Met Val Leu Val Ile Cys Pro Gln Leu Leu Leu Phe<br>170 175 180     | 581 |
| GTG TTT AAA AAC TTA GAG TGG GTG GTT TTC TTG CAA ATT TTC TTA TGG<br>Val Phe Lys Asn Leu Glu Trp Val Val Phe Leu Gln Ile Phe Leu Trp<br>185 190 195 200 | 629 |
| GGG ATT GGG ATC ACT TCG CTT GGG ATT TCC TTG CAA ATG AGG GTG TTG<br>Gly Ile Gly Ile Thr Ser Leu Gly Ile Ser Leu Gln Met Arg Val Leu<br>205 210 215     | 677 |
| CAG CTT GCG CCG GAT GCC ACG GAT GTT GCG AGT GCG ATT TAC TCA GGG<br>Gln Leu Ala Pro Asp Ala Thr Asp Val Ala Ser Ala Ile Tyr Ser Gly<br>220 225 230     | 725 |
| AGC TAT AAT GTG GGG ATT GGA TCA GGA GCG CTG TTT GGC AGT ATT GTG<br>Ser Tyr Asn Val Gly Ile Gly Ser Gly Ala Leu Phe Gly Ser Ile Val<br>235 240 245     | 773 |
| ATC CAC CAA CTA GGG CTA GGA TAT ATT GGC TTT GTG GGT GGG GCT TTA<br>Ile His Gln Leu Gly Leu Gly Tyr Ile Gly Phe Val Gly Gly Ala Leu<br>250 255 260     | 821 |
| GGT TTG TTG GCG CTC TTT TGG CTT AGA TTC ATT ACG ATA AAG TTT AAA<br>Gly Leu Leu Ala Leu Phe Trp Leu Arg Phe Ile Thr Ile Lys Phe Lys<br>265 270 275 280 | 869 |
| AAA ACA TAAAGAGCGT TAAAAGGATT AGCCCAATAA AGGAGAATCC CTTTCGCACT<br>Lys Thr                                                                             | 925 |

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

|                                                                                |
|--------------------------------------------------------------------------------|
| Met Gly Ile Ala Phe Ala His Ser Ile Phe Trp Ser Ile Thr Ala Ser<br>1 5 10 15   |
| Leu Val Ile Arg Val Ala Pro Arg Asn Lys Lys Gln Gln Ala Leu Gly<br>20 25 30    |
| Leu Leu Ala Leu Gly Ser Ser Leu Ala Met Ile Leu Gly Leu Pro Leu<br>35 40 45    |
| Gly Arg Ile Ile Gly Gln Ile Leu Asp Trp Arg Ser Thr Phe Gly Val<br>50 55 60    |
| Ile Gly Gly Val Ala Thr Leu Ile Ala Leu Leu Met Trp Lys Leu Leu<br>65 70 75 80 |
| Pro His Leu Pro Ser Arg Asn Ala Gly Thr Leu Ala Ser Val Pro Val<br>85 90 95    |
| Leu Met Lys Arg Pro Leu Leu Met Gly Ile Tyr Leu Leu Val Ile Met                |







|                                                                 |                     |                     |     |     |
|-----------------------------------------------------------------|---------------------|---------------------|-----|-----|
| 210                                                             |                     | 215                 |     | 220 |
| Lys Met Leu His Glu Thr                                         | His Lys Ile Met Gly | Val Asp Phe Pro Ile |     |     |
| 225                                                             | 230                 | 235                 | 240 |     |
| Ser Ala Thr Cys Val Arg Val Pro Val Leu Arg Ser His Ser Glu Ser |                     |                     |     |     |
|                                                                 | 245                 | 250                 | 255 |     |
| Leu Ser Ile Ala Phe Glu Lys Glu Phe Asp Leu Lys Glu Val Tyr Glu |                     |                     |     |     |
|                                                                 | 260                 | 265                 | 270 |     |
| Val Leu Lys Asn Ala Pro Ser Val Ala Val Cys Asp Asp Pro Ser His |                     |                     |     |     |
|                                                                 | 275                 | 280                 | 285 |     |
| Asn Leu Tyr Pro Thr Pro Leu Lys Ala Ser His Thr Asp Ser Val Phe |                     |                     |     |     |
|                                                                 | 290                 | 295                 | 300 |     |
| Ile Gly Arg Leu Arg Lys Asp Leu Phe Asp Lys Lys Thr Leu His Gly |                     |                     |     |     |
| 305                                                             | 310                 | 315                 | 320 |     |
| Phe Cys Val Ala Asp Gln Leu Arg Val Gly Ala Ala Thr Asn Ala Leu |                     |                     |     |     |
|                                                                 | 325                 | 330                 | 335 |     |
| Lys Ile Ala Leu His Tyr Ile Lys Asn Ala                         |                     |                     |     |     |
|                                                                 | 340                 | 345                 |     |     |

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...1359
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| TAAAATTTTA GCATACAAAT ACAAGGAAAT GGA ATG ATT ACC CCT AAA GTG TTG | 54  |
| Met Ile Thr Pro Lys Val Leu                                      |     |
| 1 5                                                              |     |
| AGC GGG TTT AAA GAC CGC TTG CCT AAA GAT GCG ATA CAA AAA GCC CAG  | 102 |
| Ser Gly Phe Lys Asp Arg Leu Pro Lys Asp Ala Ile Gln Lys Ala Gln  |     |
| 10 15 20                                                         |     |
| TTG CTT GCG AAA GTT TCA GTC GTG TTT CAA AGT TTT GGT TTT GTG CCG  | 150 |
| Leu Leu Ala Lys Val Ser Val Val Phe Gln Ser Phe Gly Phe Val Pro  |     |
| 25 30 35                                                         |     |
| ATT GAA ACC CCT CAT TTG GAA TAC GCT CAA ACG TTA TTG CCT GAT GCG  | 198 |
| Ile Glu Thr Pro His Leu Glu Tyr Ala Gln Thr Leu Leu Pro Asp Ala  |     |
| 40 45 50 55                                                      |     |
| AGC AGT GAT ATT CAA AAA GAA ATT TAT CGT TTT AAA GAC CAT GGG GAT  | 246 |
| Ser Ser Asp Ile Gln Lys Glu Ile Tyr Arg Phe Lys Asp His Gly Asp  |     |
| 60 65 70                                                         |     |
| AGA GAT GTG GCT TTA AGG TTT GAT TTG ACT GTG CCA TTA GCC CGC TTT  | 294 |
| Arg Asp Val Ala Leu Arg Phe Asp Leu Thr Val Pro Leu Ala Arg Phe  |     |

| 75  |     |     |     |     |     | 80  |     |     |     |     |     | 85  |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| GTC | TCT | TTG | CAC | CAC | CAA | ACG | CTA | GGC | ATG | CCC | TTT | AAA | CGC | TAC | GCT | 342 |  |  |
| Val | Ser | Leu | His | His | Gln | Thr | Leu | Gly | Met | Pro | Phe | Lys | Arg | Tyr | Ala |     |  |  |
|     |     | 90  |     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     |  |  |
| ATA | GGC | AAT | GTC | TTT | AGG | GGC | GAA | AGG | GCG | CAA | AAA | GGG | CGT | TAT | AGG | 390 |  |  |
| Ile | Gly | Asn | Val | Phe | Arg | Gly | Glu | Arg | Ala | Gln | Lys | Gly | Arg | Tyr | Arg |     |  |  |
|     | 105 |     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     |     |  |  |
| GAA | TTT | ACG | CAA | TGC | GAT | TTT | GAT | TTT | ATA | GGG | AGC | GAG | AGT | TTG | GTG | 438 |  |  |
| Glu | Phe | Thr | Gln | Cys | Asp | Phe | Asp | Phe | Ile | Gly | Ser | Glu | Ser | Leu | Val |     |  |  |
| 120 |     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |     |  |  |
| TGC | GAT | GCT | GAG | ATC | ATT | CAA | GTG | ATT | GTC | GCT | TCT | TTA | AAA | GCC | CTA | 486 |  |  |
| Cys | Asp | Ala | Glu | Ile | Ile | Gln | Val | Ile | Val | Ala | Ser | Leu | Lys | Ala | Leu |     |  |  |
|     |     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |     |     |  |  |
| GAT | TTA | GAA | GAT | TTT | TGC | GTC | TCT | ATC | AAC | CAC | AGA | AAA | ATT | TTG | AAC | 534 |  |  |
| Asp | Leu | Glu | Asp | Phe | Cys | Val | Ser | Ile | Asn | His | Arg | Lys | Ile | Leu | Asn |     |  |  |
|     |     |     | 155 |     |     |     |     | 160 |     |     |     |     | 165 |     |     |     |  |  |
| GGG | ATA | TGC | GAA | TAT | TTT | GGG | ATC | TCT | CAA | GTG | AAT | GAA | GCG | TTG | CGC | 582 |  |  |
| Gly | Ile | Cys | Glu | Tyr | Phe | Gly | Ile | Ser | Gln | Val | Asn | Glu | Ala | Leu | Arg |     |  |  |
|     |     | 170 |     |     |     | 175 |     |     |     |     |     | 180 |     |     |     |     |  |  |
| ATT | GTG | GAT | AAA | TTG | GAA | AAA | ATT | GGC | TTG | AAT | GGG | GTT | GAA | GAA | GAA | 630 |  |  |
| Ile | Val | Asp | Lys | Leu | Glu | Lys | Ile | Gly | Leu | Asn | Gly | Val | Glu | Glu | Glu |     |  |  |
|     | 185 |     |     |     |     | 190 |     |     |     |     | 195 |     |     |     |     |     |  |  |
| TTA | AAA | AAA | GAG | TGC | GGT | TTA | AAT | TCA | AAC | ACC | ATT | AAA | GAG | CTT | TTA | 678 |  |  |
| Leu | Lys | Lys | Glu | Cys | Gly | Leu | Asn | Ser | Asn | Thr | Ile | Lys | Glu | Leu | Leu |     |  |  |
| 200 |     |     |     |     | 205 |     |     |     |     | 210 |     |     |     |     | 215 |     |  |  |
| GAA | TTA | ATT | CAA | ATC | AAA | CAA | AAC | GAT | TTA | AGC | CAT | GCG | GAA | TTT | TTT | 726 |  |  |
| Glu | Leu | Ile | Gln | Ile | Lys | Gln | Asn | Asp | Leu | Ser | His | Ala | Glu | Phe | Phe |     |  |  |
|     |     |     |     | 220 |     |     |     |     | 225 |     |     |     |     | 230 |     |     |  |  |
| GAA | AAA | ATT | GCT | TAT | TTG | AAA | GAC | TAT | AAT | GAA | AAT | CTA | AAA | AAA | GGC | 774 |  |  |
| Glu | Lys | Ile | Ala | Tyr | Leu | Lys | Asp | Tyr | Asn | Glu | Asn | Leu | Lys | Lys | Gly |     |  |  |
|     |     |     | 235 |     |     |     |     | 240 |     |     |     |     | 245 |     |     |     |  |  |
| ATA | CAG | GAT | TTA | GAA | AGG | CTA | TAC | CAG | TTG | CTA | GGG | GAT | TTG | CAA | ATT | 822 |  |  |
| Ile | Gln | Asp | Leu | Glu | Arg | Leu | Tyr | Gln | Leu | Leu | Gly | Asp | Leu | Gln | Ile |     |  |  |
|     |     | 250 |     |     |     |     | 255 |     |     |     |     | 260 |     |     |     |     |  |  |
| TCT | CAA | AAC | CTG | TAT | AAA | ATT | GAT | TTT | TCT | ATC | GCT | AGG | GGA | TTA | GGG | 870 |  |  |
| Ser | Gln | Asn | Leu | Tyr | Lys | Ile | Asp | Phe | Ser | Ile | Ala | Arg | Gly | Leu | Gly |     |  |  |
|     | 265 |     |     |     |     | 270 |     |     |     |     | 275 |     |     |     |     |     |  |  |
| TAT | TAT | ACA | GGG | ATT | GTG | TAT | GAA | ACC | ACG | CTT | AAT | GAA | ATG | AAG | TCT | 918 |  |  |
| Tyr | Tyr | Thr | Gly | Ile | Val | Tyr | Glu | Thr | Thr | Leu | Asn | Glu | Met | Lys | Ser |     |  |  |
| 280 |     |     |     |     | 285 |     |     |     |     | 290 |     |     |     |     | 295 |     |  |  |
| TTA | GGG | AGC | GTG | TGT | TCA | GGG | GGG | CGT | TAT | GAT | CAT | TTG | ACT | AAA | AAT | 966 |  |  |
| Leu | Gly | Ser | Val | Cys | Ser | Gly | Gly | Arg | Tyr | Asp | His | Leu | Thr | Lys | Asn |     |  |  |
|     |     |     | 300 |     |     |     |     |     | 305 |     |     |     |     | 310 |     |     |  |  |



|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 65                                                              | 70  | 75  | 80  |
| Thr Val Pro Leu Ala Arg Phe Val Ser Leu His His Gln Thr Leu Gly |     |     |     |
|                                                                 | 85  | 90  | 95  |
| Met Pro Phe Lys Arg Tyr Ala Ile Gly Asn Val Phe Arg Gly Glu Arg |     |     |     |
|                                                                 | 100 | 105 | 110 |
| Ala Gln Lys Gly Arg Tyr Arg Glu Phe Thr Gln Cys Asp Phe Asp Phe |     |     |     |
|                                                                 | 115 | 120 | 125 |
| Ile Gly Ser Glu Ser Leu Val Cys Asp Ala Glu Ile Ile Gln Val Ile |     |     |     |
|                                                                 | 130 | 135 | 140 |
| Val Ala Ser Leu Lys Ala Leu Asp Leu Glu Asp Phe Cys Val Ser Ile |     |     |     |
|                                                                 | 145 | 150 | 155 |
| Asn His Arg Lys Ile Leu Asn Gly Ile Cys Glu Tyr Phe Gly Ile Ser |     |     |     |
|                                                                 | 165 | 170 | 175 |
| Gln Val Asn Glu Ala Leu Arg Ile Val Asp Lys Leu Glu Lys Ile Gly |     |     |     |
|                                                                 | 180 | 185 | 190 |
| Leu Asn Gly Val Glu Glu Glu Leu Lys Lys Glu Cys Gly Leu Asn Ser |     |     |     |
|                                                                 | 195 | 200 | 205 |
| Asn Thr Ile Lys Glu Leu Leu Glu Leu Ile Gln Ile Lys Gln Asn Asp |     |     |     |
|                                                                 | 210 | 215 | 220 |
| Leu Ser His Ala Glu Phe Phe Glu Lys Ile Ala Tyr Leu Lys Asp Tyr |     |     |     |
|                                                                 | 225 | 230 | 235 |
| Asn Glu Asn Leu Lys Lys Gly Ile Gln Asp Leu Glu Arg Leu Tyr Gln |     |     |     |
|                                                                 | 245 | 250 | 255 |
| Leu Leu Gly Asp Leu Gln Ile Ser Gln Asn Leu Tyr Lys Ile Asp Phe |     |     |     |
|                                                                 | 260 | 265 | 270 |
| Ser Ile Ala Arg Gly Leu Gly Tyr Tyr Thr Gly Ile Val Tyr Glu Thr |     |     |     |
|                                                                 | 275 | 280 | 285 |
| Thr Leu Asn Glu Met Lys Ser Leu Gly Ser Val Cys Ser Gly Gly Arg |     |     |     |
|                                                                 | 290 | 295 | 300 |
| Tyr Asp His Leu Thr Lys Asn Phe Ser Lys Glu Asn Leu Gln Gly Val |     |     |     |
|                                                                 | 305 | 310 | 315 |
| Gly Ala Ser Ile Gly Ile Asp Arg Leu Ile Val Ala Leu Ser Glu Met |     |     |     |
|                                                                 | 325 | 330 | 335 |
| Gln Leu Leu Asp Glu Arg Ser Thr Gln Ala Lys Val Leu Ile Ala Cys |     |     |     |
|                                                                 | 340 | 345 | 350 |
| Met His Glu Glu Tyr Phe Ser Tyr Ala Asn Arg Leu Ala Glu Ser Leu |     |     |     |
|                                                                 | 355 | 360 | 365 |
| Arg Gln Ser Gly Ile Phe Ser Glu Val Tyr Pro Glu Ala Gln Lys Ile |     |     |     |
|                                                                 | 370 | 375 | 380 |
| Lys Lys Pro Phe Ser Tyr Ala Asn His Lys Gly His Glu Phe Val Ala |     |     |     |
|                                                                 | 385 | 390 | 395 |
| Val Ile Gly Glu Glu Phe Lys Ser Glu Thr Leu Ser Leu Lys Asn     |     |     |     |
|                                                                 | 405 | 410 | 415 |
| Met His Ser Gly Met Gln Leu Asn Cys Leu Ser Phe Leu Lys Ala Leu |     |     |     |
|                                                                 | 420 | 425 | 430 |
| Glu Ile Ile Gly Glu Asn Asp Glu Asp Leu                         |     |     |     |
|                                                                 | 435 | 440 |     |

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:



(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 70...597  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| CACGCCCCATA GGAGAAGTGG CAGAAGTTAT GCAGCTCTTA TTAAAGAAGG AAAAATTAAA | 60  |
| GCTTGGGGG ATG AGT GAG GCA GGG TTA TCT AGC ATC CAA AAA GCC CAT CAA  | 111 |
| Met Ser Glu Ala Gly Leu Ser Ser Ile Gln Lys Ala His Gln            |     |
| 1 5 10                                                             |     |
| ATT TGC CCT TTA AGC GCG TTG CAG AGC GAA TAT TCC TTG TGG TGG CGC    | 159 |
| Ile Cys Pro Leu Ser Ala Leu Gln Ser Glu Tyr Ser Leu Trp Trp Arg    |     |
| 15 20 25 30                                                        |     |
| GAA CCT GAA AAA GAG ATT TTA GGT TTT TTA GAA AAA GAA AAA ATT GGA    | 207 |
| Glu Pro Glu Lys Glu Ile Leu Gly Phe Leu Glu Lys Glu Lys Ile Gly    |     |
| 35 40 45                                                           |     |
| TTT GTC GCT TTT TCG CCT TTG GGT AAG GGG TTT TTA GGC GCG AAA TTT    | 255 |
| Phe Val Ala Phe Ser Pro Leu Gly Lys Gly Phe Leu Gly Ala Lys Phe    |     |
| 50 55 60                                                           |     |
| GAA AAA AAT GCC ACT TTC GCT AGT GAG GAT TTT AGA AGC GTT TCT CCT    | 303 |
| Glu Lys Asn Ala Thr Phe Ala Ser Glu Asp Phe Arg Ser Val Ser Pro    |     |
| 65 70 75                                                           |     |
| AGG TTT AAT CAA GAA AAT CTA GCC AAA AAT TAC GCC TTG GTG GAA TTA    | 351 |
| Arg Phe Asn Gln Glu Asn Leu Ala Lys Asn Tyr Ala Leu Val Glu Leu    |     |
| 80 85 90                                                           |     |
| ATC CAA GAT CAT GCA CAC GCT AAA GGC GTT ACA CCA GCC CAA CTG GCT    | 399 |
| Ile Gln Asp His Ala His Ala Lys Gly Val Thr Pro Ala Gln Leu Ala    |     |
| 95 100 105 110                                                     |     |
| CTC TCA TGG ATT TTG CAC ACG CAA AAA ATC ATT GTC CCT CTC TTT GGC    | 447 |
| Leu Ser Trp Ile Leu His Thr Gln Lys Ile Ile Val Pro Leu Phe Gly    |     |
| 115 120 125                                                        |     |
| ACC ACC AAA GAA TCT AGG CTC ATA GAA AAT ATA GGG GCT TTG CAG GTT    | 495 |
| Thr Thr Lys Glu Ser Arg Leu Ile Glu Asn Ile Gly Ala Leu Gln Val    |     |
| 130 135 140                                                        |     |
| TCT TGG AGT CAA AAA GAA TTG GAG ATT TTC CAA AAA GAA TTG ACT GCA    | 543 |
| Ser Trp Ser Gln Lys Glu Leu Glu Ile Phe Gln Lys Glu Leu Thr Ala    |     |
| 145 150 155                                                        |     |
| ATC AAA ATA GAA GGG GCC CGC TAC CCT GAA AGA ATC AAT GAA ATG GTG    | 591 |
| Ile Lys Ile Glu Gly Ala Arg Tyr Pro Glu Arg Ile Asn Glu Met Val    |     |
| 160 165 170                                                        |     |
| AAT CAA TAAAAGTATT GGGTATTTAT AATTGCATTG GCTCTTTTAA AA             | 639 |
| Asn Gln                                                            |     |
| 175                                                                |     |

(2) INFORMATION FOR SEQ ID NO:282:





| 250                                                                                                                                | 255 | 260 | 265 |      |
|------------------------------------------------------------------------------------------------------------------------------------|-----|-----|-----|------|
| TTG AGC GAG CGA GAA AAT GTT TTC AAT GAA ATT GCC AGA AAA ATC AGT<br>Leu Ser Glu Arg Glu Asn Val Phe Asn Glu Ile Ala Arg Lys Ile Ser | 270 | 275 | 280 | 867  |
| GAA GCC CAC TCA GAA TTC AGT TTA GAA GAA ATT GAA TTG TCT TTA GAA<br>Glu Ala His Ser Glu Phe Ser Leu Glu Glu Ile Glu Leu Ser Leu Glu | 285 | 290 | 295 | 915  |
| AAA GTG AAA AAG ACT GAG ATA AGA CGC ATG ATC ATT AAG GAT AAA ATC<br>Lys Val Lys Lys Thr Glu Ile Arg Arg Met Ile Ile Lys Asp Lys Ile | 300 | 305 | 310 | 963  |
| CGC CCG GAT AAG CGC GCG TTA GAA GAA GTG CGG CCC ATT TTG ATA GAG<br>Arg Pro Asp Lys Arg Ala Leu Glu Glu Val Arg Pro Ile Leu Ile Glu | 315 | 320 | 325 | 1011 |
| AGC GAT TTG CTC CCT ATG GCG CAT AGC TCC ATT TTA TTC ACT AGG GGG<br>Ser Asp Leu Leu Pro Met Ala His Ser Ser Ile Leu Phe Thr Arg Gly | 330 | 335 | 340 | 1059 |
| CAA ACT CAA AGC TTA GTG GTA GGG GTT TTA GGC ACG GAT AAT GAC GCT<br>Gln Thr Gln Ser Leu Val Val Gly Val Leu Gly Thr Asp Asn Asp Ala | 350 | 355 | 360 | 1107 |
| CAA ACC CAT GAG AGT TTG GAG CAT AAA GCT CCC ATT AAA GAG CGC TTC<br>Gln Thr His Glu Ser Leu Glu His Lys Ala Pro Ile Lys Glu Arg Phe | 365 | 370 | 375 | 1155 |
| ATG TTT CAT TAT AAT TTC CCT CCT TTC TGC GTG GGC GAA GCG AGT TCT<br>Met Phe His Tyr Asn Phe Pro Pro Phe Cys Val Gly Glu Ala Ser Ser | 380 | 385 | 390 | 1203 |
| ATT GGC GCG GCT TCA AGG CGT GAA TTA GGG CAT GGG AAT TTG GCT AAA<br>Ile Gly Ala Ala Ser Arg Arg Glu Leu Gly His Gly Asn Leu Ala Lys | 395 | 400 | 405 | 1251 |
| AGA GCC TTA GAA ACG AGC ATT AAA AAT AAA GAG CAG GTG ATA CGA TTG<br>Arg Ala Leu Glu Thr Ser Ile Lys Asn Lys Glu Gln Val Ile Arg Leu | 410 | 415 | 420 | 1299 |
| GTT TCT GAG ATT TTA GAA AGC AAT GGT TCA AGC TCA ATG GCG AGC GTG<br>Val Ser Glu Ile Leu Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val | 430 | 435 | 440 | 1347 |
| TGC GCA GGC TCT TTA GCC CTT TAT GCA AGC GGT GTG GAA ATT TAC GAT<br>Cys Ala Gly Ser Leu Ala Leu Tyr Ala Ser Gly Val Glu Ile Tyr Asp | 445 | 450 | 455 | 1395 |
| TTA GTC GCT GGG GTG GCT ATG GGC ATG GTG AGC GAA GGG CAA GAT CAC<br>Leu Val Ala Gly Val Ala Met Gly Met Val Ser Glu Gly Gln Asp His | 460 | 465 | 470 | 1443 |
| GCT ATT TTA AGC GAT ATT AGC GGC TTA GAA GAC GCA GAA GGC GAT ATG<br>Ala Ile Leu Ser Asp Ile Ser Gly Leu Glu Asp Ala Glu Gly Asp Met | 475 | 480 | 485 | 1491 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| GAT TTT AAG ATT GCT GGG AAT TTA GAA GGC ATT ACG GCC ATG CAA ATG   | 1539 |
| Asp Phe Lys Ile Ala Gly Asn Leu Glu Gly Ile Thr Ala Met Gln Met   |      |
| 490 495 500 505                                                   |      |
| GAT ACC AAA ATG AGC GGT ATC AAG CTA GAA ATT TTA TAC CAA GCC TTA   | 1587 |
| Asp Thr Lys Met Ser Gly Ile Lys Leu Glu Ile Leu Tyr Gln Ala Leu   |      |
| 510 515 520                                                       |      |
| CTC CAA GCC AAA GAA GCA CGG AAA CAT ATT TTA AAA ATC ATG CAT GAA   | 1635 |
| Leu Gln Ala Lys Glu Ala Arg Lys His Ile Leu Lys Ile Met His Glu   |      |
| 525 530 535                                                       |      |
| GCG AAA GAA AAG ATT GTG ATC AAT TTT TCC CAT TTG CCC ACA ACG GAG   | 1683 |
| Ala Lys Glu Lys Ile Val Ile Asn Phe Ser His Leu Pro Thr Thr Glu   |      |
| 540 545 550                                                       |      |
| ATT TTT AAT GTC GCA CCC GAT AAA ATT GTA GAA ATT ATC GGT CAA GGG   | 1731 |
| Ile Phe Asn Val Ala Pro Asp Lys Ile Val Glu Ile Ile Gly Gln Gly   |      |
| 555 560 565                                                       |      |
| GGG CGT GTG ATT AAA GAG ATA GTA GAA AAG TTT GAA GTT AAA ATT GAT   | 1779 |
| Gly Arg Val Ile Lys Glu Ile Val Glu Lys Phe Glu Val Lys Ile Asp   |      |
| 570 575 580 585                                                   |      |
| TTG AAC AAA CCG AGC GGT GAA GTG AAA ATC ATG GGG AAT AAA GAG CGC   | 1827 |
| Leu Asn Lys Pro Ser Gly Glu Val Lys Ile Met Gly Asn Lys Glu Arg   |      |
| 590 595 600                                                       |      |
| GTT TTA AAG ACT AAG GAA TTT ATT TTA AAC TAC TTG CAT TCT TTA GAT   | 1875 |
| Val Leu Lys Thr Lys Glu Phe Ile Leu Asn Tyr Leu His Ser Leu Asp   |      |
| 605 610 615                                                       |      |
| CAA GAA TTG GAG CAA TAC GCT ATT GAT GAG GTA TTA GAA GCT CAA GTG   | 1923 |
| Gln Glu Leu Glu Gln Tyr Ala Ile Asp Glu Val Leu Glu Ala Gln Val   |      |
| 620 625 630                                                       |      |
| AAA CGA ATC GTG GAT TTT GGG GCG TTT TTA AGC TTG CCT AAG GGG GGC   | 1971 |
| Lys Arg Ile Val Asp Phe Gly Ala Phe Leu Ser Leu Pro Lys Gly Gly   |      |
| 635 640 645                                                       |      |
| GAA GGC TTG TTA AGA AAG CAA AAC ATG GAC AAG TGT CAA GTG GTT TTA   | 2019 |
| Glu Gly Leu Leu Arg Lys Gln Asn Met Asp Lys Cys Gln Val Val Leu   |      |
| 650 655 660 665                                                   |      |
| AAA GAA GGC GAT AGC ATC AGG TGT AGG GTG ATT AGC TTC AAT AAG GGT   | 2067 |
| Lys Glu Gly Asp Ser Ile Arg Cys Arg Val Ile Ser Phe Asn Lys Gly   |      |
| 670 675 680                                                       |      |
| AAA ATC GCT TTA GAT TTG GCT TAAAATTTTA AAAAGCGTTT TTTAAAAGCG TTTT | 2122 |
| Lys Ile Ala Leu Asp Leu Ala                                       |      |
| 685                                                               |      |
| TAAGCTAGTT T                                                      | 2133 |

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 688 amino acids

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Phe | Ile | Thr | Ile | Asn | Ser | Ser | Asn | Lys | Thr | Glu | Glu | Phe | Ala |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Lys | Gln | Val | Ala | Lys | Gln | Ala | Thr | Ser | Ser | Leu | Leu | Tyr | Arg | Leu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Lys | Thr | Ile | Ile | Leu | Ala | Ser | Val | Cys | Val | Glu | Arg | Glu | Pro | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Glu | Asp | Phe | Leu | Pro | Leu | Val | Val | Gln | Phe | Leu | Glu | Lys | Ser | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ala | Ala | Gly | Lys | Ile | Pro | Gly | Gly | Phe | Val | Lys | Arg | Glu | Gly | Arg | Ala |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Gln | Asp | Phe | Glu | Ile | Leu | Thr | Ser | Arg | Leu | Ile | Asp | Arg | Thr | Leu | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Pro | Leu | Phe | Pro | Lys | Asp | Tyr | Arg | Tyr | Pro | Thr | Gln | Ile | Thr | Leu | Met |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Val | Leu | Ser | His | Asp | Ile | Glu | Asn | Asp | Leu | Gln | Val | Ser | Ala | Leu | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Ala | Ser | Ala | Ala | Leu | Phe | Leu | Ala | His | Ile | Ala | Pro | Ile | Lys | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Ser | Ala | Cys | Arg | Ile | Ala | Arg | Met | Asp | Asn | Glu | Phe | Ile | Ile | Asn |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |
| Pro | Ser | Ala | Ser | Leu | Leu | Asn | Gln | Ser | Ser | Leu | Asp | Leu | Phe | Val | Ser |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Gly | Thr | Lys | Glu | Ser | Leu | Asn | Met | Ile | Glu | Met | Arg | Ser | Leu | Gly | Gln |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Lys | Leu | Asn | Ala | Leu | Glu | Glu | Pro | Leu | Met | Leu | Glu | Ala | Leu | Glu | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ala | Gln | Lys | Ser | Leu | Glu | Glu | Thr | Cys | Thr | Leu | Tyr | Glu | Glu | Ile | Phe |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Thr | Pro | His | Gln | Asn | Glu | Leu | Phe | Phe | Lys | Glu | Ser | Gln | Gly | Ile | Val |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     |     | 240 |
| Phe | Asn | Glu | Arg | Leu | Leu | Asp | Leu | Leu | Lys | Asn | Gln | Tyr | Phe | Asp | Glu |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ile | Ile | Lys | Gly | Ile | Glu | Ser | Ser | Ala | Leu | Ser | Glu | Arg | Glu | Asn | Val |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Phe | Asn | Glu | Ile | Ala | Arg | Lys | Ile | Ser | Glu | Ala | His | Ser | Glu | Phe | Ser |
|     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| Leu | Glu | Glu | Ile | Glu | Leu | Ser | Leu | Glu | Lys | Val | Lys | Lys | Thr | Glu | Ile |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Arg | Arg | Met | Ile | Ile | Lys | Asp | Lys | Ile | Arg | Pro | Asp | Lys | Arg | Ala | Leu |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     |     | 320 |
| Glu | Glu | Val | Arg | Pro | Ile | Leu | Ile | Glu | Ser | Asp | Leu | Leu | Pro | Met | Ala |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| His | Ser | Ser | Ile | Leu | Phe | Thr | Arg | Gly | Gln | Thr | Gln | Ser | Leu | Val | Val |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Gly | Val | Leu | Gly | Thr | Asp | Asn | Asp | Ala | Gln | Thr | His | Glu | Ser | Leu | Glu |
|     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| His | Lys | Ala | Pro | Ile | Lys | Glu | Arg | Phe | Met | Phe | His | Tyr | Asn | Phe | Pro |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Pro | Phe | Cys | Val | Gly | Glu | Ala | Ser | Ser | Ile | Gly | Ala | Ala | Ser | Arg | Arg |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |

09080307-061504







| 235                                                       | 240                                               | 245                                                       |      |
|-----------------------------------------------------------|---------------------------------------------------|-----------------------------------------------------------|------|
| GAG AAA CTT CAG GCT GAC<br>Glu Lys Leu Gln Ala Asp<br>250 | AAC ACG CCT TTT<br>Asn Thr Pro Phe<br>255         | AAA GGG GTT TTA CTC GCT<br>Lys Gly Val Leu Leu Ala<br>260 | 819  |
| GAA ATT GTA ATC ATA GAA<br>Glu Ile Val Ile Ile Glu<br>270 | GAA AAA GGC GTT TTA<br>Glu Lys Gly Val Leu<br>275 | GAG CCG TAT TTA TTG<br>Glu Pro Tyr Leu Leu<br>280         | 867  |
| GAT TTT AGC GTG CGT TTT<br>Asp Phe Ser Val Arg Phe<br>285 | AAA GAC ATT GAA TGC<br>Lys Asp Ile Glu Cys<br>290 | ACG ATT TTA CCC<br>Thr Ile Leu Pro<br>295                 | 915  |
| CTT TTA GAA AGC TCG CTT<br>Leu Leu Glu Ser Ser Leu<br>300 | TTA GAT TTG TGT TTG<br>Leu Asp Leu Cys Leu<br>305 | GCC ACA GCC AAA GGG<br>Ala Thr Ala Lys Gly<br>310         | 963  |
| GAA TTA CAT TCT CTT GAA<br>Glu Leu His Ser Leu Glu<br>315 | TTG GTG TTT TCT AAA<br>Leu Val Phe Ser Lys<br>320 | GAA TTT GTG ATG AGT<br>Glu Phe Val Met Ser<br>325         | 1011 |
| GTG GCG CTT GTT TCT AGG<br>Val Ala Leu Val Ser Arg<br>330 | AAT TAC CCC ACT AGC<br>Asn Tyr Pro Thr Ser<br>335 | TCT TCG CCC AAA CAA<br>Ser Ser Ser Pro Lys Gln<br>340     | 1059 |
| ACC CTT TAT ATT GAT CCG<br>Thr Leu Tyr Ile Asp Pro<br>350 | GTT GAT GAA AAA AAG<br>Val Asp Glu Lys Lys<br>355 | GGT CAT TTG ATT TTA<br>Gly His Leu Ile Leu<br>360         | 1107 |
| GGG GAG GTG GAG CAG GAT<br>Gly Glu Val Glu Gln Asp<br>365 | AAT GGC GTG TTT GAA<br>Asn Gly Val Phe Glu<br>370 | AGC AGT GGG GGG AGG<br>Ser Ser Gly Gly Arg<br>375         | 1155 |
| GTG ATC TTT GCC ATT GGT<br>Val Ile Phe Ala Ile Gly<br>380 | AGG GGA AAA TCC TTA<br>Arg Gly Lys Ser Leu<br>385 | TTA GAA GCC AGA AAC<br>Leu Leu Glu Ala Arg Asn<br>390     | 1203 |
| CAT GCT TAT GAA ATC GCT<br>His Ala Tyr Glu Ile Ala<br>395 | CAA AAG GTG CAT TTT<br>Gln Lys Val His Phe<br>400 | GAA GGC ATG TTT TAT<br>Glu Gly Met Phe Tyr<br>405         | 1251 |
| CGC AAG GAT ATT GGT TTT<br>Arg Lys Asp Ile Gly Phe<br>410 | AAG GTG TTA GAT TTG<br>Lys Val Leu Asp Leu<br>415 | AAA GAA TAT TCT TAAAG<br>Lys Glu Tyr Ser<br>420           | 1301 |
| GTTAAAGTTT AAGACAAACC AAAGAGTTTG TCTTGTTTG                |                                                   |                                                           | 1340 |

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Asp | Asn | Asn | Asn | Tyr | Asn | Val | Leu | Ile | Val | Gly | Asn | Lys | Gly | 1   | 5   | 10  | 15  |
| Arg | Glu | Tyr | Ala | Leu | Ala | Gln | Arg | Leu | Gln | Gln | Asp | Glu | Arg | Val | Asn | 20  | 25  | 30  |     |
| Ala | Leu | Tyr | Phe | Cys | Leu | Gly | Asn | Gly | Gly | Thr | Gln | Asp | Leu | Gly | Glu | 35  | 40  | 45  |     |
| Asn | Leu | Glu | Cys | Glu | His | Tyr | Glu | His | Ile | Val | Glu | Leu | Ala | Leu | Lys | 50  | 55  | 60  |     |
| Lys | Gln | Ile | His | Leu | Ala | Ile | Ile | Ser | Glu | Glu | Glu | Phe | Leu | Val | Leu | 65  | 70  | 75  | 80  |
| Gly | Leu | Thr | Glu | Met | Leu | Glu | Lys | Ala | Gly | Ile | Leu | Val | Phe | Gly | Ala | 85  | 90  | 95  |     |
| Ser | Lys | Glu | Ala | Ala | Lys | Leu | Glu | Ala | Ser | Lys | Ser | Tyr | Met | Lys | Ala | 100 | 105 | 110 |     |
| Phe | Val | Lys | Glu | Cys | Gly | Ile | Lys | Ser | Ala | Ser | Tyr | Phe | Glu | Thr | Asn | 115 | 120 | 125 |     |
| Asp | Leu | Lys | Glu | Ala | Leu | Ser | Tyr | Ile | Gln | Asn | Ala | Ser | Phe | Pro | Leu | 130 | 135 | 140 |     |
| Val | Ile | Lys | Ala | Leu | Asn | Lys | Asn | Thr | Ser | Ile | Val | Tyr | Gln | Glu | Glu | 145 | 150 | 155 | 160 |
| Glu | Ala | Ile | Lys | Ile | Leu | Glu | Asp | Ala | Phe | Lys | Gln | Ser | Asn | Glu | Pro | 165 | 170 | 175 |     |
| Val | Ile | Ile | Glu | Pro | Phe | Leu | Glu | Gly | Phe | Glu | Leu | Ser | Val | Thr | Ala | 180 | 185 | 190 |     |
| Leu | Ile | Ala | Asn | Asp | Asp | Phe | Ile | Leu | Leu | Pro | Phe | Cys | Gln | Asn | Tyr | 195 | 200 | 205 |     |
| Lys | Arg | Leu | Leu | Glu | Gly | Asp | Asn | Gly | Val | Asn | Thr | Gly | Gly | Met | Gly | 210 | 215 | 220 |     |
| Ala | Ile | Ala | Pro | Ala | Asn | Phe | Phe | Ser | Asn | Glu | Leu | Glu | Glu | Lys | Ile | 225 | 230 | 235 | 240 |
| Lys | Asn | His | Ile | Phe | Lys | Pro | Thr | Leu | Glu | Lys | Leu | Gln | Ala | Asp | Asn | 245 | 250 | 255 |     |
| Thr | Pro | Phe | Lys | Gly | Val | Leu | Leu | Ala | Glu | Ile | Val | Ile | Ile | Glu | Glu | 260 | 265 | 270 |     |
| Lys | Gly | Val | Leu | Glu | Pro | Tyr | Leu | Leu | Asp | Phe | Ser | Val | Arg | Phe | Lys | 275 | 280 | 285 |     |
| Asp | Ile | Glu | Cys | Gln | Thr | Ile | Leu | Pro | Leu | Leu | Glu | Ser | Ser | Leu | Leu | 290 | 295 | 300 |     |
| Asp | Leu | Cys | Leu | Ala | Thr | Ala | Lys | Gly | Glu | Leu | His | Ser | Leu | Glu | Leu | 305 | 310 | 315 | 320 |
| Val | Phe | Ser | Lys | Glu | Phe | Val | Met | Ser | Val | Ala | Leu | Val | Ser | Arg | Asn | 325 | 330 | 335 |     |
| Tyr | Pro | Thr | Ser | Ser | Ser | Pro | Lys | Gln | Thr | Leu | Tyr | Ile | Asp | Pro | Val | 340 | 345 | 350 |     |
| Asp | Glu | Lys | Lys | Gly | His | Leu | Ile | Leu | Gly | Glu | Val | Glu | Gln | Asp | Asn | 355 | 360 | 365 |     |
| Gly | Val | Phe | Glu | Ser | Ser | Gly | Gly | Arg | Val | Ile | Phe | Ala | Ile | Gly | Arg | 370 | 375 | 380 |     |
| Gly | Lys | Ser | Leu | Leu | Glu | Ala | Arg | Asn | His | Ala | Tyr | Glu | Ile | Ala | Gln | 385 | 390 | 395 | 400 |
| Lys | Val | His | Phe | Glu | Gly | Met | Phe | Tyr | Arg | Lys | Asp | Ile | Gly | Phe | Lys | 405 | 410 | 415 |     |
| Val | Leu | Asp | Leu | Lys | Glu | Tyr | Ser |     |     |     |     |     |     |     |     | 420 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 17...769
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TTAAAATGAA GTGAAA ATG AGA GAA ATA AAT ATG ATT TTA TAC ATT CAT ATC | 52  |
| Met Arg Glu Ile Asn Met Ile Leu Tyr Ile His Ile                   |     |
| 1 5 10                                                            |     |
| CCC TTT TGT GAA AAT AAA TGC GGC TAT TGC GCT TTC AAT TCC TAT GAA   | 100 |
| Pro Phe Cys Glu Asn Lys Cys Gly Tyr Cys Ala Phe Asn Ser Tyr Glu   |     |
| 15 20 25                                                          |     |
| AAC AAG CAT GGG TTA AAA GAA GAA TAC ACT CAA GCG TTA TGC CTG GAT   | 148 |
| Asn Lys His Gly Leu Lys Glu Glu Tyr Thr Gln Ala Leu Cys Leu Asp   |     |
| 30 35 40                                                          |     |
| TTA AAG CAT GCG TTA AGT CAA ACT GAC GAA CCA ATT GAA AGC GTT TTT   | 196 |
| Leu Lys His Ala Leu Ser Gln Thr Asp Glu Pro Ile Glu Ser Val Phe   |     |
| 45 50 55 60                                                       |     |
| ATT GGT GGC GGC ACG CCT AAC ACT TTA AGC GTG AAG GCT TTT GAA AGG   | 244 |
| Ile Gly Gly Gly Thr Pro Asn Thr Leu Ser Val Lys Ala Phe Glu Arg   |     |
| 65 70 75                                                          |     |
| ATT TTT GAA AGC ATT TAT CAA CAT GCG AGC TTG AGC TTG GAT TGT GAG   | 292 |
| Ile Phe Glu Ser Ile Tyr Gln His Ala Ser Leu Ser Leu Asp Cys Glu   |     |
| 80 85 90                                                          |     |
| ATC ACC ACT GAA GCT AAC CCC GAA TTG ATT ACT AAA GCT TGG TGT CAA   | 340 |
| Ile Thr Thr Glu Ala Asn Pro Glu Leu Ile Thr Lys Ala Trp Cys Gln   |     |
| 95 100 105                                                        |     |
| GGC TTA AAA GGT TTA GGG ATC AAC CGC TTG AGT TTA GGG GTG CAA AGT   | 388 |
| Gly Leu Lys Gly Leu Gly Ile Asn Arg Leu Ser Leu Gly Val Gln Ser   |     |
| 110 115 120                                                       |     |
| TTT AGG GAA GAT AAA TTA TTG TTT TTA GAG CGC CAA CAT TCC AAA AAT   | 436 |
| Phe Arg Glu Asp Lys Leu Leu Phe Leu Glu Arg Gln His Ser Lys Asn   |     |
| 125 130 135 140                                                   |     |
| ATC GCT CCT GCG ATA GAA ACT ATT TTA AAA AGC GGG ATT GAA AAT ATC   | 484 |
| Ile Ala Pro Ala Ile Glu Thr Ile Leu Lys Ser Gly Ile Glu Asn Ile   |     |
| 145 150 155                                                       |     |
| AGC ATT GAT TTG ATT TAT AAC ACC CCA TTA GAC AAT GAA AAC TCT CTA   | 532 |
| Ser Ile Asp Leu Ile Tyr Asn Thr Pro Leu Asp Asn Glu Asn Ser Leu   |     |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Leu | Ala | Lys | Glu | Leu | Pro | Ile | Asn | His | Leu | Ser | Ala | Tyr | Ala | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Val | Glu | Lys | Asn | Thr | Asn | Leu | Glu | Lys | Asn | Ala | Lys | Lys | Pro | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Cys | Ala | His | Phe | Asp | Asn | Val | Val | Arg | Glu | Ile | Leu | Glu | Gly | Phe | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Lys | Gln | Tyr | Glu | Cys | Leu | Ile | Thr | Leu | Glu | Ile | Ile | Lys | Ser | Asn |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Thr | Thr | Trp | Leu | Thr | Gly | Gly | Leu | Lys | Ile | Ile |     |     |     |     |     |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 76...1257
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

|             |                 |                 |                 |                 |            |     |
|-------------|-----------------|-----------------|-----------------|-----------------|------------|-----|
| GCCAAGTCAT  | TGCTTATTTTC     | AAAAGAGAGG      | GGTATTTATA      | GGGTGTTAAT      | CGTTCAAAAA | 60  |
| TACGGCGGCA  | CGAGC           | ATG GGC AGC ATA | GAA AGG ATC CAC | AAT GTC GCT CAA |            | 111 |
|             | Met Gly Ser Ile | Glu Arg Ile     | His Asn Val     | Ala Gln         |            |     |
|             | 1               | 5               | 10              |                 |            |     |
| AGG GTT TTA | GAA AGC GTT     | ACA TTA GGG     | CAT CAA GTC     | GTG GTG GTG     | GTT        | 159 |
| Arg Val Leu | Glu Ser Val     | Thr Leu Gly     | His Gln Val     | Val Val Val     | Val        |     |
|             | 15              | 20              | 25              |                 |            |     |
| TCA GCG ATG | AGC GGC GAA     | ACC GAC AGG     | CTT TTA GAA     | TTT GGC AAG     | AAT        | 207 |
| Ser Ala Met | Ser Gly Glu     | Thr Asp Arg     | Leu Leu Glu     | Phe Gly Lys     | Asn        |     |
|             | 30              | 35              | 40              |                 |            |     |
| TTT AGC CAT | AAC CCT AAC     | AAG CGA GAG     | ATG GAC AGG     | ATT GTA AGC     | GTG        | 255 |
| Phe Ser His | Asn Pro Asn     | Lys Arg Glu     | Met Asp Arg     | Ile Val Ser     | Val        |     |
|             | 45              | 50              | 55              | 60              |            |     |
| GGG GAA TTG | GTT TCA AGT     | GCG GCT TTG     | AGC ATG GCG     | TTA GAA AGG     | TAT        | 303 |
| Gly Glu Leu | Val Ser Ser     | Ala Ala Leu     | Ser Met Ala     | Leu Glu Arg     | Tyr        |     |
|             | 65              | 70              | 75              |                 |            |     |
| GGG CAT AGA | GCC ATT TCC     | TTG AGC GGG     | AAA GAA GCG     | GGC ATT TTA     | ACC        | 351 |
| Gly His Arg | Ala Ile Ser     | Leu Ser Gly     | Lys Glu Ala     | Gly Ile Leu     | Thr        |     |
|             | 80              | 85              | 90              |                 |            |     |
| AGC TCG CAT | TTT CAA AAC     | GCC GTG ATC     | CAA TCC ATT     | GAC ACC AAA     | CGC        | 399 |
| Ser Ser His | Phe Gln Asn     | Ala Val Ile     | Gln Ser Ile     | Asp Thr Lys     | Arg        |     |
|             | 95              | 100             | 105             |                 |            |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| ATC | ACA | GAG | CTT | TTA | GAA | AAA | AAC | TAC | ATT | GTG | GTG | ATC | GCT | GGG | TTT | 447  |
| Ile | Thr | Glu | Leu | Leu | Glu | Lys | Asn | Tyr | Ile | Val | Val | Ile | Ala | Gly | Phe |      |
|     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |     |     |     |     |      |
| CAA | GGC | GCT | GAT | ATT | CAA | GGT | GAA | ACA | ACG | ACT | TTA | GGG | CGT | GGG | GGG | 495  |
| Gln | Gly | Ala | Asp | Ile | Gln | Gly | Glu | Thr | Thr | Thr | Leu | Gly | Arg | Gly | Gly |      |
|     | 125 |     |     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |      |
| AGC | GAT | TTG | AGC | GCG | GTT | GCT | TTG | GCC | GGG | GCT | TTA | AAA | GCG | CAT | TTG | 543  |
| Ser | Asp | Leu | Ser | Ala | Val | Ala | Leu | Ala | Gly | Ala | Leu | Lys | Ala | His | Leu |      |
|     |     |     |     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |      |
| TGC | GAA | ATC | TAT | ACG | GAT | GTG | GAT | GGC | GTT | TAT | ACC | ACC | GAT | CCG | CGC | 591  |
| Cys | Glu | Ile | Tyr | Thr | Asp | Val | Asp | Gly | Val | Tyr | Thr | Thr | Asp | Pro | Arg |      |
|     |     |     | 160 |     |     |     |     | 165 |     |     |     |     | 170 |     |     |      |
| ATT | GAA | GAA | AAG | GCT | CAA | AAA | ATC | GCG | CAA | ATC | AGC | TAT | GAT | GAA | ATG | 639  |
| Ile | Glu | Glu | Lys | Ala | Gln | Lys | Ile | Ala | Gln | Ile | Ser | Tyr | Asp | Glu | Met |      |
|     |     |     | 175 |     |     |     | 180 |     |     |     |     | 185 |     |     |     |      |
| CTT | GAA | CTG | GCT | TCT | ATG | GGG | GCT | AAA | GTT | TTA | TTA | AAC | CGC | TCG | GTG | 687  |
| Leu | Glu | Leu | Ala | Ser | Met | Gly | Ala | Lys | Val | Leu | Leu | Asn | Arg | Ser | Val |      |
|     | 190 |     |     |     |     | 195 |     |     |     |     | 200 |     |     |     |     |      |
| GAA | TTA | GCC | AAA | AAG | CTC | AGC | GTG | AAG | TTA | GTG | ACT | CGC | AAT | TCG | TTT | 735  |
| Glu | Leu | Ala | Lys | Lys | Leu | Ser | Val | Lys | Leu | Val | Thr | Arg | Asn | Ser | Phe |      |
|     | 205 |     |     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |      |
| AAC | CAT | AGC | GAA | GGC | ACG | CTC | ATT | GTG | GCT | GAA | AAA | GAC | TTT | AAA | GGA | 783  |
| Asn | His | Ser | Glu | Gly | Thr | Leu | Ile | Val | Ala | Glu | Lys | Asp | Phe | Lys | Gly |      |
|     |     |     |     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |      |
| GAA | CGC | ATG | GAA | ACC | CCT | ATA | GTG | AGT | GGG | ATC | GCA | TTG | GAT | AAA | AAT | 831  |
| Glu | Arg | Met | Glu | Thr | Pro | Ile | Val | Ser | Gly | Ile | Ala | Leu | Asp | Lys | Asn |      |
|     |     |     | 240 |     |     |     |     | 245 |     |     |     |     | 250 |     |     |      |
| CAG | GCT | CGT | GTG | AGC | ATG | GAG | GGC | GTG | GAA | GAT | CGG | CCA | GGC | ATT | GCC | 879  |
| Gln | Ala | Arg | Val | Ser | Met | Glu | Gly | Val | Glu | Asp | Arg | Pro | Gly | Ile | Ala |      |
|     |     | 255 |     |     |     | 260 |     |     |     |     |     | 265 |     |     |     |      |
| GCT | GAA | ATC | TTT | GGC | GCT | TTA | GCG | GAG | TAT | CGC | ATT | AAC | GTG | GAT | ATG | 927  |
| Ala | Glu | Ile | Phe | Gly | Ala | Leu | Ala | Glu | Tyr | Arg | Ile | Asn | Val | Asp | Met |      |
|     | 270 |     |     |     |     | 275 |     |     |     |     | 280 |     |     |     |     |      |
| ATC | GTC | CAA | ACG | ATC | GGC | AGA | GAC | GGC | AAA | ACC | GAT | TTG | GAT | TTT | ACG | 975  |
| Ile | Val | Gln | Thr | Ile | Gly | Arg | Asp | Gly | Lys | Thr | Asp | Leu | Asp | Phe | Thr |      |
|     | 285 |     |     |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |      |
| ATC | GTT | AAA | ACC | CAA | ATA | GAA | GAA | ACC | AAG | CAA | GCC | TTA | AAG | CCT | TTT | 1023 |
| Ile | Val | Lys | Thr | Gln | Ile | Glu | Glu | Thr | Lys | Gln | Ala | Leu | Lys | Pro | Phe |      |
|     |     |     |     | 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |      |
| TTA | GCG | CAA | ATG | GAT | TCC | ATT | GAT | TAT | GAT | GAA | AAT | ATC | GCT | AAA | GTC | 1071 |
| Leu | Ala | Gln | Met | Asp | Ser | Ile | Asp | Tyr | Asp | Glu | Asn | Ile | Ala | Lys | Val |      |
|     |     |     | 320 |     |     |     |     | 325 |     |     |     |     | 330 |     |     |      |
| TCC | ATA | GTG | GGC | GTG | GGC | ATG | AAG | TCG | CAT | TCT | GGG | GTG | GCG | AGT | ATC | 1119 |
| Ser | Ile | Val | Gly | Val | Gly | Met | Lys | Ser | His | Ser | Gly | Val | Ala | Ser | Ile |      |

|                                                                   |     |     |      |
|-------------------------------------------------------------------|-----|-----|------|
| 335                                                               | 340 | 345 |      |
| GCT TTT AAA GCC CTA GCC AAA GAC AAT ATC AAT ATC ATG ATG ATT TCT   |     |     | 1167 |
| Ala Phe Lys Ala Leu Ala Lys Asp Asn Ile Asn Ile Met Met Ile Ser   |     |     |      |
| 350                                                               | 355 | 360 |      |
| ACA AGC GAG ATT AAA ATT TCG GTT TTG ATT GAC ATT AAA TAC GCT GAA   |     |     | 1215 |
| Thr Ser Glu Ile Lys Ile Ser Val Leu Ile Asp Ile Lys Tyr Ala Glu   |     |     |      |
| 365                                                               | 370 | 375 | 380  |
| TTA GCT GTT AGA ACT TTG CAT GCG GTG TAT CAA TTA GAT CAA TGAAAAATT |     |     | 1266 |
| Leu Ala Val Arg Thr Leu His Ala Val Tyr Gln Leu Asp Gln           |     |     |      |
| 385                                                               | 390 |     |      |
| TCTACGATTG GATCAAGGAA TTTGT                                       |     |     | 1291 |

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ser | Ile | Glu | Arg | Ile | His | Asn | Val | Ala | Gln | Arg | Val | Leu | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Val | Thr | Leu | Gly | His | Gln | Val | Val | Val | Val | Ser | Ala | Met | Ser |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Gly | Glu | Thr | Asp | Arg | Leu | Leu | Glu | Phe | Gly | Lys | Asn | Phe | Ser | His | Asn |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Asn | Lys | Arg | Glu | Met | Asp | Arg | Ile | Val | Ser | Val | Gly | Glu | Leu | Val |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Ser | Ala | Ala | Leu | Ser | Met | Ala | Leu | Glu | Arg | Tyr | Gly | His | Arg | Ala |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Ser | Leu | Ser | Gly | Lys | Glu | Ala | Gly | Ile | Leu | Thr | Ser | Ser | His | Phe |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gln | Asn | Ala | Val | Ile | Gln | Ser | Ile | Asp | Thr | Lys | Arg | Ile | Thr | Glu | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Glu | Lys | Asn | Tyr | Ile | Val | Val | Ile | Ala | Gly | Phe | Gln | Gly | Ala | Asp |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Gln | Gly | Glu | Thr | Thr | Thr | Leu | Gly | Arg | Gly | Gly | Ser | Asp | Leu | Ser |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Ala | Val | Ala | Leu | Ala | Gly | Ala | Leu | Lys | Ala | His | Leu | Cys | Glu | Ile | Tyr |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Thr | Asp | Val | Asp | Gly | Val | Tyr | Thr | Thr | Asp | Pro | Arg | Ile | Glu | Glu | Lys |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Gln | Lys | Ile | Ala | Gln | Ile | Ser | Tyr | Asp | Glu | Met | Leu | Glu | Leu | Ala |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Ser | Met | Gly | Ala | Lys | Val | Leu | Leu | Asn | Arg | Ser | Val | Glu | Leu | Ala | Lys |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Leu | Ser | Val | Lys | Leu | Val | Thr | Arg | Asn | Ser | Phe | Asn | His | Ser | Glu |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Thr | Leu | Ile | Val | Ala | Glu | Lys | Asp | Phe | Lys | Gly | Glu | Arg | Met | Glu |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     | 240 |





|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TAT GGT ATA GAA GCC CAA AAC GCG CTT TTA AAA ATC TTA GAA GAA CCC   | 288 |
| Tyr Gly Ile Glu Ala Gln Asn Ala Leu Leu Lys Ile Leu Glu Glu Pro   |     |
| 85 90 95                                                          |     |
| CCG AAT AAC GTT TGT TTT ATC ATG TTC GCT AAA AGC CAA AAC CAT GTG   | 336 |
| Pro Asn Asn Val Cys Phe Ile Met Phe Ala Lys Ser Gln Asn His Val   |     |
| 100 105 110                                                       |     |
| TTA GCC ACC ATT AAA TCC CGC CTA ATT AAA GAA GAC AAA CGC CAA AAA   | 384 |
| Leu Ala Thr Ile Lys Ser Arg Leu Ile Lys Glu Asp Lys Arg Gln Lys   |     |
| 115 120 125                                                       |     |
| ATC CCC CTA AAA CCT TTA GAT TTG GAT TTA TCC AAG CTG GAT TTG AAA   | 432 |
| Ile Pro Leu Lys Pro Leu Asp Leu Asp Leu Ser Lys Leu Asp Leu Lys   |     |
| 130 135 140                                                       |     |
| GAC ATT TAT GCG TTT TTA AAA AAT TTA GAC AAA GAA AAT TTT GAT TCC   | 480 |
| Asp Ile Tyr Ala Phe Leu Lys Asn Leu Asp Lys Glu Asn Phe Asp Ser   |     |
| 145 150 155 160                                                   |     |
| AGA GAA AAT CAG AGG GAA AGG ATT GAA AGC CTG TTA GAG AGC GTT AAC   | 528 |
| Arg Glu Asn Gln Arg Glu Arg Ile Glu Ser Leu Leu Glu Ser Val Asn   |     |
| 165 170 175                                                       |     |
| AGG CAT AAG ATC CCC TTA AAC GAG CAA GAA TTG CAA GCC TTT GAT TTA   | 576 |
| Arg His Lys Ile Pro Leu Asn Glu Gln Glu Leu Gln Ala Phe Asp Leu   |     |
| 180 185 190                                                       |     |
| GCG ATC AAG GCT AAC AGC TCT TAT TAC AAG CTC AGC TAT AAT CTT TTA   | 624 |
| Ala Ile Lys Ala Asn Ser Ser Tyr Tyr Lys Leu Ser Tyr Asn Leu Leu   |     |
| 195 200 205                                                       |     |
| CCC CTG CTT TTA AGC CTT TTA TCC AAA AAG AAA ACG CCA TGATTGTAAA AC | 675 |
| Pro Leu Leu Leu Ser Leu Leu Ser Lys Lys Lys Thr Pro               |     |
| 210 215 220                                                       |     |
| GCCTTAACCC TGATGCGCTC AAAAACGCTC T                                | 706 |

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Gly Tyr Ser Val Lys Asn Ser Asn Arg Leu Ile Tyr Thr Asp Asn Leu |  |
| 1 5 10 15                                                       |  |
| Glu Glu Ser Leu Glu Glu Thr Ala Ser Leu Phe Glu His His Ile Lys |  |
| 20 25 30                                                        |  |
| Phe Tyr Thr Glu Ile Ile Glu Lys Asp Lys Lys Val Ile Lys Thr Phe |  |
| 35 40 45                                                        |  |
| Asn Lys Asp Phe Lys Ile Glu His Ala Lys Glu Val Ile Ser Lys Ala |  |
| 50 55 60                                                        |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Leu | Lys | His | Ser | Glu | Leu | Asn | Ala | Phe | Leu | Ile | Ala | Ala | Pro | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Tyr | Gly | Ile | Glu | Ala | Gln | Asn | Ala | Leu | Leu | Lys | Ile | Leu | Glu | Glu | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Asn | Asn | Val | Cys | Phe | Ile | Met | Phe | Ala | Lys | Ser | Gln | Asn | His | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Ala | Thr | Ile | Lys | Ser | Arg | Leu | Ile | Lys | Glu | Asp | Lys | Arg | Gln | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Pro | Leu | Lys | Pro | Leu | Asp | Leu | Asp | Leu | Ser | Lys | Leu | Asp | Leu | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Ile | Tyr | Ala | Phe | Leu | Lys | Asn | Leu | Asp | Lys | Glu | Asn | Phe | Asp | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Arg | Glu | Asn | Gln | Arg | Glu | Arg | Ile | Glu | Ser | Leu | Leu | Glu | Ser | Val | Asn |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Arg | His | Lys | Ile | Pro | Leu | Asn | Glu | Gln | Glu | Leu | Gln | Ala | Phe | Asp | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Ile | Lys | Ala | Asn | Ser | Ser | Tyr | Tyr | Lys | Leu | Ser | Tyr | Asn | Leu | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Leu | Leu | Leu | Ser | Leu | Leu | Ser | Lys | Lys | Lys | Thr | Pro |     |     |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 58...1059
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

|             |             |             |             |             |         |     |     |
|-------------|-------------|-------------|-------------|-------------|---------|-----|-----|
| TATTCTCTCG  | CAATAATTGT  | TATTGTTATT  | GCGACAAAAC  | TTTTAGAAGG  | AGTTATT | ATG | 60  |
|             |             |             |             |             |         | Met |     |
|             |             |             |             |             |         | 1   |     |
| GGA AGT ATC | GGT AGT ATG | GGC AAA CCT | ATT GAA GGG | TTT TTA GTG | GCA     |     | 108 |
| Gly Ser Ile | Gly Ser Met | Gly Lys Pro | Ile Glu Gly | Phe Leu Val | Ala     |     |     |
|             | 5           |             | 10          |             | 15      |     |     |
| GCC ATT CAG | TTT CCT GTG | CCA ATT GTC | AAT AGC CGT | AAG GAT ATT | GAT     |     | 156 |
| Ala Ile Gln | Phe Pro Val | Pro Ile Val | Asn Ser Arg | Lys Asp Ile | Asp     |     |     |
|             | 20          |             | 25          |             | 30      |     |     |
| CAC AAT ATT | GAA AGC ATT | ATT AGA ACC | TTG CAT GCG | ACT AAA GCG | GGG     |     | 204 |
| His Asn Ile | Glu Ser Ile | Ile Arg Thr | Leu His Ala | Thr Lys Ala | Gly     |     |     |
|             | 35          |             | 40          |             | 45      |     |     |
| TAT CCG GGA | GTG GAG CTT | ATC ATT TTC | CCT GAG TAT | AGC ACG CAA | GGT     |     | 252 |
| Tyr Pro Gly | Val Glu Ile | Ile Phe Pro | Glu Tyr Ser | Thr Gln Gly |         |     |     |
|             | 50          |             | 55          |             | 60      |     | 65  |









ATGAAATCTT CTTTAAAACT TTTTATGCGG CCTT

1152

## (2) INFORMATION FOR SEQ ID NO:296:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

```

Met Ile Ala Tyr Ile Leu Lys Arg Leu Leu Leu Ile Ile Pro Thr Leu
 1 5 10 15
Leu Ala Ile Met Thr Ile Asn Phe Phe Leu Ile Gln Ser Ala Pro Gly
 20 25 30
Gly Pro Ile Glu Gln Met Met Ala Lys Ile Asn Asn Thr Gln Ser Lys
 35 40 45
Glu Ile Gln Gly Val Val Lys Glu Arg Ser Tyr Arg Ala Ser Gln Gly
 50 55 60
Leu Glu Ser Asp Leu Leu Glu Asn Leu Lys Lys Leu Tyr Gly Phe Asp
65 70 75 80
Lys Pro Ile Gly Glu Arg Tyr Leu Leu Met Leu Lys Lys Tyr Leu Gln
 85 90 95
Phe Asp Phe Gly Glu Ser Phe Tyr Arg Gln Ile Lys Val Ile Asp Leu
 100 105 110
Ile Lys Glu Lys Leu Pro Val Ser Ile Ser Leu Gly Leu Phe Ser Thr
 115 120 125
Leu Leu Ile Tyr Leu Ile Ser Ile Pro Leu Gly Ile Phe Lys Ala Lys
 130 135 140
Arg Asn Asn Glu Pro Leu Asp Val Leu Ser Ser Val Val Ile Ile Val
145 150 155 160
Ala Asn Ala Ile Pro Ala Phe Leu Phe Ala Val Val Leu Ile Val Phe
 165 170 175
Phe Ala Gly Gly Asn Tyr Trp His Trp Phe Pro Leu Lys Gly Leu Val
 180 185 190
Ser Asp Asn Phe Glu Ser Leu Ser Ala Leu Gly Lys Ile Lys Asp Tyr
 195 200 205
Leu Trp His Ile Thr Leu Pro Val Leu Cys Ile Ser Leu Gly Gly Phe
 210 215 220
Ala Ser Leu Thr Leu Leu Val Lys Asn Ser Phe Leu Asp Glu Met Gly
225 230 235 240
Lys Leu Tyr Val Leu Ser Ala Lys Ala Lys Gly Cys Ser Val Gly Arg
 245 250 255
Ile Phe Tyr Ala His Val Phe Arg Asn Ala Ile Leu Leu Val Val Ala
 260 265 270
Gly Phe Pro Gln Ala Phe Leu Gly Met Phe Phe Ser Ser Ser Leu Leu
 275 280 285
Ile Glu Ile Val Phe Ser Leu Asp Gly Leu Gly Leu Leu Gly Tyr Glu
 290 295 300
Ser Ile Val Ser Arg Asp Tyr Pro Val Val Phe Gly Ser Leu Tyr Ile
305 310 315 320
Phe Thr Leu Leu Gly Leu Val Ala Ser Leu Ile Ser Asp Leu Leu Cys
 325 330 335

```

Val Val Ile Asp Pro Arg Ile Asp Phe Glu Lys Arg  
 340 345

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...618
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| TTAAAGGTCT AAACC ATG GAT ATT AAG GCA TGT TAT CAA AAC GCT AAA GCG | 51  |
| Met Asp Ile Lys Ala Cys Tyr Gln Asn Ala Lys Ala                  |     |
| 1 5 10                                                           |     |
| TTA TTA GAG GGG CAT TTC TTG CTC AGC AGT GGG TTT CAT TCC AAT TAT  | 99  |
| Leu Leu Glu Gly His Phe Leu Leu Ser Ser Gly Phe His Ser Asn Tyr  |     |
| 15 20 25                                                         |     |
| TAT TTG CAA TCC GCT AAA GTT TTA GAA GAT CCC AAA CTA GCC GAA CAA  | 147 |
| Tyr Leu Gln Ser Ala Lys Val Leu Glu Asp Pro Lys Leu Ala Glu Gln  |     |
| 30 35 40                                                         |     |
| TTA GCG CTA GAA TTA GCC AAA CAA ATC CAA GAA GCT CAT TTG AAT ATT  | 195 |
| Leu Ala Leu Glu Leu Ala Lys Gln Ile Gln Glu Ala His Leu Asn Ile  |     |
| 45 50 55 60                                                      |     |
| GAA TGC GTG TGC TCA CCG GCT ATT GGG GGG ATT TTG GCT GGG TAT GAG  | 243 |
| Glu Cys Val Cys Ser Pro Ala Ile Gly Gly Ile Leu Ala Gly Tyr Glu  |     |
| 65 70 75                                                         |     |
| CTT GCA AGG GCT TTG GGC GTG CGT TTT ATC TTC ACC GAA AGG GTG GAT  | 291 |
| Leu Ala Arg Ala Leu Gly Val Arg Phe Ile Phe Thr Glu Arg Val Asp  |     |
| 80 85 90                                                         |     |
| AAT ACC ATG GCG TTA AGG CGT GGC TTT GAA GTC AAA AAA AAC GAA AAA  | 339 |
| Asn Thr Met Ala Leu Arg Arg Gly Phe Glu Val Lys Lys Asn Glu Lys  |     |
| 95 100 105                                                       |     |
| ATT TTA GTG TGT GAG GAC ATT ATC ACT ACG GGA AAA TCC GCT ATG GAA  | 387 |
| Ile Leu Val Cys Glu Asp Ile Ile Thr Thr Gly Lys Ser Ala Met Glu  |     |
| 110 115 120                                                      |     |
| TGC GCT AAA GTT TTA GAA GAA AAG GGT GCT CAA ATC GTG GCT TTT GGT  | 435 |
| Cys Ala Lys Val Leu Glu Glu Lys Gly Ala Gln Ile Val Ala Phe Gly  |     |
| 125 130 135 140                                                  |     |
| GCT TTA GCT AAT CGG GGC ATT TGC AAG CGT GCT CAT TCT CAT TTA AAA  | 483 |



Ala Leu Ala Asn Arg Gly Ile Cys Lys Arg Ala His Ser His Leu Lys  
145 150 155

GCC CAA GAG GGA GCG TGT TTG CCT AGC CAT TTG CCC CTT TTT GCT TTA 531  
Ala Gln Glu Gly Ala Cys Leu Pro Ser His Leu Pro Leu Phe Ala Leu  
160 165 170

GAA GAT TTT GTT TTT GAC ATG CAC AAG CCT AGT TCT TGC CCT TTA TGC 579  
Glu Asp Phe Val Phe Asp Met His Lys Pro Ser Ser Cys Pro Leu Cys  
175 180 185

GCT ACT AGC GTT GCT ATA AAG CCA GGA AGT CGT GGC AAC TAAAAAACA AA 630  
Ala Thr Ser Val Ala Ile Lys Pro Gly Ser Arg Gly Asn  
190 195 200

AAAAAATAAA ACCCCAAAAA AAAAGCAAGC GT 662

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

Met Asp Ile Lys Ala Cys Tyr Gln Asn Ala Lys Ala Leu Leu Glu Gly  
1 5 10 15  
His Phe Leu Leu Ser Ser Gly Phe His Ser Asn Tyr Tyr Leu Gln Ser  
20 25 30  
Ala Lys Val Leu Glu Asp Pro Lys Leu Ala Glu Gln Leu Ala Leu Glu  
35 40 45  
Leu Ala Lys Gln Ile Gln Glu Ala His Leu Asn Ile Glu Cys Val Cys  
50 55 60  
Ser Pro Ala Ile Gly Gly Ile Leu Ala Gly Tyr Glu Leu Ala Arg Ala  
65 70 75 80  
Leu Gly Val Arg Phe Ile Phe Thr Glu Arg Val Asp Asn Thr Met Ala  
85 90 95  
Leu Arg Arg Gly Phe Glu Val Lys Lys Asn Glu Lys Ile Leu Val Cys  
100 105 110  
Glu Asp Ile Ile Thr Thr Gly Lys Ser Ala Met Glu Cys Ala Lys Val  
115 120 125  
Leu Glu Glu Lys Gly Ala Gln Ile Val Ala Phe Gly Ala Leu Ala Asn  
130 135 140  
Arg Gly Ile Cys Lys Arg Ala His Ser His Leu Lys Ala Gln Glu Gly  
145 150 155 160  
Ala Cys Leu Pro Ser His Leu Pro Leu Phe Ala Leu Glu Asp Phe Val  
165 170 175  
Phe Asp Met His Lys Pro Ser Ser Cys Pro Leu Cys Ala Thr Ser Val  
180 185 190  
Ala Ile Lys Pro Gly Ser Arg Gly Asn  
195 200

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 40...384
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CTCTCTTTGC GCCTAAAGGC CTTTATCACC GATATTTTT ATG ATT TAT ACC CCC    | 54  |
| Met Ile Tyr Thr Pro                                               |     |
| 1 5                                                               |     |
| ATG CTT TAT ATA ATG ACT TAT GCG ATT TTA GGG AGC GCG AAG GAT TTT   | 102 |
| Met Leu Tyr Ile Met Thr Tyr Ala Ile Leu Gly Ser Ala Lys Asp Phe   |     |
| 10 15 20                                                          |     |
| AGG GAA AAC CAG AGC GCG ATT TTT TTA TGC CTG CTT TTT TAC GCC CTA   | 150 |
| Arg Glu Asn Gln Ser Ala Ile Phe Leu Cys Leu Leu Phe Tyr Ala Leu   |     |
| 25 30 35                                                          |     |
| ACA CAC AGC TTT TTT ATC GCT TTT AAA TCC CAA AGC CCT GGC ATG CGT   | 198 |
| Thr His Ser Phe Phe Ile Ala Phe Lys Ser Gln Ser Pro Gly Met Arg   |     |
| 40 45 50                                                          |     |
| TAC GCT CGG TTT AAA TTA ATC AAA AAT AAT GGC GAA AAA GTG GGC TTT   | 246 |
| Tyr Ala Arg Phe Lys Leu Ile Lys Asn Asn Gly Glu Lys Val Gly Phe   |     |
| 55 60 65                                                          |     |
| TTT TTA GCT TTG TGG CGC TTT GTT TTG TGG GTG TTG AGC ATG GGG TTA   | 294 |
| Phe Leu Ala Leu Trp Arg Phe Val Leu Trp Val Leu Ser Met Gly Leu   |     |
| 70 75 80 85                                                       |     |
| CTC ATA GGG TTT GTT ACG CCT TTT ATT TTT AAG TTT TTT TTG CAT GAC   | 342 |
| Leu Ile Gly Phe Val Thr Pro Phe Ile Phe Lys Phe Phe Leu His Asp   |     |
| 90 95 100                                                         |     |
| AAA CTC AGC GGC ACT CAT ATT GAA ACC ATC AAG GAG GCA ACA TGAAAAATT | 393 |
| Lys Leu Ser Gly Thr His Ile Glu Thr Ile Lys Glu Ala Thr           |     |
| 105 110 115                                                       |     |
| TAGTAATC                                                          | 401 |

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Met Ile Tyr Thr Pro Met Leu Tyr Ile Met Thr Tyr Ala Ile Leu Gly  
1 5 10 15  
Ser Ala Lys Asp Phe Arg Glu Asn Gln Ser Ala Ile Phe Leu Cys Leu  
20 25 30  
Leu Phe Tyr Ala Leu Thr His Ser Phe Phe Ile Ala Phe Lys Ser Gln  
35 40 45  
Ser Pro Gly Met Arg Tyr Ala Arg Phe Lys Leu Ile Lys Asn Asn Gly  
50 55 60  
Glu Lys Val Gly Phe Phe Leu Ala Leu Trp Arg Phe Val Leu Trp Val  
65 70 75 80  
Leu Ser Met Gly Leu Ile Gly Phe Val Thr Pro Phe Ile Phe Lys  
85 90 95  
Phe Phe Leu His Asp Lys Leu Ser Gly Thr His Ile Glu Thr Ile Lys  
100 105 110  
Glu Ala Thr  
115

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 53...667
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

AGCGGGGCTG GTATTTTCAGC AGAAAGCGGG ATTAAACCT TTAGAGACGC TG ATG GCT 58  
Met Ala  
1  
TGT GGG AAA GGG CAT GAC ATC ATG GAA GTT GCC TCG CCT TAT GGC TGG 106  
Cys Gly Lys Gly His Asp Ile Met Glu Val Ala Ser Pro Tyr Gly Trp  
5 10 15  
AAA AAG AAC CCG CAA AAG GTG TTG GAT TTT TAC AAC CAA AGG CGC CGA 154  
Lys Lys Asn Pro Gln Lys Val Leu Asp Phe Tyr Asn Gln Arg Arg Arg  
20 25 30

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CAG CTT TTT GAA GTT TAT CCT AAC AAA GCC CAT AAG GCT TTA GCG GAA   | 202 |
| Gln Leu Phe Glu Val Tyr Pro Asn Lys Ala His Lys Ala Leu Ala Glu   |     |
| 35 40 45 50                                                       |     |
| TTG GAA AAA CAC TAT CAA GTC AAT ATC ATC ACC CAA AAT GTA GAT GAT   | 250 |
| Leu Glu Lys His Tyr Gln Val Asn Ile Ile Thr Gln Asn Val Asp Asp   |     |
| 55 60 65                                                          |     |
| TTG CAT GAA AGA GCG GGT TCT TCT CGC ATT TTG CAC TTG CAT GGG GAA   | 298 |
| Leu His Glu Arg Ala Gly Ser Ser Arg Ile Leu His Leu His Gly Glu   |     |
| 70 75 80                                                          |     |
| TTA TTG AGC GTT CGC AGC GAG AAA GAT CCT AAT TTA GTT TAT AGG TGG   | 346 |
| Leu Leu Ser Val Arg Ser Glu Lys Asp Pro Asn Leu Val Tyr Arg Trp   |     |
| 85 90 95                                                          |     |
| GAA AAG GAC TTG AAT TTA GGC GAC TTG GCC AAA GAC AAA TCG CAA TTA   | 394 |
| Glu Lys Asp Leu Asn Leu Gly Asp Leu Ala Lys Asp Lys Ser Gln Leu   |     |
| 100 105 110                                                       |     |
| CGC CCT GAT ATT GTG TGG TTT GGC GAA GCG GTG CCT TTG CTT AAA GAA   | 442 |
| Arg Pro Asp Ile Val Trp Phe Gly Glu Ala Val Pro Leu Leu Lys Glu   |     |
| 115 120 125 130                                                   |     |
| GCG ATT TCT TTA GTC AAA CAA GCG CAT CTT TTA ATC ATC ATT GGC ACT   | 490 |
| Ala Ile Ser Leu Val Lys Gln Ala His Leu Leu Ile Ile Ile Gly Thr   |     |
| 135 140 145                                                       |     |
| TCT TTG CAA GTC TAT CCC GCC GCT AGC CTC TAC ACG CAT GCG CAT AAA   | 538 |
| Ser Leu Gln Val Tyr Pro Ala Ala Ser Leu Tyr Thr His Ala His Lys   |     |
| 150 155 160                                                       |     |
| GAC GCT CTC ATT TAT TAC ATT GAC CCT AAG GCT AAA AAC GCC CAT TTA   | 586 |
| Asp Ala Leu Ile Tyr Tyr Ile Asp Pro Lys Ala Lys Asn Ala His Leu   |     |
| 165 170 175                                                       |     |
| CCC CAG AAT GTC CAA TGC ATT AAT GAA AGC GCG GTG CAT GCC ATG CAA   | 634 |
| Pro Gln Asn Val Gln Cys Ile Asn Glu Ser Ala Val His Ala Met Gln   |     |
| 180 185 190                                                       |     |
| GAT TTA ATG CCC AAA CTC ATA GAA ATG GCT TCT TAAGAAATGT TAAAATAATT | 687 |
| Asp Leu Met Pro Lys Leu Ile Glu Met Ala Ser                       |     |
| 195 200 205                                                       |     |
| TTTATTTTTT CAGCTAACGA TTAGCAAAAA                                  | 717 |

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Cys | Gly | Lys | Gly | His | Asp | Ile | Met | Glu | Val | Ala | Ser | Pro | Tyr |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Gly | Trp | Lys | Lys | Asn | Pro | Gln | Lys | Val | Leu | Asp | Phe | Tyr | Asn | Gln | Arg |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg | Arg | Gln | Leu | Phe | Glu | Val | Tyr | Pro | Asn | Lys | Ala | His | Lys | Ala | Leu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ala | Glu | Leu | Glu | Lys | His | Tyr | Gln | Val | Asn | Ile | Ile | Thr | Gln | Asn | Val |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Asp | Asp | Leu | His | Glu | Arg | Ala | Gly | Ser | Ser | Arg | Ile | Leu | His | Leu | His |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Gly | Glu | Leu | Leu | Ser | Val | Arg | Ser | Glu | Lys | Asp | Pro | Asn | Leu | Val | Tyr |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Arg | Trp | Glu | Lys | Asp | Leu | Asn | Leu | Gly | Asp | Leu | Ala | Lys | Asp | Lys | Ser |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Gln | Leu | Arg | Pro | Asp | Ile | Val | Trp | Phe | Gly | Glu | Ala | Val | Pro | Leu | Leu |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Lys | Glu | Ala | Ile | Ser | Leu | Val | Lys | Gln | Ala | His | Leu | Leu | Ile | Ile | Ile |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Gly | Thr | Ser | Leu | Gln | Val | Tyr | Pro | Ala | Ala | Ser | Leu | Tyr | Thr | His | Ala |  |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |  |
| His | Lys | Asp | Ala | Leu | Ile | Tyr | Tyr | Ile | Asp | Pro | Lys | Ala | Lys | Asn | Ala |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| His | Leu | Pro | Gln | Asn | Val | Gln | Cys | Ile | Asn | Glu | Ser | Ala | Val | His | Ala |  |
|     |     | 180 |     |     |     | 185 |     |     |     |     |     |     | 190 |     |     |  |
| Met | Gln | Asp | Leu | Met | Pro | Lys | Leu | Ile | Glu | Met | Ala | Ser |     |     |     |  |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 23...421
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| ATTAAAGGAG TTTGAGAGTC TG ATG CAA CAA GCC ACA GAA GCA TTG AAT CAC | 52  |
| Met Gln Gln Ala Thr Glu Ala Leu Asn His                          |     |
| 1 5 10                                                           |     |
| CCC TAT TTT GGC GTT TTT GTT TTA TTG GTA TTC ACC TTT TGG GTG TTT  | 100 |
| Pro Tyr Phe Gly Val Phe Val Leu Leu Val Phe Thr Phe Trp Val Phe  |     |
| 15 20 25                                                         |     |
| AAC TTA ACC TTA AGG ATC CAA AGG TTT TTA AGC CGT AAA ATG GCT CAA  | 148 |
| Asn Leu Thr Leu Arg Ile Gln Arg Phe Leu Ser Arg Lys Met Ala Gln  |     |
| 30 35 40                                                         |     |
| AAA AAG GGC GAA AAG CTC AAG CTC GCT CCC TAT GAA TGC GGG CCT GTG  | 196 |

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 37...831
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

|            |            |            |        |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|------------|------------|--------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AGCGATCAAA | CAAGACGCTC | CCAAAAGGTT | AGTGTG | ATG | GTA | AGA | AAA | CAA | TCC |     | 54  |     |     |     |     |     |
|            |            |            |        | Met | Val | Arg | Lys | Gln | Ser |     |     |     |     |     |     |     |
|            |            |            |        | 1   |     |     |     | 5   |     |     |     |     |     |     |     |     |
| CCC        | TAT        | GAA        | GAT    | GTG | CAA | AAA | CAA | TCG | CGC | CAG | CAT | GAC | CCC | TAT | AAA | 102 |
| Pro        | Tyr        | Glu        | Asp    | Val | Gln | Lys | Gln | Ser | Arg | Gln | His | Asp | Pro | Tyr | Lys |     |
|            |            |            | 10     |     |     |     |     | 15  |     |     |     |     | 20  |     |     |     |
| ATC        | ATA        | GAA        | CCC    | ACC | CCT | AAA | AAA | TAT | TTA | GAG | GGC | AGC | GCT | TAT | GAG | 150 |
| Ile        | Ile        | Glu        | Pro    | Thr | Pro | Lys | Lys | Tyr | Leu | Glu | Gly | Ser | Ala | Tyr | Glu |     |
|            |            | 25         |        |     |     |     | 30  |     |     |     |     | 35  |     |     |     |     |
| GTC        | ATT        | TAC        | AAC    | CAC | CTT | TCT | TAC | AAA | CAT | GAG | ATT | TTA | GAC | AAA | TAC | 198 |
| Val        | Ile        | Tyr        | Asn    | His | Leu | Ser | Tyr | Lys | His | Glu | Ile | Leu | Asp | Lys | Tyr |     |
|            | 40         |            |        |     |     | 45  |     |     |     |     | 50  |     |     |     |     |     |
| ATA        | GAG        | ACT        | AAC    | ACG | GCT | GTG | TTT | TGG | ATC | AAA | AAA | GAC | GAT | ATT | TTT | 246 |
| Ile        | Glu        | Thr        | Asn    | Thr | Ala | Val | Phe | Trp | Ile | Lys | Lys | Asp | Asp | Ile | Phe |     |
| 55         |            |            |        |     | 60  |     |     |     |     | 65  |     |     |     |     | 70  |     |
| TCT        | GTC        | GCT        | ACG    | ATT | TTA | AGG | CAT | TTG | GGT | TAT | GAG | TGT | TTG | AGC | GAA | 294 |
| Ser        | Val        | Ala        | Thr    | Ile | Leu | Arg | His | Leu | Gly | Tyr | Glu | Cys | Leu | Ser | Glu |     |
|            |            |            | 75     |     |     |     |     |     | 80  |     |     |     |     | 85  |     |     |
| ATG        | AGC        | GCG        | ATA    | GAT | TTG | TGC | GCT | AAA | AAA | GGG | CAT | TTT | GAA | TTG | TTT | 342 |
| Met        | Ser        | Ala        | Ile    | Asp | Leu | Cys | Ala | Lys | Lys | Gly | His | Phe | Glu | Leu | Phe |     |
|            |            |            | 90     |     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |
| TAT        | CAG        | TTC        | GTG    | GGC | TTT | AGC | GAT | AGC | TGC | AAG | AAC | CGC | CGT | AGG | NTG | 390 |
| Tyr        | Gln        | Phe        | Val    | Gly | Phe | Ser | Asp | Ser | Cys | Lys | Asn | Arg | Arg | Arg | Xaa |     |
|            |            | 105        |        |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     |
| CGC        | GTG        | AAG        | TGC    | GTT | TTG | TTG | CCT | AAT | GAG | AGC | GTG | GAT | TCT | TTG | AGT | 438 |
| Arg        | Val        | Lys        | Cys    | Val | Leu | Leu | Pro | Asn | Glu | Ser | Val | Asp | Ser | Leu | Ser |     |
|            |            | 120        |        |     |     | 125 |     |     |     |     |     | 130 |     |     |     |     |
| TTT        | TTA        | TAC        | CGA    | TCG | GCT | AAT | TGG | AGC | GAA | AGG | GAA | GCG | TAT | GAC | ATG | 486 |
| Phe        | Leu        | Tyr        | Arg    | Ser | Ala | Asn | Trp | Ser | Glu | Arg | Glu | Ala | Tyr | Asp | Met |     |
| 135        |            |            |        |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |     |
| CTT        | GGT        | ATT        | GTG    | TTT | GAC | AAA | CAC | CCC | TAT | TTG | AAA | CGC | CTT | ATT | ATG | 534 |
| Leu        | Gly        | Ile        | Val    | Phe | Asp | Lys | His | Pro | Tyr | Leu | Lys | Arg | Leu | Ile | Met |     |

|                                                                 |     |  |     |  |     |     |
|-----------------------------------------------------------------|-----|--|-----|--|-----|-----|
|                                                                 | 155 |  | 160 |  | 165 |     |
| CCG CAT GAT TGG GTA GGC CAC CCA TTA TTG CGC TCT TAC CCG CTC AAA |     |  |     |  |     | 582 |
| Pro His Asp Trp Val Gly His Pro Leu Leu Arg Ser Tyr Pro Leu Lys |     |  |     |  |     |     |
|                                                                 | 170 |  | 175 |  | 180 |     |
| GGC GAT GAA TTC GCC CAA TGG TAT GAA GTG GAT AAA ATT TTT GGT AAA |     |  |     |  |     | 630 |
| Gly Asp Glu Phe Ala Gln Trp Tyr Glu Val Asp Lys Ile Phe Gly Lys |     |  |     |  |     |     |
|                                                                 | 185 |  | 190 |  | 195 |     |
| GAA TAC CGA GAA GTG GTG GGT AAA GAG CAG AGA GAC AGC GCA AGA GTG |     |  |     |  |     | 678 |
| Glu Tyr Arg Glu Val Val Gly Lys Glu Gln Arg Asp Ser Ala Arg Val |     |  |     |  |     |     |
|                                                                 | 200 |  | 205 |  | 210 |     |
| GAT GAA AAA GAC ACT TTC AAT TTT GCA AAA ATT GGC TAT GAA CAG GGC |     |  |     |  |     | 726 |
| Asp Glu Lys Asp Thr Phe Asn Phe Ala Lys Ile Gly Tyr Glu Gln Gly |     |  |     |  |     |     |
|                                                                 | 215 |  | 220 |  | 225 | 230 |
| AAG GGC GAA GAA TTA AAA GAA GTA GAA GAA AAG CAT GCG TTT AAG AAA |     |  |     |  |     | 774 |
| Lys Gly Glu Glu Leu Lys Glu Val Glu Glu Lys His Ala Phe Lys Lys |     |  |     |  |     |     |
|                                                                 | 235 |  | 240 |  | 245 |     |
| ATC CCT TTT GTC AAA GAT TTG CAC AAA ATC GCC CCC ACT ATC TTA AAA |     |  |     |  |     | 822 |
| Ile Pro Phe Val Lys Asp Leu His Lys Ile Ala Pro Thr Ile Leu Lys |     |  |     |  |     |     |
|                                                                 | 250 |  | 255 |  | 260 |     |
| AAG AGG CTA TAAATGGCT CAAAATTTC AAGAACTCAA CCC                  |     |  |     |  |     | 864 |
| Lys Arg Leu                                                     |     |  |     |  |     |     |
|                                                                 | 265 |  |     |  |     |     |

(2) INFORMATION FOR SEQ ID NO:306:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 265 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Val Arg Lys Gln Ser Pro Tyr Glu Asp Val Gln Lys Gln Ser Arg |  |
| 1 5 10 15                                                       |  |
| Gln His Asp Pro Tyr Lys Ile Ile Glu Pro Thr Pro Lys Lys Tyr Leu |  |
| 20 25 30                                                        |  |
| Glu Gly Ser Ala Tyr Glu Val Ile Tyr Asn His Leu Ser Tyr Lys His |  |
| 35 40 45                                                        |  |
| Glu Ile Leu Asp Lys Tyr Ile Glu Thr Asn Thr Ala Val Phe Trp Ile |  |
| 50 55 60                                                        |  |
| Lys Lys Asp Asp Ile Phe Ser Val Ala Thr Ile Leu Arg His Leu Gly |  |
| 65 70 75 80                                                     |  |
| Tyr Glu Cys Leu Ser Glu Met Ser Ala Ile Asp Leu Cys Ala Lys Lys |  |
| 85 90 95                                                        |  |
| Gly His Phe Glu Leu Phe Tyr Gln Phe Val Gly Phe Ser Asp Ser Cys |  |
| 100 105 110                                                     |  |
| Lys Asn Arg Arg Arg Xaa Arg Val Lys Cys Val Leu Leu Pro Asn Glu |  |





|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|
| GCC<br>Ala | ACC<br>Thr | ATT<br>Ile | CTC<br>Leu | ACT<br>Thr | AAC<br>Asn | ACC<br>Thr | CCA<br>Pro | ACG<br>Thr | CTC<br>Leu | ATG<br>Met | GAT<br>Asp | GAA<br>Glu | AGA<br>Arg | AAA<br>Lys | AGC<br>Ser | 297 |
|            | 70         |            |            |            |            |            | 75         |            |            |            |            | 80         |            |            |            |     |
| ATC<br>Ile | ATG<br>Met | CAA<br>Gln | ACT<br>Thr | TAT<br>Tyr | GAT<br>Asp | GTC<br>Val | AAC<br>Asn | CAC<br>His | CCC<br>Pro | CTA<br>Leu | GAG<br>Glu | TGT<br>Cys | GGC<br>Gly | GTG<br>Val | TGC<br>Cys | 345 |
|            | 85         |            |            |            |            | 90         |            |            |            |            | 95         |            |            |            |            |     |
| GAT<br>Asp | AAG<br>Lys | AGT<br>Ser | GGG<br>Gly | GAG<br>Glu | TGC<br>Cys | GAA<br>Glu | TTG<br>Leu | CAA<br>Gln | GAC<br>Asp | ATG<br>Met | ACG<br>Thr | CAT<br>His | TTA<br>Leu | ACC<br>Thr | GGC<br>Gly | 393 |
| 100        |            |            |            |            | 105        |            |            |            |            | 110        |            |            |            |            | 115        |     |
| GTA<br>Val | GAG<br>Glu | CAC<br>His | CAA<br>Gln | CCC<br>Pro | TAT<br>Tyr | GCG<br>Ala | GTG<br>Val | GCT<br>Ala | GAT<br>Asp | GAT<br>Asp | TTT<br>Phe | AAA<br>Lys | GCA<br>Ala | CTG<br>Leu | GAT<br>Asp | 441 |
|            |            |            |            |            | 120        |            |            |            | 125        |            |            |            |            | 130        |            |     |
| TTT<br>Phe | TGG<br>Trp | GCA<br>Ala | AAA<br>Lys | GCC<br>Ala | TTG<br>Leu | TAT<br>Tyr | GAT<br>Asp | CCT<br>Pro | AAT<br>Asn | TTG<br>Leu | TGC<br>Cys | ATC<br>Ile | ATG<br>Met | TGT<br>Cys | GAA<br>Glu | 489 |
|            |            |            | 135        |            |            |            |            | 140        |            |            |            |            | 145        |            |            |     |
| AGG<br>Arg | TGC<br>Cys | GTA<br>Val | ACC<br>Thr | ACT<br>Thr | TGT<br>Cys | AAG<br>Lys | GAC<br>Asp | AAT<br>Asn | GTG<br>Val | GGC<br>Gly | GAA<br>Glu | AAC<br>Asn | AAC<br>Asn | CTT<br>Leu | AAA<br>Lys | 537 |
|            |            | 150        |            |            |            |            | 155        |            |            |            |            | 160        |            |            |            |     |
| GCC<br>Ala | ACT<br>Thr | AAA<br>Lys | GCC<br>Ala | GAC<br>Asp | TTG<br>Leu | CAT<br>His | GCT<br>Ala | CCG<br>Pro | GAT<br>Asp | AAA<br>Lys | TTT<br>Phe | AAA<br>Lys | GAC<br>Asp | AGC<br>Ser | ATG<br>Met | 585 |
|            | 165        |            |            |            |            | 170        |            |            |            |            | 175        |            |            |            |            |     |
| TCC<br>Ser | AAA<br>Lys | GAC<br>Asp | GCT<br>Ala | TTT<br>Phe | AGC<br>Ser | GTG<br>Val | TGG<br>Trp | AGT<br>Ser | CGT<br>Arg | AAG<br>Lys | CAA<br>Gln | AAA<br>Lys | GGC<br>Gly | ATT<br>Ile | ATT<br>Ile | 633 |
| 180        |            |            |            |            | 185        |            |            |            |            | 190        |            |            |            |            | 195        |     |
| TCT<br>Ser | TTT<br>Phe | GTG<br>Val | GGC<br>Gly | AGC<br>Ser | GTG<br>Val | CCT<br>Pro | TGC<br>Cys | TAT<br>Tyr | GAT<br>Asp | TGC<br>Cys | GGG<br>Gly | GAA<br>Glu | TGC<br>Cys | ATT<br>Ile | GCA<br>Ala | 681 |
|            |            |            |            | 200        |            |            |            |            | 205        |            |            |            |            | 210        |            |     |
| GTA<br>Val | TGC<br>Cys | CCT<br>Pro | GTG<br>Val | GGC<br>Gly | GCT<br>Ala | TTG<br>Leu | AGC<br>Ser | TAT<br>Tyr | AAA<br>Lys | GAT<br>Asp | TTC<br>Phe | GCT<br>Ala | TAC<br>Tyr | ACG<br>Thr | GCT<br>Ala | 729 |
|            |            | 215        |            |            |            |            |            | 220        |            |            |            |            | 225        |            |            |     |
| AAC<br>Asn | GCA<br>Ala | TGG<br>Trp | GAG<br>Glu | TTA<br>Leu | AAA<br>Lys | AAG<br>Lys | ATC<br>Ile | CAT<br>His | TCT<br>Ser | ACT<br>Thr | TGT<br>Cys | TCG<br>Ser | CAT<br>His | TGC<br>Cys | TCG<br>Ser | 777 |
|            |            | 230        |            |            |            |            | 235        |            |            |            |            | 240        |            |            |            |     |
| GCC<br>Ala | GGG<br>Gly | TGT<br>Cys | TTG<br>Leu | ATT<br>Ile | TCT<br>Ser | TAT<br>Tyr | GAT<br>Asp | GTG<br>Val | CGC<br>Arg | CAT<br>His | TTT<br>Phe | GAT<br>Asp | ACT<br>Thr | CTA<br>Leu | GGC<br>Gly | 825 |
|            | 245        |            |            |            |            | 250        |            |            |            |            | 255        |            |            |            |            |     |
| GAA<br>Glu | GAA<br>Glu | TCT<br>Ser | AAA<br>Lys | ATT<br>Ile | TTT<br>Phe | AGA<br>Arg | GTG<br>Val | CTT<br>Leu | AAT<br>Asn | GAT<br>Asp | TTT<br>Phe | TAC<br>Tyr | CAT<br>His | AAC<br>Asn | CCT<br>Pro | 873 |
| 260        |            |            |            |            | 265        |            |            |            |            | 270        |            |            |            |            | 275        |     |
| ATT<br>Ile | TGT<br>Cys | GGG<br>Gly | GCA<br>Ala | GGC<br>Gly | CGT<br>Arg | TTC<br>Phe | GCT<br>Ala | TTT<br>Phe | GAT<br>Asp | GTG<br>Val | AGC<br>Ser | TCT<br>Ser | AGC<br>Ser | CCT<br>Pro | AAA<br>Lys | 921 |
|            |            |            |            | 280        |            |            |            | 285        |            |            |            |            |            | 290        |            |     |
| GGC<br>Gly | AGT<br>Ser | GCT<br>Ala | AAT<br>Asn | CTT<br>Leu | AAA<br>Lys | GAA<br>Glu | GCG<br>Ala | CAA<br>Gln | AAC<br>Asn | GCC<br>Ala | CTC<br>Leu | AAA<br>Lys | GAA<br>Glu | TGC<br>Cys | GAA<br>Glu | 969 |









Gln Leu Glu Gly Thr Ile Thr Asn Ile Glu Gly Arg Val Leu Pro Leu  
645 650 655  
Lys Pro Ala Leu Arg Phe Glu Gly Tyr Asp Leu Ser Asp Ile Met Gln  
660 665 670  
Gly Phe Gly Phe Val Glu Glu Asn Leu Ile Glu Cys Thr His Lys Leu  
675 680 685  
Pro Thr Glu Ala Gly Phe Lys Ala Ile Glu Phe Asp Tyr Leu Thr Asn  
690 695 700  
Tyr Phe Ala Asn Asp Arg Val Asn His Arg Gly Tyr Leu Leu Gly Thr  
705 710 715 720  
Ser His Phe Glu Lys Ser Ala Lys Glu Cys Glu Thr Ile Glu Cys Glu  
725 730 735  
Pro Ile Lys Pro Leu Lys Glu Lys Ile Ala Phe Asn Ala Tyr Leu Lys  
740 745 750  
Tyr Pro Glu Thr Gln Phe Asn Asn Ala Thr Asn Lys Ser Glu Asn Leu  
755 760 765  
Gln Leu Lys Ala Gly Val Tyr Val Ser Lys Ala Phe Leu Lys Lys Leu  
770 775 780  
Asn Lys Glu Val Gly Gln Asn Ile Thr Leu Ser Lys Glu Glu Glu Glu  
785 790 795 800  
Leu Thr Gly Val Leu Tyr Leu Asp Glu Ser Leu Asp Gln Glu Val Phe  
805 810 815  
Val Ile Ser Pro Ser Leu Leu Lys Asn His Ser Gly Phe Phe Arg Glu  
820 825 830  
Gly Val Phe Asp Ser Val Asp Leu Lys Glu Gln Ala  
835 840

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 44...343
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

|                                                                 |            |            |            |     |     |     |     |     |    |
|-----------------------------------------------------------------|------------|------------|------------|-----|-----|-----|-----|-----|----|
| AAATCCATGG                                                      | GAAAAATCAC | ACGCAATTTA | TAAAGGAATC | TCT | ATG | ATA | GGG | TTA | 55 |
|                                                                 |            |            |            |     | Met | Ile | Gly | Leu |    |
|                                                                 |            |            |            |     | 1   |     |     |     |    |
| AAC CAC TAT TTG ATT GTT TCA GGG TTG CTC TTT TGC ATT GGT TTA GCG | 103        |            |            |     |     |     |     |     |    |
| Asn His Tyr Leu Ile Val Ser Gly Leu Leu Phe Cys Ile Gly Leu Ala |            |            |            |     |     |     |     |     |    |
| 5 10 15 20                                                      |            |            |            |     |     |     |     |     |    |
| GGC ATG CTG AAA CGC AAA AAC ATT CTG TTA CTC TTT TTT TCT ACA GAA | 151        |            |            |     |     |     |     |     |    |
| Gly Met Leu Lys Arg Lys Asn Ile Leu Leu Leu Phe Phe Ser Thr Glu |            |            |            |     |     |     |     |     |    |
| 25 30 35                                                        |            |            |            |     |     |     |     |     |    |
| ATC ATG CTC AAT GCG ATC AAT ATC GGT TTT GTA GCG ATC TCT AAA TAC | 199        |            |            |     |     |     |     |     |    |

Ile Met Leu Asn Ala Ile Asn Ile Gly Phe Val Ala Ile Ser Lys Tyr  
40 45 50

ACG CAT AAT TTA GAC GGG CAG ATG TTT GCG CTC TTT ATT ATC TCT ATT 247  
Thr His Asn Leu Asp Gly Gln Met Phe Ala Leu Phe Ile Ile Ser Ile  
55 60 65

GCC GCT AGT GAG GTG GCT ATT GGT TTG GGC TTG GTG ATT TTG TGG TTT 295  
Ala Ala Ser Glu Val Ala Ile Gly Leu Gly Leu Val Ile Leu Trp Phe  
70 75 80

AAG AAA TTC AAA AGC TTA GAT ATT GAT TCT TTA AAC GCT ATG AAA GGT T 344  
Lys Lys Phe Lys Ser Leu Asp Ile Asp Ser Leu Asn Ala Met Lys Gly  
85 90 95 100

GAGCATGCAA TATTCTTCTT TGCTGTCAGT GGTG 378

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

Met Ile Gly Leu Asn His Tyr Leu Ile Val Ser Gly Leu Leu Phe Cys  
1 5 10 15  
Ile Gly Leu Ala Gly Met Leu Lys Arg Lys Asn Ile Leu Leu Phe  
20 25 30  
Phe Ser Thr Glu Ile Met Leu Asn Ala Ile Asn Ile Gly Phe Val Ala  
35 40 45  
Ile Ser Lys Tyr Thr His Asn Leu Asp Gly Gln Met Phe Ala Leu Phe  
50 55 60  
Ile Ile Ser Ile Ala Ala Ser Glu Val Ala Ile Gly Leu Gly Leu Val  
65 70 75 80  
Ile Leu Trp Phe Lys Lys Phe Lys Ser Leu Asp Ile Asp Ser Leu Asn  
85 90 95  
Ala Met Lys Gly  
100

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...627
- (D) OTHER INFORMATION:



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CCGGTGAAT AAGTC ATG CAA GCA GTG ATT TTA GCG AAT GGG GAG TTT CCT   | 51  |
| Met Gln Ala Val Ile Leu Ala Asn Gly Glu Phe Pro                   |     |
| 1 5 10                                                            |     |
| AAA TCT CAA AAA TGC TTA GAC CTT TTA AAA AAC GCT CCC TTT TTA ATC   | 99  |
| Lys Ser Gln Lys Cys Leu Asp Leu Leu Lys Asn Ala Pro Phe Leu Ile   |     |
| 15 20 25                                                          |     |
| GCA TGC GAT GGG GCT GTT ACC TCA TTA CAT GCG CTT CAA TTC AAA CCC   | 147 |
| Ala Cys Asp Gly Ala Val Thr Ser Leu His Ala Leu Gln Phe Lys Pro   |     |
| 30 35 40                                                          |     |
| AGC GTT GTT ATA GGC GAT CTA GAT AGC ATT GAT TCG CAT TTG AAA GCT   | 195 |
| Ser Val Val Ile Gly Asp Leu Asp Ser Ile Asp Ser His Leu Lys Ala   |     |
| 45 50 55 60                                                       |     |
| TTG TAT AAC CCT ATA CGC ATG AGT GAA CAA AAC AGC AAC GAT TTG TCC   | 243 |
| Leu Tyr Asn Pro Ile Arg Met Ser Glu Gln Asn Ser Asn Asp Leu Ser   |     |
| 65 70 75                                                          |     |
| AAA GCC TTT TTT TAT GCT TTA AAT AAA GGC TGT GAT GAC TTT ATT TTT   | 291 |
| Lys Ala Phe Phe Tyr Ala Leu Asn Lys Gly Cys Asp Asp Phe Ile Phe   |     |
| 80 85 90                                                          |     |
| TTA GGG TTG AAT GGC AAG CGA GAA GAT CAC GCT TTA GCG AAC ACT TTT   | 339 |
| Leu Gly Leu Asn Gly Lys Arg Glu Asp His Ala Leu Ala Asn Thr Phe   |     |
| 95 100 105                                                        |     |
| TTA TTG TTG GAA TAT TTT AAA TTT TGC CAA AAA ATC CAA GCC ATA AGC   | 387 |
| Leu Leu Leu Glu Tyr Phe Lys Phe Cys Gln Lys Ile Gln Ala Ile Ser   |     |
| 110 115 120                                                       |     |
| GAC TAT GGT CTT TTT AGG GTG TTA GAA ACC CCT TTC ACT TTG CCC AGT   | 435 |
| Asp Tyr Gly Leu Phe Arg Val Leu Glu Thr Pro Phe Thr Leu Pro Ser   |     |
| 125 130 135 140                                                   |     |
| TTT AAA GGG GAA CAA ATC TCG CTT TTT AGC CTG GAT CTT AAA GCC CAA   | 483 |
| Phe Lys Gly Glu Gln Ile Ser Leu Phe Ser Leu Asp Leu Lys Ala Gln   |     |
| 145 150 155                                                       |     |
| TTC ACT TCT AAA AAC CTC AAA TAC CCC TTA AAA AAC TTG CGT TTA AAA   | 531 |
| Phe Thr Ser Lys Asn Leu Lys Tyr Pro Leu Lys Asn Leu Arg Leu Lys   |     |
| 160 165 170                                                       |     |
| ACG CTC TTT TCT GGC TCG CTC AAT GAA GCT ACA GAT AGT TAT TTT AGC   | 579 |
| Thr Leu Phe Ser Gly Ser Leu Asn Glu Ala Thr Asp Ser Tyr Phe Ser   |     |
| 175 180 185                                                       |     |
| CTT AGC TCT ACA CCT AAA TCG GTG GTG TTG GTG TAT CAA AAA TTC TTA T | 628 |
| Leu Ser Ser Thr Pro Lys Ser Val Val Leu Val Tyr Gln Lys Phe Leu   |     |
| 190 195 200                                                       |     |
| AAGCGGGTTT TGTTAGGCAA GTTTTTGTCT GTATA                            | 663 |

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

```

Met Gln Ala Val Ile Leu Ala Asn Gly Glu Phe Pro Lys Ser Gln Lys
 1 5 10 15
Cys Leu Asp Leu Leu Lys Asn Ala Pro Phe Leu Ile Ala Cys Asp Gly
 20 25 30
Ala Val Thr Ser Leu His Ala Leu Gln Phe Lys Pro Ser Val Val Ile
 35 40 45
Gly Asp Leu Asp Ser Ile Asp Ser His Leu Lys Ala Leu Tyr Asn Pro
 50 55 60
Ile Arg Met Ser Glu Gln Asn Ser Asn Asp Leu Ser Lys Ala Phe Phe
 65 70 75 80
Tyr Ala Leu Asn Lys Gly Cys Asp Asp Phe Ile Phe Leu Gly Leu Asn
 85 90 95
Gly Lys Arg Glu Asp His Ala Leu Ala Asn Thr Phe Leu Leu Leu Glu
 100 105 110
Tyr Phe Lys Phe Cys Gln Lys Ile Gln Ala Ile Ser Asp Tyr Gly Leu
 115 120 125
Phe Arg Val Leu Glu Thr Pro Phe Thr Leu Pro Ser Phe Lys Gly Glu
 130 135 140
Gln Ile Ser Leu Phe Ser Leu Asp Leu Lys Ala Gln Phe Thr Ser Lys
 145 150 155 160
Asn Leu Lys Tyr Pro Leu Lys Asn Leu Arg Leu Lys Thr Leu Phe Ser
 165 170 175
Gly Ser Leu Asn Glu Ala Thr Asp Ser Tyr Phe Ser Leu Ser Ser Thr
 180 185 190
Pro Lys Ser Val Val Leu Val Tyr Gln Lys Phe Leu
 195 200

```

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 17...1048
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:



| 225                                                               | 230 | 235 |      |
|-------------------------------------------------------------------|-----|-----|------|
| AGA CCC ATT GCT AAC ACG GAG TAT TCA GGC GAT TAC GCT CAA AGA GAT   |     |     | 772  |
| Arg Pro Ile Ala Asn Thr Glu Tyr Ser Gly Asp Tyr Ala Gln Arg Asp   |     |     |      |
| 240                                                               | 245 | 250 |      |
| GAC GCT AAA GAC TTG AGC GCT AAG ATT GAA AGC ATG AAT TTG AGC GCT   |     |     | 820  |
| Asp Ala Lys Asp Leu Ser Ala Lys Ile Glu Ser Met Asn Leu Ser Ala   |     |     |      |
| 255                                                               | 260 | 265 |      |
| AGG TGT TTT AAT TGC TTG GAT AAA ATC GGC ATC AAG TAT GTG GGC GAA   |     |     | 868  |
| Arg Cys Phe Asn Cys Leu Asp Lys Ile Gly Ile Lys Tyr Val Gly Glu   |     |     |      |
| 270                                                               | 275 | 280 |      |
| CTC GTG TTG ATG AGC GAA GAA GAG CTT AAG GGC GTG AAA AAC ATG GGT   |     |     | 916  |
| Leu Val Leu Met Ser Glu Glu Glu Leu Lys Gly Val Lys Asn Met Gly   |     |     |      |
| 285                                                               | 290 | 295 | 300  |
| AAA AAA TCC TAT GAT GAA ATC GCT GAA AAA TTG AAT GAT TTG GGC TAT   |     |     | 964  |
| Lys Lys Ser Tyr Asp Glu Ile Ala Glu Lys Leu Asn Asp Leu Gly Tyr   |     |     |      |
| 305                                                               | 310 | 315 |      |
| CCG GTA GGC ACA GAA TTA AGC CCT GAA CAA AGA GAG AGT TTA AAG AAA   |     |     | 1012 |
| Pro Val Gly Thr Glu Leu Ser Pro Glu Gln Arg Glu Ser Leu Lys Lys   |     |     |      |
| 320                                                               | 325 | 330 |      |
| AGA TTA GAA AAA TTA GAA GAT AAA GGA GGT AAC GAC TGATGAGACA CAAACA |     |     | 1064 |
| Arg Leu Glu Lys Leu Glu Asp Lys Gly Gly Asn Asp                   |     |     |      |
| 335                                                               | 340 |     |      |
| CGGATACCGC AAGCTTGGGA GAACCAGCTC GCACAGAAAG GC                    |     |     | 1106 |

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Val | Ile | Lys | Thr | Ala | Pro | Leu | Ile | Pro | Ser | Glu | Ile | Lys | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Glu | Lys | Glu | Gly | Asn | Arg | Val | Lys | Ile | Ser | Leu | Ala | Pro | Phe | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Gly | Tyr | Ala | Val | Thr | Leu | Ala | His | Pro | Ile | Arg | Arg | Leu | Leu | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Ser | Ser | Val | Gly | Tyr | Ala | Pro | Val | Gly | Leu | Lys | Ile | Glu | Gly | Val |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| His | His | Glu | Phe | Asp | Ser | Leu | Arg | Gly | Val | Thr | Glu | Asp | Val | Ser | Leu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Phe | Ile | Met | Asn | Leu | Lys | Asn | Ile | Arg | Phe | Ile | Ala | Lys | Ala | Leu | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | Gln | Asp | Ser | Ser | Leu | Glu | Asn | Gln | Ser | Val | Val | Val | Asp | Tyr | Ser |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |



|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AGT TCC AGA GAG ATT TTA GAA GCG GTA GGC ATT TCT TTT GAC AAG CGC   | 147 |
| Ser Ser Arg Glu Ile Leu Glu Ala Val Gly Ile Ser Phe Asp Lys Arg   |     |
| 30 35 40                                                          |     |
| GTG CAT GAA TTG AGC GAA GAT GAA GTG TCT AGC ATC GCT AAA AAA ATC   | 195 |
| Val His Glu Leu Ser Glu Asp Glu Val Ser Ser Ile Ala Lys Lys Ile   |     |
| 45 50 55 60                                                       |     |
| CAA CAA AGC TAC CTA GTA GAG GGC GAT TTG CGT AAA AAA GTT CAA ATG   | 243 |
| Gln Gln Ser Tyr Leu Val Glu Gly Asp Leu Arg Lys Lys Val Gln Met   |     |
| 65 70 75                                                          |     |
| GAT ATT AAA TCT TTA ATG GAC TTG GGG AAT TAT CGT GGG ATC AGG CAT   | 291 |
| Asp Ile Lys Ser Leu Met Asp Leu Gly Asn Tyr Arg Gly Ile Arg His   |     |
| 80 85 90                                                          |     |
| CGT AAG GGT CTT CCT GTG AGA GGT CAA ACC ACT AAA AAT AAC GCT AGG   | 339 |
| Arg Lys Gly Leu Pro Val Arg Gly Gln Thr Thr Lys Asn Asn Ala Arg   |     |
| 95 100 105                                                        |     |
| ACT CGT AAG GGT AAG AAA AAA ACC GTG GGT AGC AAG TAGCGAATAA GGAGAT | 391 |
| Thr Arg Lys Gly Lys Lys Thr Val Gly Ser Lys                       |     |
| 110 115 120                                                       |     |
| GATGATTTAA TGGCTAAGAG AAATGTAACG GC                               | 423 |

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ala Arg Ile Ala Gly Val Asp Leu Pro Lys Lys Lys Arg Val Glu |  |
| 1 5 10 15                                                       |  |
| Tyr Ala Leu Thr Tyr Ile Tyr Gly Ile Gly Leu Lys Ser Ser Arg Glu |  |
| 20 25 30                                                        |  |
| Ile Leu Glu Ala Val Gly Ile Ser Phe Asp Lys Arg Val His Glu Leu |  |
| 35 40 45                                                        |  |
| Ser Glu Asp Glu Val Ser Ser Ile Ala Lys Lys Ile Gln Gln Ser Tyr |  |
| 50 55 60                                                        |  |
| Leu Val Glu Gly Asp Leu Arg Lys Lys Val Gln Met Asp Ile Lys Ser |  |
| 65 70 75 80                                                     |  |
| Leu Met Asp Leu Gly Asn Tyr Arg Gly Ile Arg His Arg Lys Gly Leu |  |
| 85 90 95                                                        |  |
| Pro Val Arg Gly Gln Thr Thr Lys Asn Asn Ala Arg Thr Arg Lys Gly |  |
| 100 105 110                                                     |  |
| Lys Lys Lys Thr Val Gly Ser Lys                                 |  |
| 115 120                                                         |  |

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 649 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 19...621  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AAGCGTAGGG TGTTTTTA ATG ATT TTT TAT AGA AAG GAA GCT ACA ATG AAC | 51  |
| Met Ile Phe Tyr Arg Lys Glu Ala Thr Met Asn                     |     |
| 1 5 10                                                          |     |
| GCA TTG AAA AAA TTA AGT TTC TGC GCC TTG TTA TCC CTA GGC CTC TTC | 99  |
| Ala Leu Lys Lys Leu Ser Phe Cys Ala Leu Leu Ser Leu Gly Leu Phe |     |
| 15 20 25                                                        |     |
| GCT CAA ACA GCG CAT GCT AAG CAT TTA AAG GGC ACG ATT AAC TAT CCT | 147 |
| Ala Gln Thr Ala His Ala Lys His Leu Lys Gly Thr Ile Asn Tyr Pro |     |
| 30 35 40                                                        |     |
| GAT TGG CTT GAA ATC AAT TTT TTT GAC GAA AAA AAC CCG CCC AAT CAA | 195 |
| Asp Trp Leu Glu Ile Asn Phe Phe Asp Glu Lys Asn Pro Pro Asn Gln |     |
| 45 50 55                                                        |     |
| TAT GTC GGA TCG GCT TCA ATT TCT GGT AAA AGG AAC GAT TTT TAC GCC | 243 |
| Tyr Val Gly Ser Ala Ser Ile Ser Gly Lys Arg Asn Asp Phe Tyr Ala |     |
| 60 65 70 75                                                     |     |
| AAT TAC ATC CCC TAT GAT GAC CAA TTG CCC CCT GAA CAA AAC GCT GAA | 291 |
| Asn Tyr Ile Pro Tyr Asp Asp Gln Leu Pro Pro Glu Gln Asn Ala Glu |     |
| 80 85 90                                                        |     |
| AAA ATC GCT CTT TTA AGG GCC AGA ATA AAC GCT TAC AGC ACT TTA GAG | 339 |
| Lys Ile Ala Leu Leu Arg Ala Arg Ile Asn Ala Tyr Ser Thr Leu Glu |     |
| 95 100 105                                                      |     |
| AGC ATT TTA CTC ACT AAA ATG CAC AAT CGT ATT GTT AAG GTG CTT CAA | 387 |
| Ser Ile Leu Leu Thr Lys Met His Asn Arg Ile Val Lys Val Leu Gln |     |
| 110 115 120                                                     |     |
| GTT AAA AAT AAT GTT ATC AGC CAT TTA TTC GGG CTT GTT GAT TTT TTA | 435 |
| Val Lys Asn Asn Val Ile Ser His Leu Phe Gly Leu Val Asp Phe Leu |     |
| 125 130 135                                                     |     |
| ACC TCT AAA TCC ATT TTG GCT AAA AGG TTC GTG GAT ACC ACA AAT CAT | 483 |
| Thr Ser Lys Ser Ile Leu Ala Lys Arg Phe Val Asp Thr Thr Asn His |     |
| 140 145 150 155                                                 |     |
| CGT GTG TAT GTC ATG GTG CAA TTC CCT TTC ATT CAG CCT GAA GAC TTG | 531 |
| Arg Val Tyr Val Met Val Gln Phe Pro Phe Ile Gln Pro Glu Asp Leu |     |
| 160 165 170                                                     |     |

ATC GCT TAC TTT AAA GCC AAA CGC ATC GAC CTT TCT TCA GCG AGC GCT 579  
 Ile Ala Tyr Phe Lys Ala Lys Arg Ile Asp Leu Ser Ser Ala Ser Ala  
                   175                                  180                                  185

ACC CAT CTC AGC GCC CTT TTA AAT AAG GCG TTG TTC CAC CTC TAAGAGTTT 630  
 Thr His Leu Ser Ala Leu Leu Asn Lys Ala Leu Phe His Leu  
                   190                                  195                                  200

GGGATTTAAG ATGCGGTTT 649

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Phe | Tyr | Arg | Lys | Glu | Ala | Thr | Met | Asn | Ala | Leu | Lys | Lys | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Phe | Cys | Ala | Leu | Leu | Ser | Leu | Gly | Leu | Phe | Ala | Gln | Thr | Ala | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Lys | His | Leu | Lys | Gly | Thr | Ile | Asn | Tyr | Pro | Asp | Trp | Leu | Glu | Ile |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Asn | Phe | Phe | Asp | Glu | Lys | Asn | Pro | Pro | Asn | Gln | Tyr | Val | Gly | Ser | Ala |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ser | Ile | Ser | Gly | Lys | Arg | Asn | Asp | Phe | Tyr | Ala | Asn | Tyr | Ile | Pro | Tyr |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Asp | Gln | Leu | Pro | Pro | Glu | Gln | Asn | Ala | Glu | Lys | Ile | Ala | Leu | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Arg | Ala | Arg | Ile | Asn | Ala | Tyr | Ser | Thr | Leu | Glu | Ser | Ile | Leu | Leu | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Met | His | Asn | Arg | Ile | Val | Lys | Val | Leu | Gln | Val | Lys | Asn | Asn | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Ser | His | Leu | Phe | Gly | Leu | Val | Asp | Phe | Leu | Thr | Ser | Lys | Ser | Ile |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Leu | Ala | Lys | Arg | Phe | Val | Asp | Thr | Thr | Asn | His | Arg | Val | Tyr | Val | Met |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Val | Gln | Phe | Pro | Phe | Ile | Gln | Pro | Glu | Asp | Leu | Ile | Ala | Tyr | Phe | Lys |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ala | Lys | Arg | Ile | Asp | Leu | Ser | Ser | Ala | Ser | Ala | Thr | His | Leu | Ser | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Leu | Asn | Lys | Ala | Leu | Phe | His | Leu |     |     |     |     |     |     |     |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA



(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...513
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GCATGCTCTT AGAGT ATG TCT GTA TCG CAT GTT GCT TTA ATC TTA AGG AAA  | 51  |
| Met Ser Val Ser His Val Ala Leu Ile Leu Arg Lys                   |     |
| 1 5 10                                                            |     |
| TTG TTT TAT CAT AGA CAA GGA GTT TTT ATG GGC GGT TTT TCA GTG GGA   | 99  |
| Leu Phe Tyr His Arg Gln Gly Val Phe Met Gly Gly Phe Ser Val Gly   |     |
| 15 20 25                                                          |     |
| ATG TTG AAA GAT TAT GTG GAC ATA TTT GTT TTT GCG GTG CTT GGC GTG   | 147 |
| Met Leu Lys Asp Tyr Val Asp Ile Phe Val Phe Ala Val Leu Gly Val   |     |
| 30 35 40                                                          |     |
| GCC AGT TTT TTA GCT TTG TGG TTT GCG ATT GAA AGG GTT ATT TTT TAT   | 195 |
| Ala Ser Phe Leu Ala Leu Trp Phe Ala Ile Glu Arg Val Ile Phe Tyr   |     |
| 45 50 55 60                                                       |     |
| TCT AAA GTC GAT TTG AAA GCT TAT GAC GAT ATA GAT GCC CTG AAT TTG   | 243 |
| Ser Lys Val Asp Leu Lys Ala Tyr Asp Asp Ile Asp Ala Leu Asn Leu   |     |
| 65 70 75                                                          |     |
| GAT TTA ACC AAG AAT CTA ACC ATT CTC TAT GTG ATT TTT TCT AAC GCG   | 291 |
| Asp Leu Thr Lys Asn Leu Thr Ile Leu Tyr Val Ile Phe Ser Asn Ala   |     |
| 80 85 90                                                          |     |
| CCT TAT GTG GGC TTA TTA GGG ACG GTT TTA GGG ATT ATG GTG ATT TTC   | 339 |
| Pro Tyr Val Gly Leu Leu Gly Thr Val Leu Gly Ile Met Val Ile Phe   |     |
| 95 100 105                                                        |     |
| TAT GAC ATG GGC GTG AGC GGC GGG ATG GAC GCT AAA ACG ATC ATG GTA   | 387 |
| Tyr Asp Met Gly Val Ser Gly Gly Met Asp Ala Lys Thr Ile Met Val   |     |
| 110 115 120                                                       |     |
| GGT TTG TCT TTG GCT TTA AAA GCG ACC GCT CTA GGG CTT GCT GTG GCG   | 435 |
| Gly Leu Ser Leu Ala Leu Lys Ala Thr Ala Leu Gly Leu Ala Val Ala   |     |
| 125 130 135 140                                                   |     |
| ATT CCC ACT TTG ATC GCT TAT AAT AGC TTG TTG AGA AAA TCC GAT GTT   | 483 |
| Ile Pro Thr Leu Ile Ala Tyr Asn Ser Leu Leu Arg Lys Ser Asp Val   |     |
| 145 150 155                                                       |     |
| TTG AGC GAA AAA TTC AGG ATC ATG AAA AAA TGAAAAGCAT CAGAAGAGGC GAT | 536 |
| Leu Ser Glu Lys Phe Arg Ile Met Lys Lys                           |     |
| 160 165                                                           |     |
| GGGC                                                              | 540 |

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Val | Ser | His | Val | Ala | Leu | Ile | Leu | Arg | Lys | Leu | Phe | Tyr | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Gln | Gly | Val | Phe | Met | Gly | Gly | Phe | Ser | Val | Gly | Met | Leu | Lys | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Val | Asp | Ile | Phe | Val | Phe | Ala | Val | Leu | Gly | Val | Ala | Ser | Phe | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Leu | Trp | Phe | Ala | Ile | Glu | Arg | Val | Ile | Phe | Tyr | Ser | Lys | Val | Asp |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Lys | Ala | Tyr | Asp | Asp | Ile | Asp | Ala | Leu | Asn | Leu | Asp | Leu | Thr | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asn | Leu | Thr | Ile | Leu | Tyr | Val | Ile | Phe | Ser | Asn | Ala | Pro | Tyr | Val | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Leu | Gly | Thr | Val | Leu | Gly | Ile | Met | Val | Ile | Phe | Tyr | Asp | Met | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Ser | Gly | Gly | Met | Asp | Ala | Lys | Thr | Ile | Met | Val | Gly | Leu | Ser | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Leu | Lys | Ala | Thr | Ala | Leu | Gly | Leu | Ala | Val | Ala | Ile | Pro | Thr | Leu |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Ala | Tyr | Asn | Ser | Leu | Leu | Arg | Lys | Ser | Asp | Val | Leu | Ser | Glu | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Phe | Arg | Ile | Met | Lys | Lys |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 165 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...723
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

|            |            |      |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|------------|------------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| TCATGAATTA | AACCCTAGCG | AACA | ATG | AAG | CTT | TTT | GAC | TAC | GCT | CCT | TTG |     | 51  |     |     |    |
|            |            |      | Met | Lys | Leu | Phe | Asp | Tyr | Ala | Pro | Leu |     |     |     |     |    |
|            |            |      | 1   |     |     |     | 5   |     |     |     |     |     |     |     |     |    |
| AGT        | TTG        | GCT  | TGG | CGG | GAG | TTT | TTG | CAA | AGC | GAA | TTT | AAA | AAG | CCT | TAT | 99 |
| Ser        | Leu        | Ala  | Trp | Arg | Glu | Phe | Leu | Gln | Ser | Glu | Phe | Lys | Lys | Pro | Tyr |    |
| 10         |            |      |     | 15  |     |     |     |     | 20  |     |     |     |     | 25  |     |    |



- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

```

Met Lys Leu Phe Asp Tyr Ala Pro Leu Ser Leu Ala Trp Arg Glu Phe
 1 5 10 15
Leu Gln Ser Glu Phe Lys Lys Pro Tyr Phe Leu Glu Ile Glu Lys Arg
 20 25 30
Tyr Leu Glu Ala Leu Lys Ile Pro Lys Thr Ile Phe Pro Lys Ser Ser
 35 40 45
Asn Leu Phe Tyr Ala Leu Asn Leu Thr Pro Pro Cys Ala Val Lys Ile
 50 55 60
Ile Leu Leu Gly Gln Asp Pro Tyr His Ser Thr Tyr Leu Glu Asn Asp
 65 70 75 80
Gln Glu Leu Pro Val Ala Met Gly Leu Ser Phe Ser Val Glu Lys Asn
 85 90 95
Ala Pro Ile Pro Pro Ser Leu Lys Asn Ile Phe Lys Glu Leu His Ala
100 105 110
Asn Leu Gly Val Pro Val Pro Cys Gly Asp Leu Ser Ala Trp Ala
115 120 125
Lys Arg Gly Met Leu Leu Leu Asn Ala Ile Leu Ser Val Glu Lys Asn
130 135 140
Gln Ala Ala Ser His Gln Tyr Ile Gly Trp Glu Ala Phe Ser Asp Gln
145 150 155 160
Ile Leu Met Arg Leu Phe Glu Thr Thr Ala Pro Leu Ile Val Val Leu
165 170 175
Leu Gly Lys Val Ala Gln Lys Lys Ile Ala Leu Ile Pro Lys Asn Lys
180 185 190
His Ile Ile Ile Thr Ala Pro His Pro Ser Pro Leu Ser Arg Gly Phe
195 200 205
Leu Gly Ser Gly Val Phe Thr Ser Val Gln Lys Ala Tyr Arg Glu Val
210 215 220
Tyr Arg Lys Asp Phe Asp Phe Ser Leu
225 230

```

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...1179
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

AAGAAGAAAT AAAAATC ATG GGG TTT TTA TTT GAA AAA TCG TTA ATG AGT

51



|                                                                  |      |
|------------------------------------------------------------------|------|
| TTG CCT AAG ACT ATT CAA AAC CTT TCT TTT GAT TAT TTC TCG CTT TCA  | 771  |
| Leu Pro Lys Thr Ile Gln Asn Leu Ser Phe Asp Tyr Phe Ser Leu Ser  |      |
| 240 245 250                                                      |      |
| AAT AAG CAA TTT AAA ACC TTA TCT TTT TCA ACC ATT CCC ACT CAA GAC  | 819  |
| Asn Lys Gln Phe Lys Thr Leu Ser Phe Ser Thr Ile Pro Thr Gln Asp  |      |
| 255 260 265                                                      |      |
| ACT ACC GGT ATT CAA AGC GAT CTC ATC CCT AAA AAC AAT TTT TTA GTC  | 867  |
| Thr Thr Gly Ile Gln Ser Asp Leu Ile Pro Lys Asn Asn Phe Leu Val  |      |
| 270 275 280                                                      |      |
| TTT TCT AAT GTG GCG TTG CTC GCT TTG TGC GTG TTT TTC TTG GTG CTG  | 915  |
| Phe Ser Asn Val Ala Leu Leu Ala Leu Cys Val Phe Phe Leu Val Leu  |      |
| 285 290 295                                                      |      |
| TTT TTC ATT TTT GGG CGC AAA CTC ATT TTT TTA GGG CTT GGG ATT TTG  | 963  |
| Phe Phe Ile Phe Gly Arg Lys Leu Ile Phe Leu Gly Leu Gly Ile Leu  |      |
| 300 305 310 315                                                  |      |
| TGC TTA GGG TTT GTT TTG TAT CAC CTT TTA TTC ACG CAA AAA TCA GCC  | 1011 |
| Cys Leu Gly Phe Val Leu Tyr His Leu Leu Phe Thr Gln Lys Ser Ala  |      |
| 320 325 330                                                      |      |
| CTA TTG CTC GCT CAT AAA AAA ATC CGC ATT CTG CCC ACG CAA AAT TCC  | 1059 |
| Leu Leu Leu Ala His Lys Lys Ile Arg Ile Leu Pro Thr Gln Asn Ser  |      |
| 335 340 345                                                      |      |
| ACC ATT TTA GGG CTT TCT AAA AAT GAA ATG CCG ATT AAA ATC TTA GGC  | 1107 |
| Thr Ile Leu Gly Leu Ser Lys Asn Glu Met Pro Ile Lys Ile Leu Gly  |      |
| 350 355 360                                                      |      |
| TCG CAT GAT GAT TAT TAT AAA ATC CTA ACG CCG CAT GAA CAA ATA GGA  | 1155 |
| Ser His Asp Asp Tyr Tyr Lys Ile Leu Thr Pro His Glu Gln Ile Gly  |      |
| 365 370 375                                                      |      |
| TGG GTC AAA AAA GAT GAA GTC AAA TAAAAAGTCC AATCGTTTAA GAGCGATTTA | 1209 |
| Trp Val Lys Lys Asp Glu Val Lys                                  |      |
| 380 385                                                          |      |
| TAGAGCTTTA GTGATCGCTA TAGGACTAGC TGT                             | 1242 |

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Gly Phe Leu Phe Glu Lys Ser Leu Met Ser Phe Phe Ala His Pro |  |
| 1 5 10 15                                                       |  |
| Ile Lys Ile Leu Lys Ile Ile Ser Leu Ile Leu Ser Phe Leu Val Ser |  |
| 20 25 30                                                        |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Leu | Val | Ala | Glu | Asn | Ala | His | Glu | Pro | Glu | Glu | Ile | Lys | Ala | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Ala | Tyr | Val | Lys | Ile | Pro | Gln | Leu | Glu | Asp | Leu | Glu | Asn | Asn | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Tyr | Ile | Gly | Gln | Ile | Ile | Gly | Val | Thr | Tyr | Asp | Leu | Leu | Leu | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asp | Ala | Glu | Phe | Leu | Glu | Ala | Lys | Ile | Lys | Asp | Gly | Leu | Asp | Lys | Thr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Ile | Glu | Leu | Leu | Asn | Lys | Met | Pro | Lys | Trp | Lys | Lys | Val | Glu | Lys |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Leu | Phe | Arg | Ala | Thr | Tyr | Tyr | Tyr | Lys | Ile | Lys | Gly | Ile | Lys | Ala |
|     |     | 115 |     |     |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Ile | Ile | Pro | Ser | Leu | Glu | Val | Ser | Ala | Phe | Ser | Asn | Lys | Asp | Lys | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Asp | His | Ser | Ile | Ala | Pro | Lys | Val | Thr | Leu | Gln | Val | Thr | Asp | Leu |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Lys | Asn | Pro | Arg | Tyr | Ala | Asn | Val | Met | Ala | Lys | Asp | Leu | Gln | Val |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Gln | Tyr | Lys | Thr | Lys | Asp | Tyr | Asp | Asp | Lys | Asn | Asn | Ile | Leu | Val |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Met | Glu | Ile | Ala | Phe | Lys | Glu | Ala | Thr | Trp | Glu | Asp | Phe | His | Ile | Lys |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | Ala | Ile | Lys | Gln | Gly | Phe | Asp | Asn | Ala | Ser | Leu | Asn | Gln | Ile | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Lys | Glu | Gly | Ser | Val | Phe | Tyr | Tyr | Cys | Val | Leu | Pro | Lys | Thr | Ile |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Gln | Asn | Leu | Ser | Phe | Asp | Tyr | Phe | Ser | Leu | Ser | Asn | Lys | Gln | Phe | Lys |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Thr | Leu | Ser | Phe | Ser | Thr | Ile | Pro | Thr | Gln | Asp | Thr | Thr | Gly | Ile | Gln |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Asp | Leu | Ile | Pro | Lys | Asn | Asn | Phe | Leu | Val | Phe | Ser | Asn | Val | Ala |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Leu | Ala | Leu | Cys | Val | Phe | Phe | Leu | Val | Leu | Phe | Phe | Ile | Phe | Gly |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Arg | Lys | Leu | Ile | Phe | Leu | Gly | Leu | Gly | Ile | Leu | Cys | Leu | Gly | Phe | Val |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |
| Leu | Tyr | His | Leu | Leu | Phe | Thr | Gln | Lys | Ser | Ala | Leu | Leu | Leu | Ala | His |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Lys | Lys | Ile | Arg | Ile | Leu | Pro | Thr | Gln | Asn | Ser | Thr | Ile | Leu | Gly | Leu |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ser | Lys | Asn | Glu | Met | Pro | Ile | Lys | Ile | Leu | Gly | Ser | His | Asp | Asp | Tyr |
|     |     | 355 |     |     |     |     | 360 |     |     |     | 365 |     |     |     |     |
| Tyr | Lys | Ile | Leu | Thr | Pro | His | Glu | Gln | Ile | Gly | Trp | Val | Lys | Lys | Asp |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Glu | Val | Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 385 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 34...1395  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

|            |            |             |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|------------|-------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| TTCTAATCTC | AAAAATGGGT | GGTGTATTATA | ACA | ATG | ACA | AAA | CGA | CTT | TTT | AAA |     | 54  |     |     |     |     |
|            |            |             |     | Met | Thr | Lys | Arg | Leu | Phe | Lys |     |     |     |     |     |     |
|            |            |             |     | 1   |     |     |     | 5   |     |     |     |     |     |     |     |     |
| GGG        | TTG        | TTA         | GCG | GTT | TCT | CTT | GCT | GTG | AGT | TTG | CAT | GGT | GGT | GAA | GTT | 102 |
| Gly        | Leu        | Leu         | Ala | Val | Ser | Leu | Ala | Val | Ser | Leu | His | Gly | Gly | Glu | Val |     |
|            | 10         |             |     |     |     | 15  |     |     |     |     | 20  |     |     |     |     |     |
| AAG        | GAA        | AAA         | AAG | CCG | GTT | AAG | CCG | GTT | AAA | GAA | GAT | CCG | CAA | GAA | TTA | 150 |
| Lys        | Glu        | Lys         | Lys | Pro | Val | Lys | Pro | Val | Lys | Glu | Asp | Pro | Gln | Glu | Leu |     |
|            | 25         |             |     |     |     | 30  |     |     |     |     | 35  |     |     |     |     |     |
| GCG        | GCT        | AAA         | AGG | GTG | GAA | GCG | TTC | AGT | CGT | TTC | TCT | AAT | GTG | GTT | TCA | 198 |
| Ala        | Ala        | Lys         | Arg | Val | Glu | Ala | Phe | Ser | Arg | Phe | Ser | Asn | Val | Val | Ser |     |
| 40         |            |             |     |     | 45  |     |     |     | 50  |     |     |     |     |     | 55  |     |
| GAA        | ATT        | GAA         | AAA | AAA | TAT | GTG | GAT | AAA | ATC | AGC | ATT | TCT | GAG | ATC | ATG | 246 |
| Glu        | Ile        | Glu         | Lys | Lys | Tyr | Val | Asp | Lys | Ile | Ser | Ile | Ser | Glu | Ile | Met |     |
|            |            |             |     | 60  |     |     |     | 65  |     |     |     |     | 70  |     |     |     |
| ACT        | AAA        | GCG         | ATT | GAA | GGC | TTG | CTC | TCT | AAT | TTG | GAC | GCG | CAT | TCA | GCG | 294 |
| Thr        | Lys        | Ala         | Ile | Glu | Gly | Leu | Leu | Ser | Asn | Leu | Asp | Ala | His | Ser | Ala |     |
|            |            |             | 75  |     |     |     |     | 80  |     |     |     | 85  |     |     |     |     |
| TAT        | TTG        | AAT         | GAA | AAG | AAG | TTT | AAG | GAA | TTT | CAA | GCC | CAA | ACC | GAG | GGC | 342 |
| Tyr        | Leu        | Asn         | Glu | Lys | Lys | Phe | Lys | Glu | Phe | Gln | Ala | Gln | Thr | Glu | Gly |     |
|            | 90         |             |     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     |
| GAA        | TTT        | GGG         | GGG | CTT | GGG | ATC | ACG | GTG | GGC | ATG | CGC | GAT | GGC | GTT | TTA | 390 |
| Glu        | Phe        | Gly         | Gly | Leu | Gly | Ile | Thr | Val | Gly | Met | Arg | Asp | Gly | Val | Leu |     |
|            | 105        |             |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     |     |
| ACC        | GTT        | ATT         | GCC | CCT | TTA | GAA | GGC | ACT | CCA | GCT | TAC | AAG | GCT | GGG | GTT | 438 |
| Thr        | Val        | Ile         | Ala | Pro | Leu | Glu | Gly | Thr | Pro | Ala | Tyr | Lys | Ala | Gly | Val |     |
| 120        |            |             |     |     | 125 |     |     |     | 130 |     |     |     |     |     | 135 |     |
| AAG        | TCA        | GGC         | GAT | AAC | ATT | TTA | AAA | ATC | AAT | AAC | GAA | AGC | ACG | CTG | AGC | 486 |
| Lys        | Ser        | Gly         | Asp | Asn | Ile | Leu | Lys | Ile | Asn | Asn | Glu | Ser | Thr | Leu | Ser |     |
|            |            |             |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |     |     |
| ATG        | AGC        | ATT         | GAT | GAT | GCG | ATC | AAC | CTC | ATG | CGC | GGC | AAG | CCA | AAA | ACC | 534 |
| Met        | Ser        | Ile         | Asp | Asp | Ala | Ile | Asn | Leu | Met | Arg | Gly | Lys | Pro | Lys | Thr |     |
|            |            |             | 155 |     |     |     |     | 160 |     |     |     |     | 165 |     |     |     |
| CCT        | ATT        | CAG         | ATC | ACC | GTT | GTA | AGA | AAA | AAC | GAG | CCA | AAA | CCT | TTA | GTG | 582 |
| Pro        | Ile        | Gln         | Ile | Thr | Val | Val | Arg | Lys | Asn | Glu | Pro | Lys | Pro | Leu | Val |     |
|            |            | 170         |     |     |     |     | 175 |     |     |     |     | 180 |     |     |     |     |
| TTT        | AAC        | ATC         | ATT | AGA | GAC | ATC | ATT | AAA | CTC | CCC | TCT | GTC | TAT | GTG | AAA | 630 |
| Phe        | Asn        | Ile         | Ile | Arg | Asp | Ile | Ile | Lys | Leu | Pro | Ser | Val | Tyr | Val | Lys |     |
|            | 185        |             |     |     |     | 190 |     |     |     |     | 195 |     |     |     |     |     |





435

ACTCATGGGG TTTTATTTG AAAAATCGTT AATGAGTTTT TTCGCTCATC CAATC 1455

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

|            |            |            |            |            |     |            |            |            |            |            |            |            |            |     |           |
|------------|------------|------------|------------|------------|-----|------------|------------|------------|------------|------------|------------|------------|------------|-----|-----------|
| Met<br>1   | Thr        | Lys        | Arg        | Leu<br>5   | Phe | Lys        | Gly        | Leu<br>10  | Ala        | Val        | Ser        | Leu<br>15  | Ala        | Val |           |
| Ser        | Leu        | His        | Gly<br>20  | Gly        | Glu | Val        | Lys<br>25  | Glu        | Lys        | Lys        | Pro        | Val<br>30  | Lys        | Pro | Val       |
| Lys        | Glu        | Asp<br>35  | Pro        | Gln        | Glu | Leu        | Ala<br>40  | Ala        | Lys        | Arg        | Val<br>45  | Glu        | Ala        | Phe | Ser       |
| Arg        | Phe<br>50  | Ser        | Asn        | Val        | Val | Ser<br>55  | Glu        | Ile        | Glu        | Lys        | Lys<br>60  | Tyr        | Val        | Asp | Lys       |
| Ile<br>65  | Ser        | Ile        | Ser        | Glu<br>70  | Ile | Met        | Thr        | Lys        | Ala<br>75  | Ile        | Glu        | Gly        | Leu        | Leu | Ser<br>80 |
| Asn        | Leu        | Asp        | Ala        | His<br>85  | Ser | Ala        | Tyr        | Leu<br>90  | Asn        | Glu        | Lys        | Lys        | Phe        | Lys | Glu       |
| Phe        | Gln        | Ala        | Gln<br>100 | Thr        | Glu | Gly        | Glu        | Phe<br>105 | Gly        | Gly        | Leu        | Gly        | Ile        | Thr | Val       |
| Gly        | Met        | Arg<br>115 | Asp        | Gly        | Val | Leu        | Thr<br>120 | Val        | Ile        | Ala        | Pro        | Leu<br>125 | Glu        | Gly | Thr       |
| Pro        | Ala<br>130 | Tyr        | Lys        | Ala        | Gly | Val<br>135 | Lys        | Ser        | Gly        | Asp        | Asn<br>140 | Ile        | Leu        | Lys | Ile       |
| Asn<br>145 | Asn        | Glu        | Ser        | Thr<br>150 | Leu | Ser        | Met        | Ser        | Ile        | Asp<br>155 | Ala        | Ile        | Asn        | Leu |           |
| Met        | Arg        | Gly        | Lys        | Pro<br>165 | Lys | Thr        | Pro        | Ile<br>170 | Gln        | Ile        | Thr        | Val        | Val        | Arg | Lys       |
| Asn        | Glu        | Pro        | Lys<br>180 | Pro        | Leu | Val        | Phe<br>185 | Asn        | Ile        | Ile        | Arg        | Asp<br>190 | Ile        | Ile | Lys       |
| Leu        | Pro        | Ser<br>195 | Val        | Tyr        | Val | Lys        | Lys<br>200 | Ile        | Lys        | Glu        | Thr        | Pro<br>205 | Tyr        | Leu | Tyr       |
| Val        | Arg<br>210 | Val        | Ser        | Gly        | Phe | Asp<br>215 | Lys        | Asn        | Val        | Thr        | Lys<br>220 | Ser        | Val        | Leu | Glu       |
| Gly<br>225 | Leu        | Lys        | Ala        | Asn<br>230 | Pro | Lys        | Ala        | Lys        | Gly        | Ile<br>235 | Val        | Leu        | Asp        | Leu | Arg       |
| Gly        | Asn        | Pro        | Gly<br>245 | Gly        | Leu | Leu        | Asn        | Gln        | Ala<br>250 | Val        | Gly        | Leu        | Ser        | Asn | Leu       |
| Phe        | Ile        | Lys        | Glu<br>260 | Gly        | Val | Leu        | Val        | Ser<br>265 | Gln        | Lys        | Gly        | Lys        | Asn<br>270 | Lys | Glu       |
| Glu        | Asn        | Leu<br>275 | Glu        | Tyr        | Lys | Ala        | Asn<br>280 | Gly        | Arg        | Ala        | Pro        | Tyr<br>285 | Thr        | Asn | Leu       |
| Pro        | Ile<br>290 | Ala        | Val        | Leu        | Val | Asn<br>295 | Gly        | Gly        | Ser        | Ala        | Ser<br>300 | Ala        | Ser        | Glu | Ile       |

Val Ala Gly Ala Leu Gln Asp His Lys Arg Ala Val Ile Ile Gly Glu  
 305 310 315 320  
 Lys Thr Phe Gly Lys Gly Ser Val Gln Met Leu Leu Pro Val Asn Lys  
 325 330 335  
 Asp Glu Ala Ile Lys Ile Thr Thr Ala Arg Tyr Tyr Leu Pro Ser Gly  
 340 345 350  
 Arg Thr Ile Gln Ala Lys Gly Ile Thr Pro Asp Ile Val Ile Tyr Pro  
 355 360 365  
 Gly Lys Val Pro Glu Asn Glu Asn Lys Phe Ser Leu Lys Glu Ala Asp  
 370 375 380  
 Leu Lys His His Leu Glu Gln Glu Leu Lys Lys Ile Asp Asp Lys Thr  
 385 390 395 400  
 Pro Asn Ser Lys Glu Ala Asp Lys Asp Lys Lys Asn Glu Glu Glu Lys  
 405 410 415  
 Glu Ile Thr Pro Lys Met Ile Asn Asp Asp Ile Gln Leu Lys Thr Ala  
 420 425 430  
 Ile Asp Ser Leu Lys Thr Trp Ser Ile Val Asp Glu Lys Met Asp Glu  
 435 440 445  
 Lys Ala Pro Lys Lys Lys  
 450

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...1098
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GATATAAAAG GTTAGTTAAT C ATG GAT TTT TTA AAA GAA AAC TTA AAC ACT | 51  |
| Met Asp Phe Leu Lys Glu Asn Leu Asn Thr                         |     |
| 1 5 10                                                          |     |
| ATC ATA GAG GGG GAT TGT TTA GAA AAA TTG AAA GAC TTT CCT AAC AGA | 99  |
| Ile Ile Glu Gly Asp Cys Leu Glu Lys Leu Lys Asp Phe Pro Asn Arg |     |
| 15 20 25                                                        |     |
| AGC GTT GAT TTT ATC TTT GCT GAC CCC CCA TAT TTT ATG CAA ACA GAG | 147 |
| Ser Val Asp Phe Ile Phe Ala Asp Pro Pro Tyr Phe Met Gln Thr Glu |     |
| 30 35 40                                                        |     |
| GGG GAA TTG AAG CGT TTT GAA GGC ACA AAA TTT CAA GGC GTT GAG GAT | 195 |
| Gly Glu Leu Lys Arg Phe Glu Gly Thr Lys Phe Gln Gly Val Glu Asp |     |
| 45 50 55                                                        |     |
| TAT TGG GAT AAA TTT GGC TCT TTT AAG GAA TAC GAT GCC TTT TGT TTG | 243 |
| Tyr Trp Asp Lys Phe Gly Ser Phe Lys Glu Tyr Asp Ala Phe Cys Leu |     |
| 60 65 70                                                        |     |

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GGT TGG TTG AAA GAA TGC CAA AGG ATT TTA AAA GAT AAT GGC AGT ATT | 291 |
| Gly Trp Leu Lys Glu Cys Gln Arg Ile Leu Lys Asp Asn Gly Ser Ile |     |
| 75 80 85 90                                                     |     |
| TGT GTG ATA GGG AGT TTT CAA AAT ATT TTT AGA ATT GGT TTT CAT TTG | 339 |
| Cys Val Ile Gly Ser Phe Gln Asn Ile Phe Arg Ile Gly Phe His Leu |     |
| 95 100 105                                                      |     |
| CAA AAT TTA GGG TTT TGG ATA CTC AAT GAT ATT ATT TGG CAC AAG AGT | 387 |
| Gln Asn Leu Gly Phe Trp Ile Leu Asn Asp Ile Ile Trp His Lys Ser |     |
| 110 115 120                                                     |     |
| AAT CCG GTG CCT AAT TTT GCT GGC AAG AGA TTA TGC AAC GCC CAT GAG | 435 |
| Asn Pro Val Pro Asn Phe Ala Gly Lys Arg Leu Cys Asn Ala His Glu |     |
| 125 130 135                                                     |     |
| ACG CTT ATT TGG TGT GCT AAA CAC AAA AAC AGC AAA GTT GCC TTT AAT | 483 |
| Thr Leu Ile Trp Cys Ala Lys His Lys Asn Ser Lys Val Ala Phe Asn |     |
| 140 145 150                                                     |     |
| TAT AAA ACA ATG AAG TAC CTC AAT AAC GAC AAA CAA GAA AAA TCG GTT | 531 |
| Tyr Lys Thr Met Lys Tyr Leu Asn Asn Asp Lys Gln Glu Lys Ser Val |     |
| 155 160 165 170                                                 |     |
| TGG CAA ATC CCT ATT TGC ATG GGT AAC GAA AGA CTA AAA GAT GCG CAA | 579 |
| Trp Gln Ile Pro Ile Cys Met Gly Asn Glu Arg Leu Lys Asp Ala Gln |     |
| 175 180 185                                                     |     |
| GGT AAA AAA GTG CAT TCC ACG CAA AAA CCA GAA GCG CTT TTA AAA AAA | 627 |
| Gly Lys Lys Val His Ser Thr Gln Lys Pro Glu Ala Leu Leu Lys Lys |     |
| 190 195 200                                                     |     |
| ATC ATT TTA AGC GCG ACT AAA CCT AAA GAT ATT ATT TTA GAT CCC TTT | 675 |
| Ile Ile Leu Ser Ala Thr Lys Pro Lys Asp Ile Ile Leu Asp Pro Phe |     |
| 205 210 215                                                     |     |
| TTT GGC ACA GGC ACA ACA GGG GCT GTG GCT AAA TCC ATG AAC AGG TAT | 723 |
| Phe Gly Thr Gly Thr Thr Gly Ala Val Ala Lys Ser Met Asn Arg Tyr |     |
| 220 225 230                                                     |     |
| TTT ATT GGT ATT GAA AAA GAT TCT TTT TAT ATT AAA GAA GCG GCA AAA | 771 |
| Phe Ile Gly Ile Glu Lys Asp Ser Phe Tyr Ile Lys Glu Ala Ala Lys |     |
| 235 240 245 250                                                 |     |
| CGC CTG AAT AAC ACT AGG GAT AAA AGC GAT TTT ATC ACT AAT TTA GAT | 819 |
| Arg Leu Asn Asn Thr Arg Asp Lys Ser Asp Phe Ile Thr Asn Leu Asp |     |
| 255 260 265                                                     |     |
| TTA GAA ACT AAA CCC CCA AAA ATA CCT ATG AGT CTT TTA ATT TCT AAA | 867 |
| Leu Glu Thr Lys Pro Pro Lys Ile Pro Met Ser Leu Leu Ile Ser Lys |     |
| 270 275 280                                                     |     |
| CAA TTA TTA AAA ATC GGG GAT TTT TTA TAC TCA CCT AAC AAA GAA AAA | 915 |
| Gln Leu Leu Lys Ile Gly Asp Phe Leu Tyr Ser Pro Asn Lys Glu Lys |     |
| 285 290 295                                                     |     |
| ATT TGT CAA GTT TTA GAA AAC GGA CAA GTG AGG GAT AAT GAA AAC TAT | 963 |
| Ile Cys Gln Val Leu Glu Asn Gly Gln Val Arg Asp Asn Glu Asn Tyr |     |







| 315                                                                                                                                                   | 320 | 325 |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----|------|
| CAT GAG CAA ATC GCT GAA ATT TCA AGG GAG CTT AAA ACT TTA GCC AGA<br>His Glu Gln Ile Ala Glu Ile Ser Arg Glu Leu Lys Thr Leu Ala Arg<br>330 335 340     |     |     | 1062 |
| GAA TTA GAA ATC CCT ATC ATA GCG TTA GTG CAA CTC AAC CGC AGC CTA<br>Glu Leu Glu Ile Pro Ile Ile Ala Leu Val Gln Leu Asn Arg Ser Leu<br>345 350 355     |     |     | 1110 |
| GAA AAC CGA GAC GAT AAA CGG CCC ATT CTT TCG GAT ATC AAA GAC AGC<br>Glu Asn Arg Asp Asp Lys Arg Pro Ile Leu Ser Asp Ile Lys Asp Ser<br>360 365 370 375 |     |     | 1158 |
| GGG GGG ATT GAA CAA GAC GCT GAT ATT GTT TTA TTT TTA TAT AGA GGC<br>Gly Gly Ile Glu Gln Asp Ala Asp Ile Val Leu Phe Leu Tyr Arg Gly<br>380 385 390     |     |     | 1206 |
| TAT ATC TAT CAA ATG AGG GCT GAA GAC AAC AAA ATA GAC AAA CTC AAA<br>Tyr Ile Tyr Gln Met Arg Ala Glu Asp Asn Lys Ile Asp Lys Leu Lys<br>395 400 405     |     |     | 1254 |
| AAA GAA GGT AAA ATT GAA GAG GCG CAA GAG TTG TAC TTA AAA GTT AAT<br>Lys Glu Gly Lys Ile Glu Glu Ala Gln Glu Leu Tyr Leu Lys Val Asn<br>410 415 420     |     |     | 1302 |
| GAA GAA AGG CGT ATC CAC AAG CAA AAT GGC AGC ATT GAA GAG GCT GAA<br>Glu Glu Arg Arg Ile His Lys Gln Asn Gly Ser Ile Glu Glu Ala Glu<br>425 430 435     |     |     | 1350 |
| ATC ATT GTG GCT AAA AAC AGG AAT GGG GCT ACA GGA ACG GTT TAT ACG<br>Ile Ile Val Ala Lys Asn Arg Asn Gly Ala Thr Gly Thr Val Tyr Thr<br>440 445 450 455 |     |     | 1398 |
| CGC TTT AAC GCT CCT TTC ACG CGC TAT GAA GAC ATG CCC ATA GAT TCC<br>Arg Phe Asn Ala Pro Phe Thr Arg Tyr Glu Asp Met Pro Ile Asp Ser<br>460 465 470     |     |     | 1446 |
| CAT TTA GAA GAA GGG CAA GAA ACT AAA GTG GAT TAT GAT ATA GTT ACA<br>His Leu Glu Glu Gly Gln Glu Thr Lys Val Asp Tyr Asp Ile Val Thr<br>475 480 485     |     |     | 1494 |
| ACT TGAAAGACAA AACTTTTTCAG GGGGCGTTTG AACTTCTTA<br>Thr                                                                                                |     |     | 1536 |

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | His | Leu | Lys | His | Leu | Gln | Gln | Leu | Gln | Asn | Ile | Glu | Arg | Ile |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Leu | Ser | Gly | Ile | Val | Leu | Ala | Asn | His | Lys | Ile | Glu | Glu | Val | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Val | Leu | Glu | Pro | Ser | Asp | Phe | Tyr | Tyr | Pro | Pro | Asn | Gly | Leu | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Glu | Ile | Ala | Leu | Lys | Leu | His | Glu | Glu | Asp | Cys | Pro | Ile | Asp | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Phe | Ile | Arg | Gln | Lys | Met | Pro | Lys | Asp | Lys | Gln | Ile | Lys | Glu | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asp | Leu | Val | Ala | Ile | Phe | Ala | Ala | Ser | Pro | Ile | Asp | Asn | Ile | Glu | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Val | Glu | Glu | Ile | Lys | Asn | Ala | Ser | Ile | Lys | Arg | Lys | Leu | Phe | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Ala | Asn | Thr | Ile | Arg | Glu | Gln | Ala | Leu | Glu | Ser | Ala | Gln | Lys | Ser |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Ser | Asp | Ile | Leu | Gly | Ala | Val | Glu | Arg | Glu | Val | Tyr | Ala | Leu | Leu | Asn |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Ser | Thr | Ile | Glu | Gly | Phe | Arg | Asn | Ile | Lys | Glu | Val | Leu | Glu | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Met | Asp | Leu | Ile | Thr | Glu | Asn | Gln | Arg | Lys | Gly | Ser | Leu | Glu | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Thr | Gly | Ile | Pro | Thr | Gly | Phe | Val | Gln | Leu | Asp | Asn | Tyr | Thr | Ser | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Phe | Asn | Lys | Gly | Ser | Leu | Val | Ile | Ile | Gly | Ala | Arg | Pro | Ser | Met | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Thr | Ser | Leu | Met | Met | Asn | Met | Val | Leu | Ser | Ala | Leu | Asn | Asp | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Arg | Gly | Val | Ala | Val | Phe | Ser | Leu | Glu | Met | Ser | Ala | Glu | Gln | Leu | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Leu | Arg | Ala | Leu | Ser | Asp | Leu | Thr | Ser | Ile | Asn | Met | His | Asp | Leu | Glu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ser | Gly | Arg | Leu | Asp | Asp | Asp | Gln | Trp | Glu | Asn | Leu | Ala | Lys | Cys | Phe |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asp | His | Leu | Ser | Gln | Lys | Lys | Leu | Phe | Phe | Tyr | Asp | Lys | Ser | Tyr | Val |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Arg | Ile | Glu | Gln | Ile | Arg | Leu | Gln | Leu | Arg | Lys | Leu | Lys | Ser | Gln | His |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Lys | Glu | Leu | Gly | Ile | Ala | Phe | Ile | Asp | Tyr | Leu | Gln | Leu | Met | Ser | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ser | Lys | Ala | Thr | Lys | Glu | Arg | His | Glu | Gln | Ile | Ala | Glu | Ile | Ser | Arg |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Glu | Leu | Lys | Thr | Leu | Ala | Arg | Glu | Leu | Glu | Ile | Pro | Ile | Ile | Ala | Leu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Val | Gln | Leu | Asn | Arg | Ser | Leu | Glu | Asn | Arg | Asp | Asp | Lys | Arg | Pro | Ile |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Leu | Ser | Asp | Ile | Lys | Asp | Ser | Gly | Gly | Ile | Glu | Gln | Asp | Ala | Asp | Ile |
|     | 370 |     |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |
| Val | Leu | Phe | Leu | Tyr | Arg | Gly | Tyr | Ile | Tyr | Gln | Met | Arg | Ala | Glu | Asp |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Asn | Lys | Ile | Asp | Lys | Leu | Lys | Lys | Glu | Gly | Lys | Ile | Glu | Glu | Ala | Gln |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Glu | Leu | Tyr | Leu | Lys | Val | Asn | Glu | Glu | Arg | Arg | Ile | His | Lys | Gln | Asn |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Gly | Ser | Ile | Glu | Glu | Ala | Glu | Ile | Ile | Val | Ala | Lys | Asn | Arg | Asn | Gly |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Ala | Thr | Gly | Thr | Val | Tyr | Thr | Arg | Phe | Asn | Ala | Pro | Phe | Thr | Arg | Tyr |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Asp | Met | Pro | Ile | Asp | Ser | His | Leu | Glu | Glu | Gly | Gln | Glu | Thr | Lys |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Val | Asp | Tyr | Asp | Ile | Val | Thr | Thr |     |     |     |     |     |     |     |     |
|     |     |     |     | 485 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 98...1207
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| GAAACGCATA AGGGGGTTGG CTATCGCTTT AACCCACTAT GAAAAAAAAAT CCCTTAAACT | 60  |
| CTTTTITAGGG ATTTATTTAG GCTCTTCGTT TGTGTTG ATG CTA GTG ATT AGC GTT  | 115 |
| Met Leu Val Ile Ser Val                                            |     |
| 1 5                                                                |     |
| TTA GCG TTT AAC TAT GAA AAA AAC GAA AAA ATC AAA ATG ATA CGC ATG    | 163 |
| Leu Ala Phe Asn Tyr Glu Lys Asn Glu Lys Ile Lys Met Ile Arg Met    |     |
| 10 15 20                                                           |     |
| GAC ATG GAC AAA ATG GCT TCT AAG ATC GCT AGC GAA GTG ATT GCC TTG    | 211 |
| Asp Met Asp Lys Met Ala Ser Lys Ile Ala Ser Glu Val Ile Ala Leu    |     |
| 25 30 35                                                           |     |
| CAC ATG CAA ACG CAT GGG GAT TAT CAA AAC GCT TTA AAC GCT CTC ATT    | 259 |
| His Met Gln Thr His Gly Asp Tyr Gln Asn Ala Leu Asn Ala Leu Ile    |     |
| 40 45 50                                                           |     |
| TCA CGC TAT AAA GAC GCT TCC ATA GCC CTT TTT GAT AGT AAA AAG CGT    | 307 |
| Ser Arg Tyr Lys Asp Ala Ser Ile Ala Leu Phe Asp Ser Lys Lys Arg    |     |
| 55 60 65 70                                                        |     |
| GTT TTG TAT TCT AAT ATC CCT GAA AGC GCC AAT TTG ATT AAA AAC CAT    | 355 |
| Val Leu Tyr Ser Asn Ile Pro Glu Ser Ala Asn Leu Ile Lys Asn His    |     |
| 75 80 85                                                           |     |
| AAA GAA GCG GGC TTT TTT AGT TTT AGG GGA GAG TAT TAC CTA TTG AGC    | 403 |
| Lys Glu Ala Gly Phe Phe Ser Phe Arg Gly Glu Tyr Tyr Leu Leu Ser    |     |
| 90 95 100                                                          |     |
| GAT GAA ACT TTC GCT CAC TTA GGC GTG GCT AAA ATG CTT TTT AAA AAT    | 451 |
| Asp Glu Thr Phe Ala His Leu Gly Val Ala Lys Met Leu Phe Lys Asn    |     |
| 105 110 115                                                        |     |
| TCT AAA CCC CTT CAT TTT TCT TCT TTG TAT CGT AAC ATT GTT TTA GTG    | 499 |
| Ser Lys Pro Leu His Phe Ser Ser Leu Tyr Arg Asn Ile Val Leu Val    |     |





Arg Phe Asn Ser Gly Val Leu Gly Tyr Gly Ile Gly Leu Gly Leu Val  
 325 330 335  
 Lys Lys Val Cys Glu Lys Tyr Lys Met Arg Leu Glu Ile His Ser Glu  
 340 345 350  
 Pro Ser Leu Lys Gly Ser Phe Tyr Glu Asn Ser Phe Cys Val Gln Phe  
 355 360 365  
 Gln Gly  
 370

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 703 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 60...665
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

GGGATAGTTT TAAAAATGAT GAAGAGTTTT TAACATTTTC TTACGCTTGG ATTGATAAA A 60  
 Me

TGC TGC CCA AAC TTA AAG ACA CAG GGA GTT TTT ATA TCT TTA ATA CCC 108  
 t Leu Pro Lys Leu Lys Asp Thr Gly Ser Phe Tyr Ile Phe Asn Thr Pr  
 1 5 10 15

CTT TTA ATT GCG CTT TAT TTT TAG CGT ATT TGC ACC ATA AAA AAG TGC 156  
 o Phe Asn Cys Ala Leu Phe Leu Ala Tyr Leu His His Lys Lys Val Hi  
 20 25 30

ATT TTT TAA ATT TTA TCA CTT GGG TTA AAA AAG ATG GGT TTG CCA ACG 204  
 s Phe Leu Asn Phe Ile Thr Trp Val Lys Lys Asp Gly Phe Ala Asn Al  
 35 40 45

CCA AAA AGC GTT ATA ACC ACG CGC AAG AAA GCA TTT TAT TTT ATA GCA 252  
 a Lys Lys Arg Tyr Asn His Ala Gln Glu Ser Ile Leu Phe Tyr Ser Me  
 50 55 60 6

TGC ACA AGA AAA ACT ACA CCT TTA ATG CCG ATG AGA TTC GCA TCG CTT 300  
 t His Lys Lys Asn Tyr Thr Phe Asn Ala Asp Glu Ile Arg Ile Ala Ty  
 5 70 75 80

ATG AAT CCG CTG AAC GCA TCA AAC ATG CTC AAA GTA AGG GGA TTT TAA 348  
 r Glu Ser Ala Glu Arg Ile Lys His Ala Gln Ser Lys Gly Ile Leu Ly  
 85 90 95

AAA ATA ACA AAC GCT GGT TCC CTA ACC CTA AGG GCA AAT TAT GCC TTG 396  
 s Asn Asn Lys Arg Trp Phe Pro Asn Pro Lys Gly Lys Leu Cys Leu As  
 100 105 110











```

Ser Leu Thr Glu Ala Gly Tyr Val Gly Glu Asp Val Glu Asn Ile Leu
180 185 190
Thr Arg Leu Leu Gln Ala Ser Asp Trp Asn Val Gln Lys Ala Gln Lys
195 200 205
Gly Ile Val Phe Ile Asp Glu Ile Asp Lys Ile Ser Arg Leu Ser Glu
210 215 220
Asn Arg Ser Ile Thr Arg Asp Val Ser Gly Glu Gly Val Gln Gln Ala
225 230 235 240
Leu Leu Lys Ile Val Glu Gly Ser Leu Val Asn Ile Pro Pro Lys Gly
245 250 255
Gly Arg Lys His Pro Glu Gly Asn Phe Ile Gln Ile Asp Thr Ser Asp
260 265 270
Ile Leu Phe Ile Cys Ala Gly Ala Phe Asp Gly Leu Ala Glu Ile Ile
275 280 285
Lys Lys Arg Thr Thr Gln Asn Val Leu Gly Phe Thr Gln Glu Lys Met
290 295 300
Ser Lys Lys Glu Gln Glu Ala Ile Leu His Leu Val Gln Thr His Asp
305 310 315 320
Leu Val Thr Tyr Gly Leu Ile Pro Glu Leu Ile Gly Arg Leu Pro Val
325 330 335
Leu Ser Thr Leu Asp Ser Ile Ser Leu Glu Ala Met Val Asp Ile Leu
340 345 350
Gln Lys Pro Lys Asn Ala Leu Ile Lys Gln Tyr Gln Gln Leu Phe Lys
355 360 365
Met Asp Glu Val Asp Leu Ile Phe Glu Glu Glu Ala Ile Lys Glu Ile
370 375 380
Ala Gln Leu Ala Leu Glu Arg Lys Thr Gly Ala Arg Gly Leu Arg Ala
385 390 395 400
Ile Ile Glu Asp Phe Cys Leu Asp Ile Met Phe Asp Leu Pro Lys Leu
405 410 415
Lys Gly Ser Glu Val Arg Ile Thr Lys Asp Cys Val Leu Lys Gln Ala
420 425 430
Glu Pro Leu Ile Ile Ala Lys Thr His Ser Lys Ile Leu Pro
435 440 445

```

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 911 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...858
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

```

AGTGTTAGAA AAAACTTTGC TTTGAAATTT GGC ATG AAA GCA GGC ATT ATT GGT 54
Met Lys Ala Gly Ile Ile Gly
1 5
TTA GGG CTT ATG GGG GGG AGT TTA GGG CTA GCC TTG CAA GAA TGG GGG 102

```



CAA GCT AAG GCG TGG ATA GAA AAT AAC GAT TAT GAA AGC CTT GCA GAA 822  
 Gln Ala Lys Ala Trp Ile Glu Asn Asn Asp Tyr Glu Ser Leu Ala Glu  
           250                          255                          260

TGG ATG GCG CAA GCG AAC AAA CTC CAG GAG TTC ATG TAAAGTAAAA TGATGT 874  
 Trp Met Ala Gln Ala Asn Lys Leu Gln Glu Phe Met  
           265                          270                          275

AAAATAATTT AAAATTTTTT ATATTGTTGT TTTTAGG 911

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ala | Gly | Ile | Ile | Gly | Leu | Gly | Leu | Met | Gly | Gly | Ser | Leu | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ala | Leu | Gln | Glu | Trp | Gly | Arg | Phe | Lys | Ser | Val | Ile | Gly | Tyr | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Asn | Ala | Leu | His | Ala | Lys | Leu | Ala | Leu | Thr | Leu | Gly | Leu | Val | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Cys | Val | Gly | Phe | Glu | Lys | Ile | Leu | Glu | Cys | Asp | Val | Ile | Phe | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ala | Ile | Pro | Val | Glu | Gly | Ile | Ile | Gly | Cys | Leu | Lys | Lys | Met | Thr | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Lys | Lys | Ser | Ala | Thr | Ile | Ile | Asp | Leu | Gly | Gly | Ala | Lys | Ala | Gln |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ile | Ile | Arg | Asn | Ile | Pro | Lys | Ser | Ile | Arg | Lys | Asn | Phe | Ile | Ala | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| His | Pro | Met | Cys | Gly | Thr | Glu | Phe | Tyr | Gly | Pro | Lys | Ala | Ser | Val | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Leu | Tyr | Glu | Asn | Ala | Leu | Val | Ile | Leu | Cys | Asp | Leu | Glu | Asp | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Gly | Thr | Glu | Gln | Val | Glu | Ile | Ala | Lys | Glu | Ile | Phe | Leu | Gly | Val | Lys |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Ala | Arg | Leu | Ile | Lys | Met | Lys | Ser | Asn | Glu | His | Asp | Thr | His | Val | Ala |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Tyr | Ile | Ser | His | Leu | Pro | His | Val | Leu | Ser | Tyr | Ala | Leu | Ala | Asn | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 |     |     |     |
| Val | Leu | Lys | Gln | Asn | Asp | Pro | Glu | Met | Ile | Leu | Ser | Leu | Ala | Gly | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Phe | Arg | Asp | Met | Ser | Arg | Leu | Ser | Lys | Ser | Ser | Pro | Leu | Met | Trp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Asp | Ile | Phe | Lys | Gln | Asn | Arg | Asp | Asn | Val | Leu | Glu | Ala | Ile | Lys |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Lys | Cys | Glu | Lys | Glu | Ile | Val | Gln | Ala | Lys | Ala | Trp | Ile | Glu | Asn | Asn |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Asp | Tyr | Glu | Ser | Leu | Ala | Glu | Trp | Met | Ala | Gln | Ala | Asn | Lys | Leu | Gln |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Glu | Phe | Met |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 275 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 73...267
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

AATAATTTAA AATTTTTTAT ATTGTTGTTT TTAGGGGTGC GAGGAGCGAA ATGGGGTATT 60  
TGGATTGTTT TT ATG GAT TAT AGG CTG TTT CAT ATG GAT AGC ATG GAT TTA 111  
Met Asp Tyr Arg Leu Phe His Met Asp Ser Met Asp Leu  
1 5 10  
CCC AGC AAC CAG CAA ACA ACC ATA AGA GAT TAT CTT AAA CCC GGA TCT 159  
Pro Ser Asn Gln Gln Thr Thr Ile Arg Asp Tyr Leu Lys Pro Gly Ser  
15 20 25  
ATT GTT GTG TTT GCC ATA ATT GTA ATA ATA ATT TCA TCT CAT TTC TCC 207  
Ile Val Val Phe Ala Ile Ile Val Ile Ile Ile Ser Ser His Phe Ser  
30 35 40 45  
AAC GCC TAT AAA ACC CTT ATC GCT TCT AAT AAA AAA CCA GTT TTA AGC 255  
Asn Ala Tyr Lys Thr Leu Ile Ala Ser Asn Lys Lys Pro Val Leu Ser  
50 55 60  
CAT TTA GAA ATT TGATTCTTA AACCTTTTTA TCAAAAATAC CGGTGTT 304  
His Leu Glu Ile  
65

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

Met Asp Tyr Arg Leu Phe His Met Asp Ser Met Asp Leu Pro Ser Asn  
1 5 10 15  
Gln Gln Thr Thr Ile Arg Asp Tyr Leu Lys Pro Gly Ser Ile Val Val  
20 25 30  
Phe Ala Ile Ile Val Ile Ile Ile Ser Ser His Phe Ser Asn Ala Tyr  
35 40 45

Lys Thr Leu Ile Ala Ser Asn Lys Lys Pro Val Leu Ser His Leu Glu  
 50 55 60  
 Ile  
 65

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...237
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AGCTCACATT TTAGAAAAAT ATTTAAAGGG AGA ATG ATG CAA AAT AGC GTT AAA  | 54  |
| Met Met Gln Asn Ser Val Lys                                       |     |
| 1 5                                                               |     |
| AAA TTA GAA TAT GAA GAG CGT TTC AAT GAC GCT CTT TTG AAA TTA CAA   | 102 |
| Lys Leu Glu Tyr Glu Glu Arg Phe Asn Asp Ala Leu Leu Lys Leu Gln   |     |
| 10 15 20                                                          |     |
| GCA TGC CAA GAA GAA AAG CAG GTA ACG AGT TGT TTG AAA TGC GAG CAG   | 150 |
| Ala Cys Gln Glu Glu Lys Gln Val Thr Ser Cys Leu Lys Cys Glu Gln   |     |
| 25 30 35                                                          |     |
| GTT TTG AAT TGC AAG ATC CGC AAC AGC TAT GTG GAT GCG GCT TAT GAG   | 198 |
| Val Leu Asn Cys Lys Ile Arg Asn Ser Tyr Val Asp Ala Ala Tyr Glu   |     |
| 40 45 50 55                                                       |     |
| AGC ATG AGT TTA GGC GAA CGG GGC GGG TTT GAT TTC AAT TAAATGGGAT TA | 249 |
| Ser Met Ser Leu Gly Glu Arg Gly Gly Phe Asp Phe Asn               |     |
| 60 65                                                             |     |
| AAATGGCTAG TAATACTACC TT                                          | 271 |

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

Met Met Gln Asn Ser Val Lys Lys Leu Glu Tyr Glu Glu Arg Phe Asn

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| 1   |     | 5   |     | 10  |     | 15  |
| Asp | Ala | Leu | Leu | Lys | Leu | Gln |
|     |     | 20  |     | 25  |     | 30  |
| Ser | Cys | Leu | Lys | Cys | Glu | Gln |
|     |     | 35  |     | 40  |     | 45  |
| Tyr | Val | Asp | Ala | Ala | Tyr | Glu |
|     |     | 50  |     | 55  |     | 60  |
| Phe | Asp | Phe | Asn |     |     |     |
| 65  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 27...524
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

|            |            |        |     |     |     |     |     |     |     |     |     |     |
|------------|------------|--------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AAAAGGCTTT | TTAAAAGGAC | ACACCA | ATG | AGC | GAA | CCA | TTA | GAA | ACA | TTA | GAC | 53  |
|            |            |        | Met | Ser | Glu | Pro | Leu | Glu | Thr | Leu | Asp |     |
|            |            |        | 1   |     |     |     | 5   |     |     |     |     |     |
| AAG        | GAT        | AAA    | CAA | GCT | ATG | AGT | GAA | GCA | ATT | AAA | AAA | 101 |
| Lys        | Asp        | Lys    | Gln | Ala | Met | Ser | Glu | Ala | Ile | Lys | Lys |     |
| 10         |            |        | 15  |     |     |     | 20  |     |     |     | 25  |     |
| GAC        | AAA        | GAA    | AAC | CTC | GCA | CGA | GTC | AAA | GCA | GAC | AAA | 149 |
| Asp        | Lys        | Glu    | Asn | Leu | Ala | Arg | Val | Lys | Ala | Asp | Lys |     |
|            |            |        | 30  |     |     |     | 35  |     |     |     | 40  |     |
| GAT        | GAA        | AGT    | GAA | AAA | GGC | TAC | GAA | AAA | GAC | GAT | GAC | 197 |
| Asp        | Glu        | Ser    | Glu | Lys | Gly | Tyr | Glu | Lys | Asp | Asp | Asp |     |
|            |            |        | 45  |     |     |     | 50  |     |     |     | 55  |     |
| AAT        | CTT        | GAC    | AAA | GAA | ATC | GCT | AAA | GAC | AAA | GCT | AGC | 245 |
| Asn        | Leu        | Asp    | Lys | Glu | Ile | Ala | Lys | Asp | Lys | Ala | Ser |     |
|            |            |        | 60  |     |     |     | 65  |     |     |     | 70  |     |
| GAG        | CTT        | TAT    | GAA | GAG | GAC | GAT | AGA | GTT | AAA | CGA | GAC | 293 |
| Glu        | Leu        | Tyr    | Glu | Glu | Asp | Asp | Arg | Val | Lys | Arg | Asp |     |
|            |            |        | 75  |     |     |     | 80  |     |     |     | 85  |     |
| GAT        | GCC        | TTG    | CGT | GAT | AAA | GAA | AAA | GCC | AAA | GAT | GAC | 341 |
| Asp        | Ala        | Leu    | Arg | Asp | Lys | Glu | Lys | Ala | Lys | Asp | Asp |     |
|            |            |        | 90  |     |     |     | 95  |     |     |     | 100 |     |
| AGA        | GCG        | GAC    | GAT | GAC | ACC | ATA | GAG | GAC | GAT | GAG | GAA | 389 |
| Arg        | Ala        | Asp    | Asp | Asp | Thr | Ile | Glu | Asp | Asp | Glu | Glu |     |
|            |            |        |     |     |     |     |     |     |     | Tyr | Gly |     |
|            |            |        |     |     |     |     |     |     |     | Asp | Asp |     |





(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 82...2283

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

|                                                                 |            |            |                                         |            |            |     |
|-----------------------------------------------------------------|------------|------------|-----------------------------------------|------------|------------|-----|
| CAACAAGCTA                                                      | ACCAAAGCAT | TGAAGAAGCT | TTACAGAATG                              | TCCCGGGTCT | GCAAATTAGG | 60  |
| AATGCGACAG                                                      | GTGTAGGGGC | T          | ATG CCT ACT ATC CAA ATC CGT GGC TTT GGA | 111        |            |     |
|                                                                 |            | Met        | Pro Thr Ile Gln Ile Arg Gly Phe Gly     |            |            |     |
|                                                                 |            | 1          | 5                                       | 10         |            |     |
| GCT GGG GGT TCA GGG CAT AGC GAT GCG ACG CTG ATG TTA GTC AAT GGT | 159        |            |                                         |            |            |     |
| Ala Gly Gly Ser Gly His Ser Asp Ala Thr Leu Met Leu Val Asn Gly |            |            |                                         |            |            |     |
|                                                                 | 15         |            | 20                                      |            | 25         |     |
| ATT CCT GTT TAT ATG GCC CCC TAC GCT CAC ATT GAG CTA GAC ATT TTC | 207        |            |                                         |            |            |     |
| Ile Pro Val Tyr Met Ala Pro Tyr Ala His Ile Glu Leu Asp Ile Phe |            |            |                                         |            |            |     |
|                                                                 | 30         |            | 35                                      |            | 40         |     |
| CCC GTT ACC TTT CAA GCC ATT GAT CGC ATT GAT GTG ATC AAG GGT GGA | 255        |            |                                         |            |            |     |
| Pro Val Thr Phe Gln Ala Ile Asp Arg Ile Asp Val Ile Lys Gly Gly |            |            |                                         |            |            |     |
|                                                                 | 45         |            | 50                                      |            | 55         |     |
| GGC AGC GTG CAA TAC GGG CCT AAC ACT TAT GGG GGT ATT GTC AAT ATC | 303        |            |                                         |            |            |     |
| Gly Ser Val Gln Tyr Gly Pro Asn Thr Tyr Gly Gly Ile Val Asn Ile |            |            |                                         |            |            |     |
|                                                                 | 60         |            | 65                                      |            | 70         |     |
| ATC ACT AAG CCT ATC CCT AAT CAA TGG GAA AAC CAA GCG GCT GAA AGG | 351        |            |                                         |            |            |     |
| Ile Thr Lys Pro Ile Pro Asn Gln Trp Glu Asn Gln Ala Ala Glu Arg |            |            |                                         |            |            |     |
|                                                                 | 75         |            | 80                                      |            | 85         | 90  |
| ATC ACT TAT TGG GCT AAG GCT AGA AAC GCT GGG TTT GCC GCT CCT CCT | 399        |            |                                         |            |            |     |
| Ile Thr Tyr Trp Ala Lys Ala Arg Asn Ala Gly Phe Ala Ala Pro Pro |            |            |                                         |            |            |     |
|                                                                 | 95         |            | 100                                     |            | 105        |     |
| GAT AAA ACC GGC GAT CCT TCT TTC ATC AAG TCT TTA GGC AAC AAC CTC | 447        |            |                                         |            |            |     |
| Asp Lys Thr Gly Asp Pro Ser Phe Ile Lys Ser Leu Gly Asn Asn Leu |            |            |                                         |            |            |     |
|                                                                 | 110        |            | 115                                     |            | 120        |     |
| CTC TAT AAC ACT TAT GTG AGG AGT GGA GGG ATG ATC AAT AAG CAT GTG | 495        |            |                                         |            |            |     |
| Leu Tyr Asn Thr Tyr Val Arg Ser Gly Gly Met Ile Asn Lys His Val |            |            |                                         |            |            |     |
|                                                                 | 125        |            | 130                                     |            | 135        |     |
| GGT ATC CAA GCG CAA GCT AAC TGG GTT AGA GGA CAA GGC TTT AGG GAC | 543        |            |                                         |            |            |     |
| Gly Ile Gln Ala Gln Ala Asn Trp Val Arg Gly Gln Gly Phe Arg Asp |            |            |                                         |            |            |     |
|                                                                 | 140        |            | 145                                     |            | 150        |     |
| AAT AGC CCC TCT AAC ATT TCA AAC TAT TGG CTA GAT GGA GTC TAT GAC | 591        |            |                                         |            |            |     |
| Asn Ser Pro Ser Asn Ile Ser Asn Tyr Trp Leu Asp Gly Val Tyr Asp |            |            |                                         |            |            |     |
|                                                                 | 155        |            | 160                                     |            | 165        | 170 |
| ATC AAT GAA AAC AAT GGG ATT AAA GCC TAT TAC CAA TAC TAC GAT TTT | 639        |            |                                         |            |            |     |
| Ile Asn Glu Asn Asn Gly Ile Lys Ala Tyr Tyr Gln Tyr Tyr Asp Phe |            |            |                                         |            |            |     |
|                                                                 | 175        |            | 180                                     |            | 185        |     |





GTT CTT AAT AGC GGT TAT CAA TGC GAA GCT TGG TGT ATG ACC CAA CAT 2079  
Val Leu Asn Ser Gly Tyr Gln Cys Glu Ala Trp Cys Met Thr Gln His  
655 660 665

GAA GGG CTC TTG CCT TGG TAT TGG GTG TGG AAT ATC CAA GTG AGC CAA 2127  
Glu Gly Leu Leu Pro Trp Tyr Trp Val Trp Asn Ile Gln Val Ser Gln  
670 675 680

ATT TTC TGG GAA AAC GGG AGA CAC AGA GTT ACA GGA AGC TTG CAA ATC 2175  
Ile Phe Trp Glu Asn Gly Arg His Arg Val Thr Gly Ser Leu Gln Ile  
685 690 695

AAT AAT ATC TTC AAC ATG AAG TAT TAT TTT ACA GGG ATT GGC TCT AGC 2223  
Asn Asn Ile Phe Asn Met Lys Tyr Tyr Phe Thr Gly Ile Gly Ser Ser  
700 705 710

CCT GCA GGC TTG CAA CCT GCG CCT GGA AGA TCG GTT ACA GCG TAT TTG 2271  
Pro Ala Gly Leu Gln Pro Ala Pro Gly Arg Ser Val Thr Ala Tyr Leu  
715 720 725 730

AAC TAC ACT TTC TAAAGGCTTT AAAAAGGAGG GGGTTATTGC GCGATGATGA GCCG 2327  
Asn Tyr Thr Phe

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 734 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Met Pro Thr Ile Gln Ile Arg Gly Phe Gly Ala Gly Gly Ser Gly His  
1 5 10 15  
Ser Asp Ala Thr Leu Met Leu Val Asn Gly Ile Pro Val Tyr Met Ala  
20 25 30  
Pro Tyr Ala His Ile Glu Leu Asp Ile Phe Pro Val Thr Phe Gln Ala  
35 40 45  
Ile Asp Arg Ile Asp Val Ile Lys Gly Gly Gly Ser Val Gln Tyr Gly  
50 55 60  
Pro Asn Thr Tyr Gly Gly Ile Val Asn Ile Ile Thr Lys Pro Ile Pro  
65 70 75 80  
Asn Gln Trp Glu Asn Gln Ala Ala Glu Arg Ile Thr Tyr Trp Ala Lys  
85 90 95  
Ala Arg Asn Ala Gly Phe Ala Ala Pro Pro Asp Lys Thr Gly Asp Pro  
100 105 110  
Ser Phe Ile Lys Ser Leu Gly Asn Asn Leu Leu Tyr Asn Thr Tyr Val  
115 120 125  
Arg Ser Gly Gly Met Ile Asn Lys His Val Gly Ile Gln Ala Gln Ala  
130 135 140  
Asn Trp Val Arg Gly Gln Gly Phe Arg Asp Asn Ser Pro Ser Asn Ile  
145 150 155 160  
Ser Asn Tyr Trp Leu Asp Gly Val Tyr Asp Ile Asn Glu Asn Asn Gly



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 625 |     | 630 |     | 635 |     | 640 |     |     |     |     |     |     |     |     |     |
| Tyr | Tyr | Ser | Gly | Gly | Asn | Asn | Tyr | Glu | Ser | Val | Leu | Asn | Ser | Gly | Tyr |
|     |     |     |     | 645 |     |     |     | 650 |     |     |     |     |     | 655 |     |
| Gln | Cys | Glu | Ala | Trp | Cys | Met | Thr | Gln | His | Glu | Gly | Leu | Leu | Pro | Trp |
|     |     |     | 660 |     |     |     |     | 665 |     |     |     |     | 670 |     |     |
| Tyr | Trp | Val | Trp | Asn | Ile | Gln | Val | Ser | Gln | Ile | Phe | Trp | Glu | Asn | Gly |
|     |     | 675 |     |     |     |     | 680 |     |     |     |     | 685 |     |     |     |
| Arg | His | Arg | Val | Thr | Gly | Ser | Leu | Gln | Ile | Asn | Asn | Ile | Phe | Asn | Met |
|     | 690 |     |     |     |     | 695 |     |     |     | 700 |     |     |     |     |     |
| Lys | Tyr | Tyr | Phe | Thr | Gly | Ile | Gly | Ser | Ser | Pro | Ala | Gly | Leu | Gln | Pro |
| 705 |     |     |     |     | 710 |     |     |     |     | 715 |     |     |     |     | 720 |
| Ala | Pro | Gly | Arg | Ser | Val | Thr | Ala | Tyr | Leu | Asn | Tyr | Thr | Phe |     |     |
|     |     |     | 725 |     |     |     |     |     | 730 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 37...204
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CATTGGAGAT TGTGCCATTC TTTGATTTTA TCTAAA ATG TCT TTA GGG GCA GTG | 54  |
| Met Ser Leu Gly Ala Val                                         |     |
| 1 5                                                             |     |
| ATT AAG CTT ATT TTT TGT TAT AAA TTA GAG GGG GTA ATA TTA GAT TTA | 102 |
| Ile Lys Leu Ile Phe Cys Tyr Lys Leu Glu Gly Val Ile Leu Asp Leu |     |
| 10 15 20                                                        |     |
| AAG CGC ATC AAT TTC AAA TCC TAT TAT CCC AAT AAT AAA AAT GCA TTA | 150 |
| Lys Arg Ile Asn Phe Lys Ser Tyr Tyr Pro Asn Asn Lys Asn Ala Leu |     |
| 25 30 35                                                        |     |
| TTT ATC AAC AAT AAA AAA ATC CAT TAT CTA GTG CCT CAA AGG TTC ATA | 198 |
| Phe Ile Asn Asn Lys Lys Ile His Tyr Leu Val Pro Gln Arg Phe Ile |     |
| 40 45 50                                                        |     |
| TTG CTT TAACTTGCT ATGGACGATT AGAAATCG                           | 232 |
| Leu Leu                                                         |     |
| 55                                                              |     |

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Leu | Gly | Ala | Val | Ile | Lys | Leu | Ile | Phe | Cys | Tyr | Lys | Leu | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Val | Ile | Leu | Asp | Leu | Lys | Arg | Ile | Asn | Phe | Lys | Ser | Tyr | Tyr | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Asn | Lys | Asn | Ala | Leu | Phe | Ile | Asn | Asn | Lys | Lys | Ile | His | Tyr | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Pro | Gln | Arg | Phe | Ile | Leu | Leu |     |     |     |     |     |     |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1142 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 24...1094  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CTTTTAGAAT TAGGGCTTAA AGC ATG AAA GCT AGT ATT TAT GAT TTC ACT CTA | 53  |
| Met Lys Ala Ser Ile Tyr Asp Phe Thr Leu                           |     |
| 1 5 10                                                            |     |
| AAG GAA TTG AGC CAG CTT TTA AAA CCA AGC TTT AGG GCT AAA CAG CTT   | 101 |
| Lys Glu Leu Ser Gln Leu Leu Lys Pro Ser Phe Arg Ala Lys Gln Leu   |     |
| 15 20 25                                                          |     |
| TAT TTG TGG CTC TAT GCG AAG TAT AAA ACA AGC TTT AAG GAC ATG CAA   | 149 |
| Tyr Leu Trp Leu Tyr Ala Lys Tyr Lys Thr Ser Phe Lys Asp Met Gln   |     |
| 30 35 40                                                          |     |
| AAT AAT TTT TCA AAA GAT TTT ATC GCT TAT TTG GAG CGA GAA TTT GCT   | 197 |
| Asn Asn Phe Ser Lys Asp Phe Ile Ala Tyr Leu Glu Arg Glu Phe Ala   |     |
| 45 50 55                                                          |     |
| TTG CGC ACG ATA GAA ATC ACG CAT GTG AGG GAG AGC GTT GAT GGC TCT   | 245 |
| Leu Arg Thr Ile Glu Ile Thr His Val Arg Glu Ser Val Asp Gly Ser   |     |
| 60 65 70                                                          |     |
| AAA AAA TAC CTT TTT AAA TCT TTA AGA GAC AAC CAC ACT TTT GAA GCG   | 293 |
| Lys Lys Tyr Leu Phe Lys Ser Leu Arg Asp Asn His Thr Phe Glu Ala   |     |
| 75 80 85 90                                                       |     |







Lys Asp Leu Asn Asp Ser Leu Asp Cys Ala Lys Lys Leu Leu Lys Leu  
 275 280 285  
 Leu Asn Gly Ile Lys Ser Lys Val Asn Leu Ile Leu Phe Asn Pro His  
 290 295 300  
 Glu Gly Ser Lys Phe Glu Arg Pro Ser Leu Glu Asn Ala Arg Met Phe  
 305 310 315 320  
 Ala Asp Phe Leu Asn Ser Lys Gly Leu Leu Cys Thr Ile Arg Glu Ser  
 325 330 335  
 Lys Ala Leu Asp Ile Glu Ala Ala Cys Gly Gln Leu Arg Glu Lys Lys  
 340 345 350  
 Leu Ser Gln Gln Ile  
 355

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...987
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG CCC ATT CTT TTT GAT TGT AAC GCT ATT GCT TCA CAA GTT TTA AAA | 48  |
| Met Pro Ile Leu Phe Asp Cys Asn Ala Ile Ala Ser Gln Val Leu Lys |     |
| 1 5 10 15                                                       |     |
| GAT GAA GCG AGC GCG CTT TTA GAA AGC GTT GGA CAA TTC CAA AAA CCC | 96  |
| Asp Glu Ala Ser Ala Leu Leu Glu Ser Val Gly Gln Phe Gln Lys Pro |     |
| 20 25 30                                                        |     |
| AAC GAT TTA GAA GCG ATT GTC AAA CTC ATT TTA AAA AGC CAA GAA AAT | 144 |
| Asn Asp Leu Glu Ala Ile Val Lys Leu Ile Leu Lys Ser Gln Glu Asn |     |
| 35 40 45                                                        |     |
| GGG GGT AAG CTT GTG ATA GTG GGT GTG GGT AAG AGC GCT TTA GTG GCG | 192 |
| Gly Gly Lys Leu Val Ile Val Gly Val Gly Lys Ser Ala Leu Val Ala |     |
| 50 55 60                                                        |     |
| CAA AAA ATC GTT GCT TCC ATG CTA AGC ACC GGT AAC AGG AGC GCG TTT | 240 |
| Gln Lys Ile Val Ala Ser Met Leu Ser Thr Gly Asn Arg Ser Ala Phe |     |
| 65 70 75 80                                                     |     |
| TTA CAC CCC ACA GAA GCC ATG CAT GGG GAT TTG GGC ATG GTG GAA AAA | 288 |
| Leu His Pro Thr Glu Ala Met His Gly Asp Leu Gly Met Val Glu Lys |     |
| 85 90 95                                                        |     |
| AAC GAT GTG GTT TTA ATG ATT AGC TAT GGG GGC GAG TCT TTA GAA TTA | 336 |
| Asn Asp Val Val Leu Met Ile Ser Tyr Gly Gly Glu Ser Leu Glu Leu |     |
| 100 105 110                                                     |     |



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 329 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Ile | Leu | Phe | Asp | Cys | Asn | Ala | Ile | Ala | Ser | Gln | Val | Leu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Glu | Ala | Ser | Ala | Leu | Leu | Glu | Ser | Val | Gly | Gln | Phe | Gln | Lys | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Asp | Leu | Glu | Ala | Ile | Val | Lys | Leu | Ile | Leu | Lys | Ser | Gln | Glu | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Gly | Lys | Leu | Val | Ile | Val | Gly | Val | Gly | Lys | Ser | Ala | Leu | Val | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gln | Lys | Ile | Val | Ala | Ser | Met | Leu | Ser | Thr | Gly | Asn | Arg | Ser | Ala | Phe |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Leu | His | Pro | Thr | Glu | Ala | Met | His | Gly | Asp | Leu | Gly | Met | Val | Glu | Lys |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asn | Asp | Val | Val | Leu | Met | Ile | Ser | Tyr | Gly | Gly | Glu | Ser | Leu | Glu | Leu |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Leu | Asn | Leu | Val | Ser | His | Leu | Lys | Arg | Leu | Ser | His | Lys | Ile | Ile | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Thr | Lys | Ser | Pro | Asn | Ser | Ser | Leu | Ser | Lys | Leu | Gly | Asp | Tyr | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Ser | Leu | Lys | Ile | Gln | Lys | Glu | Ala | Cys | Pro | Ile | Asn | Thr | Ala | Pro |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     |     | 160 |
| Thr | Thr | Ser | Thr | Thr | Leu | Thr | Leu | Ala | Leu | Gly | Asp | Val | Leu | Met | Ala |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Cys | Leu | Met | Arg | Ala | Lys | Asn | Phe | Ser | Gln | Glu | Asp | Phe | Ala | Ser | Phe |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| His | Pro | Gly | Gly | Leu | Leu | Gly | Lys | Lys | Leu | Phe | Val | Lys | Val | Lys | Asp |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Leu | Gln | Thr | Thr | Asn | Leu | Pro | Leu | Ile | Ala | Pro | Ser | Thr | Ser | Phe |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Lys | Asp | Ala | Leu | Ile | Glu | Met | Ser | Glu | Lys | Arg | Leu | Gly | Ser | Ala | Ile |
| 225 |     |     |     | 230 |     |     |     | 235 |     |     |     |     |     |     | 240 |
| Leu | Val | Asn | Glu | Ala | Asn | Glu | Leu | Val | Gly | Val | Leu | Ser | Asp | Gly | Asp |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Val | Arg | Arg | Ala | Leu | Leu | Lys | Gly | Val | Ser | Leu | Lys | Ser | Glu | Val | Arg |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| His | Phe | Ala | Thr | Leu | Lys | Pro | Lys | Ser | Phe | Lys | Asn | Leu | Asp | Ala | Leu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Leu | Glu | Ala | Leu | Glu | Phe | Leu | Glu | Arg | His | Lys | Ile | Gln | Leu | Leu |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |
| Val | Cys | Val | Asp | Asp | His | Asn | Lys | Val | Leu | Gly | Val | Leu | His | Leu | His |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |
| Gln | Leu | Leu | Glu | Leu | Gly | Leu | Lys | Ala |     |     |     |     |     |     |     |
|     |     |     |     | 325 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:353:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 991 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 64...939  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| TCCTTAAAC ATTTGAAGTA TAATACACTC TTATGGTCAA ATATTAAGTT TAGGAAAAGC | 60  |
| TGC ATG TGG AGT TTC ATT CAA AAA ATC TTT AAG GCT TTA ATC ATC GCA  | 108 |
| Met Trp Ser Phe Ile Gln Lys Ile Phe Lys Ala Leu Ile Ile Ala      |     |
| 1 5 10 15                                                        |     |
| CCT TTA GAT TTT ATC ACG AAG TAT TTC AAG TCG TTT GTG CTG TTA CTC  | 156 |
| Pro Leu Asp Phe Ile Thr Lys Tyr Phe Lys Ser Phe Val Leu Leu Leu  |     |
| 20 25 30                                                         |     |
| ATT GTA TTA GTC TTT TTT AGC GCT AAA GAA AGC GCG CCA AGC GCC CCG  | 204 |
| Ile Val Leu Val Phe Phe Ser Ala Lys Glu Ser Ala Pro Ser Ala Pro  |     |
| 35 40 45                                                         |     |
| CCT AAT CTC GCT AAA CTC TAT TTA AAT GGG GCG ATT TTT AGC ACC GAG  | 252 |
| Pro Asn Leu Ala Lys Leu Tyr Leu Asn Gly Ala Ile Phe Ser Thr Glu  |     |
| 50 55 60                                                         |     |
| GAT TTT GAC AAA GAA GTG GAT AAA ATC CTA AAA ACC CCT AGC ATT AAG  | 300 |
| Asp Phe Asp Lys Glu Val Asp Lys Ile Leu Lys Thr Pro Ser Ile Lys  |     |
| 65 70 75                                                         |     |
| GGC GTT TTG CTT TTG ATT GAC TCT CCT GGT GGG GCG GTG TCA GCG AGC  | 348 |
| Gly Val Leu Leu Leu Ile Asp Ser Pro Gly Gly Ala Val Ser Ala Ser  |     |
| 80 85 90 95                                                      |     |
| GTG GAA TTG AGC GAA AAA ATC GCT GAT TTG AAG CAA AAA ATG CCC GTT  | 396 |
| Val Glu Leu Ser Glu Lys Ile Ala Asp Leu Lys Gln Lys Met Pro Val  |     |
| 100 105 110                                                      |     |
| TTA GCG TAT GCT AGG GGG GTT ATG GCG AGC GGG AGC TAT TAT GCG GGC  | 444 |
| Leu Ala Tyr Ala Arg Gly Val Met Ala Ser Gly Ser Tyr Tyr Ala Gly  |     |
| 115 120 125                                                      |     |
| ATG CAA GCG AGC GAA GTT TAT GCC TCT AAA GCG AGT TTG ATA GGA TCC  | 492 |
| Met Gln Ala Ser Glu Val Tyr Ala Ser Lys Ala Ser Leu Ile Gly Ser  |     |
| 130 135 140                                                      |     |
| ATT GGG GTG ATT TTT TCA GGT GCG AAT GTG GAA AAT TTG CTC AAT AAA  | 540 |
| Ile Gly Val Ile Phe Ser Gly Ala Asn Val Glu Asn Leu Leu Asn Lys  |     |
| 145 150 155                                                      |     |
| GTC GGC GTA GCC ACT CAA GGC GTG CAT GCG GGC GAA TAC AAA GAA ATA  | 588 |
| Val Gly Val Ala Thr Gln Gly Val His Ala Gly Glu Tyr Lys Glu Ile  |     |
| 160 165 170 175                                                  |     |





|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | Thr | Val | Lys | Ile | Ile | Ser | Lys | Thr | Asp | Asn | Ile | Glu | Ile | Gln |     |
| 40  |     |     |     |     |     | 45  |     |     |     |     | 50  |     |     |     |     |     |
| GAC | TTG | AAG | CTC | AAT | CGT | GGC | AAT | TGT | GAG | CAT | GAT | CAA | AAT | TTC | TTG | 246 |
| Asp | Leu | Lys | Leu | Asn | Arg | Gly | Asn | Cys | Glu | His | Asp | Gln | Asn | Phe | Leu |     |
| 55  |     |     |     |     | 60  |     |     |     |     | 65  |     |     |     |     | 70  |     |
| GTA | AAG | TTA | ATC | CAA | GAA | ACA | GCC | AAT | ACA | TAC | CTG | TTT | GCA | TCA | GAA | 294 |
| Val | Lys | Leu | Ile | Gln | Glu | Thr | Ala | Asn | Thr | Tyr | Leu | Phe | Ala | Ser | Glu |     |
|     |     |     |     | 75  |     |     |     |     | 80  |     |     |     |     | 85  |     |     |
| AAA | GAA | AAA | GCG | ATC | AAA | AAC | CAC | CAA | GCA | AAA | ATC | GCA | AGA | CTT | CAA | 342 |
| Lys | Glu | Lys | Ala | Ile | Lys | Asn | His | Gln | Ala | Lys | Ile | Ala | Arg | Leu | Gln |     |
|     |     |     | 90  |     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |
| AAA | GAT | TTA | GAA | GAA | CTC | ACA | CAG | CAT | GTG | CAA | CAA | TCC | AAT | AAT | CTT | 390 |
| Lys | Asp | Leu | Glu | Glu | Leu | Thr | Gln | His | Val | Gln | Gln | Ser | Asn | Asn | Leu |     |
|     |     | 105 |     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     |
| GAT | AAA | TTG | TTA | GAA | AAT | GGA | GGA | CTA | TTC | GTT | AGT | GGC | CAT | GAT | TAT | 438 |
| Asp | Lys | Leu | Leu | Glu | Asn | Gly | Gly | Leu | Phe | Val | Ser | Gly | His | Asp | Tyr |     |
|     | 120 |     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     |     |
| AAA | TAT | ACA | AAA | GAT | GAT | AAC | CCA | ATA | TAT | GTT | GTT | AAG | AGG | ATG | CTT | 486 |
| Lys | Tyr | Thr | Lys | Asp | Asp | Asn | Pro | Ile | Tyr | Val | Val | Lys | Arg | Met | Leu |     |
|     | 135 |     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |     |
| GAT | AAC | CTT | GAT | AGC | TAT | AAA | TAT | GAA | TCA | GAC | GAC | GTG | CTA | GAC | GTG | 534 |
| Asp | Asn | Leu | Asp | Ser | Tyr | Lys | Tyr | Glu | Ser | Asp | Asp | Val | Leu | Asp | Val |     |
|     |     |     |     | 155 |     |     |     |     | 160 |     |     |     |     | 165 |     |     |
| CCA | TAT | GAG | AAG | CTA | TTG | GAA | ATA | AGC | ATT | GCT | ATT | GAA | GAC | ACT | AAA | 582 |
| Pro | Tyr | Glu | Lys | Leu | Leu | Glu | Ile | Ser | Ile | Ala | Ile | Glu | Asp | Thr | Lys |     |
|     |     |     | 170 |     |     |     |     | 175 |     |     |     |     | 180 |     |     |     |
| AAC | CCC | AAA | GAC | TAC | CCT | TAT | ATC | AAC | CTT | AAA | GAA | CTC | AAA | AAA | TTA | 630 |
| Asn | Pro | Lys | Asp | Tyr | Pro | Tyr | Ile | Asn | Leu | Lys | Glu | Leu | Lys | Lys | Leu |     |
|     |     | 185 |     |     |     |     | 190 |     |     |     |     | 195 |     |     |     |     |
| ATA | GAT | AGT | ATT | ATT | GAT | GAT | CAT | GGT | TAT | ATG | GCC | GAT | GGC | TTT | TTG | 678 |
| Ile | Asp | Ser | Ile | Ile | Asp | Asp | His | Gly | Tyr | Met | Ala | Asp | Gly | Phe | Leu |     |
|     | 200 |     |     |     | 205 |     |     |     |     |     | 210 |     |     |     |     |     |
| AAT | GAA | TAT | TCT | AAT | AGG | GTA | TCA | AAA | AAA | GGT | CTC | CAA | ATC | CTT | GCT | 726 |
| Asn | Glu | Tyr | Ser | Asn | Arg | Val | Ser | Lys | Lys | Gly | Leu | Gln | Ile | Leu | Ala |     |
|     | 215 |     |     |     | 220 |     |     |     |     | 225 |     |     |     |     | 230 |     |
| AAA | CTA | AAA | TCC | ATG | TGG | CCT | AGC | GTA | GGG | AAA | TTT | TAT | TTC | GCC | TCT | 774 |
| Lys | Leu | Lys | Ser | Met | Trp | Pro | Ser | Val | Gly | Lys | Phe | Tyr | Phe | Ala | Ser |     |
|     |     |     |     | 235 |     |     |     |     | 240 |     |     |     |     | 245 |     |     |
| TTG | AAA | GAG | GCT | ATC | CCA | AGG | CAT | GCC | AAA | GAA | GTT | ACT | GAC | AAG | ATG | 822 |
| Leu | Lys | Glu | Ala | Ile | Pro | Arg | His | Ala | Lys | Glu | Val | Thr | Asp | Lys | Met |     |
|     |     |     | 250 |     |     |     |     | 255 |     |     |     |     | 260 |     |     |     |
| ATT | AGC | TCT | GAA | GAA | AAA | TCT | ATC | AAA | GCC | AAT | CAA | GTC | AAA | CTC | ACT | 870 |
| Ile | Ser | Ser | Glu | Glu | Lys | Ser | Ile | Lys | Ala | Asn | Gln | Val | Lys | Leu | Thr |     |
|     |     | 265 |     |     |     |     | 270 |     |     |     |     | 275 |     |     |     |     |





|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Leu | Gln | Ile | Leu | Ala | Lys | Leu | Lys | Ser | Met | Trp | Pro | Ser | Val | Gly |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Lys | Phe | Tyr | Phe | Ala | Ser | Leu | Lys | Glu | Ala | Ile | Pro | Arg | His | Ala | Lys |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Val | Thr | Asp | Lys | Met | Ile | Ser | Ser | Glu | Glu | Lys | Ser | Ile | Lys | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asn | Gln | Val | Lys | Leu | Thr | Glu | Ala | Lys | Gln | Asp | Ile | Asp | Lys | Met | Glu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Lys | Ile | Ile | Lys | Asp | Leu | Glu | Ser | Lys | Lys | Asn | Thr | Leu | Ser | Val | Tyr |
|     | 290 |     |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     |
| Leu | Lys | Phe | Gly | Glu | Ser | Phe | Thr | Ala | His | Tyr | Lys | Cys | Gln | Asn | Leu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ile | Glu | Val | Gly | Val | Lys | Thr | Asp | Lys | Gly | Ser | Trp | Thr | Phe | Asn | Phe |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |

Asn Arg

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 847 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 94...807
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

|            |            |            |            |            |            |     |     |     |     |     |     |     |     |     |     |     |
|------------|------------|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GCCTTGACGC | ATGTTTTTGA | AGTTTATCCT | AAAGTCAATA | TTTTTTTAAA | AATCCTTCAC | 60  |     |     |     |     |     |     |     |     |     |     |
| AAAGAAGGGG | CTTACCACAA | GCTTATTTCT | CGC        | ATG        | TGT        | TTG | GTC | AAA | GAC | AAG | 114 |     |     |     |     |     |
|            |            |            | Met        | Cys        | Leu        | Val | Lys | Asp | Lys |     |     |     |     |     |     |     |
|            |            |            | 1          |            |            |     | 5   |     |     |     |     |     |     |     |     |     |
| CTC        | AAA        | GAC        | ATT        | ATC        | AGC        | GTC | AAA | AGC | GCG | CTT | TCT | TTT | TCG | TTA | AAA | 162 |
| Leu        | Lys        | Asp        | Ile        | Ile        | Ser        | Val | Lys | Ser | Ala | Leu | Ser | Phe | Ser | Leu | Lys |     |
|            | 10         |            |            |            |            | 15  |     |     |     |     | 20  |     |     |     |     |     |
| GGG        | GAT        | TTT        | GAC        | TGC        | CCT        | TTA | GAA | GAA | AAC | TCG | CTC | TTT | AAA | GCC | CTC | 210 |
| Gly        | Asp        | Phe        | Asp        | Cys        | Pro        | Leu | Glu | Glu | Asn | Ser | Leu | Phe | Lys | Ala | Leu |     |
|            | 25         |            |            |            | 30         |     |     |     |     | 35  |     |     |     |     |     |     |
| CAA        | ATT        | TTA        | AAG        | AAT        | TTT        | TTA | AAA | TCA | AAA | AAT | TTC | TCT | CAT | TCT | GTC | 258 |
| Gln        | Ile        | Leu        | Lys        | Asn        | Phe        | Leu | Lys | Ser | Lys | Asn | Phe | Ser | His | Ser | Val |     |
| 40         |            |            |            | 45         |            |     |     |     | 50  |     |     |     |     | 55  |     |     |
| ATC        | AAA        | TCC        | CTA        | GAC        | ACC        | CTA | GCG | ATT | GAA | GTG | GAA | AAA | AAC | ATC | CCC | 306 |
| Ile        | Lys        | Ser        | Leu        | Asp        | Thr        | Leu | Ala | Ile | Glu | Val | Glu | Lys | Asn | Ile | Pro |     |
|            |            |            | 60         |            |            |     |     | 65  |     |     |     |     | 70  |     |     |     |
| ACT        | CAA        | GCC        | GGA        | TTA        | GGC        | GGT | GGG | AGC | ACT | GAT | GCT | GGG | GGG | CTA | TTG | 354 |
| Thr        | Gln        | Ala        | Gly        | Leu        | Gly        | Gly | Gly | Ser | Thr | Asp | Ala | Gly | Gly | Leu | Leu |     |



Ala Leu Ser Phe Ser Leu Lys Gly Asp Phe Asp Cys Pro Leu Glu Glu  
 20 25 30  
 Asn Ser Leu Phe Lys Ala Leu Gln Ile Leu Lys Asn Phe Leu Lys Ser  
 35 40 45  
 Lys Asn Phe Ser His Ser Val Ile Lys Ser Leu Asp Thr Leu Ala Ile  
 50 55 60  
 Glu Val Glu Lys Asn Ile Pro Thr Gln Ala Gly Leu Gly Gly Gly Ser  
 65 70 75 80  
 Thr Asp Ala Gly Gly Leu Leu Tyr His Leu Asn Gln Ile Phe Asp Trp  
 85 90 95  
 Arg Leu Ser Leu Glu Glu Leu Tyr Ser Met Gly Ser Leu Val Gly Ala  
 100 105 110  
 Asp Thr Asn Phe Phe Ile Ser Gln Tyr Lys Ser Thr Asn Ala Thr Ser  
 115 120 125  
 Tyr Gly Glu Val Ile Glu Asn Phe Glu Glu Glu Pro Leu Glu Asn Arg  
 130 135 140  
 Leu Glu Ile Tyr Ala Pro Asn His Val Phe Cys Ser Thr Lys Ala Val  
 145 150 155 160  
 Tyr Gln Ala Tyr Lys Pro Glu Thr Cys Phe Ser Gln Ala Lys Glu Trp  
 165 170 175  
 Leu Lys Lys Pro Ser Leu Glu Cys Leu Lys Thr Tyr Asp Arg Asn Gly  
 180 185 190  
 Leu Asn Asp Leu Leu Lys Pro Ala Leu Leu Thr Asn Gln Ala Leu Lys  
 195 200 205  
 Asp Ile Glu Ser Glu Leu Gly Lys Glu Trp Phe Phe Ser Gly Ser Gly  
 210 215 220  
 Ser Ala Phe Phe Arg Leu Lys Pro Met Gln Lys Gly Gly Glu  
 225 230 235

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 28...1047
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| TGAAACTATC CATTAAAGG TGTGAAA ATG GCA AAT TTA GAA AAT TTA GAC TGG | 54  |
| Met Ala Asn Leu Glu Asn Leu Asp Trp                              |     |
| 1 5                                                              |     |
| AAA AAT TTA GGC TTT AGC TAC ATT AAA ACG GAT TTT CGC TTC ATC GCC  | 102 |
| Lys Asn Leu Gly Phe Ser Tyr Ile Lys Thr Asp Phe Arg Phe Ile Ala  |     |
| 10 15 20 25                                                      |     |
| ACT TAT AAA AAC GGC TCT TGG TCG CAA GGC GGA TTG GTG AGC GAA AAC  | 150 |
| Thr Tyr Lys Asn Gly Ser Trp Ser Gln Gly Gly Leu Val Ser Glu Asn  |     |
| 30 35 40                                                         |     |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|
| ATG<br>Met | TTA<br>Leu | CAA<br>Gln | CTC<br>Leu | AGC<br>Ser | GAA<br>Glu | GGC<br>Gly | TCG<br>Ser | CCG<br>Pro | GTC<br>Val | TTG<br>Leu | CAC<br>His | TAC<br>Tyr | GGG<br>Gly | CAG<br>Gln | GCT<br>Ala | 198 |
| 45         |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| TGT<br>Cys | TTT<br>Phe | GAA<br>Glu | GGC<br>Gly | TTG<br>Leu | AAG<br>Lys | GCT<br>Ala | TAC<br>Tyr | CGC<br>Arg | TCT<br>Ser | CAA<br>Gln | AAG<br>Lys | GGG<br>Gly | AAA<br>Lys | GCT<br>Ala | TTA<br>Leu | 246 |
| 60         |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| CTC<br>Leu | TTT<br>Phe | CGC<br>Arg | CCT<br>Pro | TTA<br>Leu | GAA<br>Glu | AAC<br>Asn | GCC<br>Ala | AAA<br>Lys | CGC<br>Arg | TTG<br>Leu | CAA<br>Gln | ACT<br>Thr | TCA<br>Ser | TGC<br>Cys | GAA<br>Glu | 294 |
| 75         |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| AGA<br>Arg | CTG<br>Leu | CTC<br>Leu | ATG<br>Met | CCC<br>Pro | AAA<br>Lys | GTG<br>Val | AGC<br>Ser | GAA<br>Glu | GAG<br>Glu | CTG<br>Leu | TTT<br>Phe | TTA<br>Leu | AGG<br>Arg | GCA<br>Ala | TGC<br>Cys | 342 |
| 90         |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| GCT<br>Ala | GAA<br>Glu | GTG<br>Val | GTG<br>Val | AAA<br>Lys | GCG<br>Ala | AAT<br>Asn | CAA<br>Gln | AAA<br>Lys | TGG<br>Trp | CTC<br>Leu | GCT<br>Ala | CCT<br>Pro | TAT<br>Tyr | AAA<br>Lys | AGC<br>Ser | 390 |
| 110        |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| GGG<br>Gly | GCG<br>Ala | AGT<br>Ser | TTG<br>Leu | TAT<br>Tyr | TTG<br>Leu | CGC<br>Arg | CCT<br>Pro | TTT<br>Phe | GTC<br>Val | ATA<br>Ile | GGC<br>Gly | GTA<br>Val | GGG<br>Gly | GAT<br>Asp | AAT<br>Asn | 438 |
| 125        |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| TTG<br>Leu | GGG<br>Gly | GTG<br>Val | AAG<br>Lys | CCG<br>Pro | GCT<br>Ala | AAT<br>Asn | GAA<br>Glu | TAC<br>Tyr | CTT<br>Leu | TTT<br>Phe | ATC<br>Ile | GTG<br>Val | TTT<br>Phe | TGT<br>Cys | GCG<br>Ala | 486 |
| 140        |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| CCT<br>Pro | GTG<br>Val | GGG<br>Gly | GCG<br>Ala | TAT<br>Tyr | TTT<br>Phe | AAG<br>Lys | GGG<br>Gly | GGT<br>Gly | ATA<br>Ile | GAA<br>Glu | AAA<br>Lys | GGG<br>Gly | GGG<br>Gly | GCT<br>Ala | AGG<br>Arg | 534 |
| 155        |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| TTT<br>Phe | ATC<br>Ile | ACT<br>Thr | ACG<br>Thr | ATT<br>Ile | TTT<br>Phe | GAT<br>Asp | AGG<br>Arg | GCC<br>Ala | GCG<br>Ala | CCT<br>Pro | AAA<br>Lys | GGC<br>Gly | ACC<br>Thr | GGT<br>Gly | GGG<br>Gly | 582 |
| 170        |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| GTG<br>Val | AAA<br>Lys | GTG<br>Val | GGA<br>Gly | GGG<br>Gly | AAT<br>Asn | TAC<br>Tyr | GCT<br>Ala | GCA<br>Ala | AGC<br>Ser | CTG<br>Leu | TTA<br>Leu | GCC<br>Ala | CAT<br>His | AAA<br>Lys | ATG<br>Met | 630 |
| 190        |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| GCC<br>Ala | ACA<br>Thr | GAG<br>Glu | CAA<br>Gln | GGC<br>Gly | TAT<br>Tyr | GAT<br>Asp | GAT<br>Asp | TGC<br>Cys | ATT<br>Ile | TAT<br>Tyr | TTA<br>Leu | GAC<br>Asp | CCT<br>Pro | ACT<br>Thr | ACG<br>Thr | 678 |
| 205        |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| CAC<br>His | ACT<br>Thr | AAA<br>Lys | ATT<br>Ile | GAA<br>Glu | GAA<br>Glu | GTG<br>Val | GGG<br>Gly | GCG<br>Ala | GCG<br>Ala | AAT<br>Asn | TTT<br>Phe | TTT<br>Phe | GGC<br>Gly | ATC<br>Ile | ACG<br>Thr | 726 |
| 220        |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| CAT<br>His | GAT<br>Asp | GAT<br>Asp | GCC<br>Ala | TTT<br>Phe | ATC<br>Ile | ACC<br>Thr | CCG<br>Pro | CAT<br>His | TCG<br>Ser | CCA<br>Pro | AGC<br>Ser | ATT<br>Ile | CTG<br>Leu | CCA<br>Pro | AGC<br>Ser | 774 |
| 235        |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| ATT<br>Ile | ACC<br>Thr | AAA<br>Lys | AAA<br>Lys | AGC<br>Ser | TTG<br>Leu | ATG<br>Met | GTT<br>Val | TTG<br>Leu | GCT<br>Ala | AAA<br>Lys | GAA<br>Glu | TAT<br>Tyr | TTG<br>Leu | AAC<br>Asn | CTC<br>Leu | 822 |
| 250        |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| AAA<br>Lys | GTA<br>Val | GAA<br>Glu | GAG<br>Glu | AGG<br>Arg | GAA<br>Glu | ATC<br>Ile | CTA<br>Leu | ATG<br>Met | GAT<br>Asp | GAG<br>Glu | TTG<br>Leu | GAT<br>Asp | GCG<br>Ala | TTT<br>Phe | AAA<br>Lys | 870 |

|                                                                   |     |     |      |
|-------------------------------------------------------------------|-----|-----|------|
| 270                                                               | 275 | 280 |      |
| GAA GCT GGA GCG TGC GGG ACA GCT GCG ATC ATT ACG CCC ATT AAA GAA   |     |     | 918  |
| Glu Ala Gly Ala Cys Gly Thr Ala Ala Ile Ile Thr Pro Ile Lys Glu   |     |     |      |
| 285                                                               | 290 | 295 |      |
| ATC GTG CAC AAC AAC AAG TCT TAT TTT TTT GAA GCG CCG GGC CAT ATT   |     |     | 966  |
| Ile Val His Asn Asn Lys Ser Tyr Phe Phe Glu Ala Pro Gly His Ile   |     |     |      |
| 300                                                               | 305 | 310 |      |
| ACT AAA CGA CTC TAT GAT TTG CTT TTA TCC ATC CAA CAA GGC GAA CAA   |     |     | 1014 |
| Thr Lys Arg Leu Tyr Asp Leu Leu Leu Ser Ile Gln Gln Gly Glu Gln   |     |     |      |
| 315                                                               | 320 | 325 |      |
| GAA GCC CCC AAA GAT TGG ATT TTT GAA GTT GGC TAAAAGGTTA AAATTTATAG |     |     | 1067 |
| Glu Ala Pro Lys Asp Trp Ile Phe Glu Val Gly                       |     |     |      |
| 330                                                               | 335 | 340 |      |
| CTGTATGCCG CATAAAATAA GGGCG                                       |     |     | 1092 |

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asn | Leu | Glu | Asn | Leu | Asp | Trp | Lys | Asn | Leu | Gly | Phe | Ser | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Lys | Thr | Asp | Phe | Arg | Phe | Ile | Ala | Thr | Tyr | Lys | Asn | Gly | Ser | Trp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Gln | Gly | Gly | Leu | Val | Ser | Glu | Asn | Met | Leu | Gln | Leu | Ser | Glu | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Ser | Pro | Val | Leu | His | Tyr | Gly | Gln | Ala | Cys | Phe | Glu | Gly | Leu | Lys | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Tyr | Arg | Ser | Gln | Lys | Gly | Lys | Ala | Leu | Leu | Phe | Arg | Pro | Leu | Glu | Asn |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Lys | Arg | Leu | Gln | Thr | Ser | Cys | Glu | Arg | Leu | Leu | Met | Pro | Lys | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Glu | Glu | Leu | Phe | Leu | Arg | Ala | Cys | Ala | Glu | Val | Val | Lys | Ala | Asn |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Gln | Lys | Trp | Leu | Ala | Pro | Tyr | Lys | Ser | Gly | Ala | Ser | Leu | Tyr | Leu | Arg |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Pro | Phe | Val | Ile | Gly | Val | Gly | Asp | Asn | Leu | Gly | Val | Lys | Pro | Ala | Asn |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Glu | Tyr | Leu | Phe | Ile | Val | Phe | Cys | Ala | Pro | Val | Gly | Ala | Tyr | Phe | Lys |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Gly | Gly | Ile | Glu | Lys | Gly | Gly | Ala | Arg | Phe | Ile | Thr | Thr | Ile | Phe | Asp |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Arg | Ala | Ala | Pro | Lys | Gly | Thr | Gly | Gly | Val | Lys | Val | Gly | Gly | Asn | Tyr |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Ala | Ala | Ser | Leu | Leu | Ala | His | Lys | Met | Ala | Thr | Glu | Gln | Gly | Tyr | Asp |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |

```

Asp Cys Ile Tyr Leu Asp Pro Thr Thr His Thr Lys Ile Glu Glu Val
210 215 220
Gly Ala Ala Asn Phe Phe Gly Ile Thr His Asp Asp Ala Phe Ile Thr
225 230 235 240
Pro His Ser Pro Ser Ile Leu Pro Ser Ile Thr Lys Lys Ser Leu Met
 245 250 255
Val Leu Ala Lys Glu Tyr Leu Asn Leu Lys Val Glu Glu Arg Glu Ile
 260 265 270
Leu Met Asp Glu Leu Asp Ala Phe Lys Glu Ala Gly Ala Cys Gly Thr
 275 280 285
Ala Ala Ile Ile Thr Pro Ile Lys Glu Ile Val His Asn Asn Lys Ser
290 295 300
Tyr Phe Phe Glu Ala Pro Gly His Ile Thr Lys Arg Leu Tyr Asp Leu
305 310 315 320
Leu Leu Ser Ile Gln Gln Gly Glu Gln Glu Ala Pro Lys Asp Trp Ile
 325 330 335
Phe Glu Val Gly
 340

```

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...2067
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

```

GTTATAATTT TATTTTTTAA AAGGATACCC ATG AAT AAA GTT CAA TCT ATT GAT 54
 Met Asn Lys Val Gln Ser Ile Asp
 1 5

CCT TTA ATC GCT GAT AAG TTC AAC AAC GAG TTA AGA AGT TAT AAC CTA 102
Pro Leu Ile Ala Asp Lys Phe Asn Asn Glu Leu Arg Ser Tyr Asn Leu
10 15 20

GAA TAC AAA CTA GAG CAA GAA AGC CTG AAT AAA GAA ATT GAT GAA GCT 150
Glu Tyr Lys Leu Glu Gln Glu Ser Leu Asn Lys Glu Ile Asp Glu Ala
25 30 35 40

TTA AAA AAT TAC GCT TCT AAA AAT GGG GGT TTA GGG GGT AAC CGC CCT 198
Leu Lys Asn Tyr Ala Ser Lys Asn Gly Gly Leu Gly Gly Asn Arg Pro
45 50 55

GAT GTG AAA CTT TTA TTA AAC ACA CAA GAC CCC AAC AGA AGA GTC CCT 246
Asp Val Lys Leu Leu Leu Asn Thr Gln Asp Pro Asn Arg Arg Val Pro
60 65 70

ATT TTA ATA GAA TAC AAA GGG CTA AAA GAT AAG CTC ATT AAA TTA GAC 294

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ile | Leu | Ile | Glu | Tyr | Lys | Gly | Leu | Lys | Asp | Lys | Leu | Ile | Lys | Leu | Asp |     |  |
|     |     | 75  |     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     |  |
| AAA | AAC | AAA | CTG | GTA | GAA | AAC | TTT | AAA | AAC | CAT | GAG | CCT | CAT | TAT | AAA | 342 |  |
| Lys | Asn | Lys | Leu | Val | Glu | Asn | Phe | Lys | Asn | His | Glu | Pro | His | Tyr | Lys |     |  |
|     |     | 90  |     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     |  |
| AAC | ATT | AGA | GAA | TAC | GCC | CTA | AAT | GGG | GCT | TTG | CAT | TAC | GCT | AAT | GCG | 390 |  |
| Asn | Ile | Arg | Glu | Tyr | Ala | Leu | Asn | Gly | Ala | Leu | His | Tyr | Ala | Asn | Ala |     |  |
|     |     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |     |  |
| ATT | TTA | CAC | CAC | ACG | AGC | TAC | ACT | GAA | TGC | ATC | GCC | ATA | GGC | ATT | ACA | 438 |  |
| Ile | Leu | His | His | Thr | Ser | Tyr | Thr | Glu | Cys | Ile | Ala | Ile | Gly | Ile | Thr |     |  |
|     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |     |     |  |
| GGC | TAT | AAA | GAC | AAT | AAG | GGC | GGC | ATA | TGC | TCT | CAA | ATC | GCT | GTC | TAT | 486 |  |
| Gly | Tyr | Lys | Asp | Asn | Lys | Gly | Gly | Ile | Cys | Ser | Gln | Ile | Ala | Val | Tyr |     |  |
|     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |     |     |     |  |
| TAT | GTG | AAT | AAA | AGC | AAT | CTA | GGC | ATG | GGG | ATA | GAT | GTT | TCA | AAA | GGC | 534 |  |
| Tyr | Val | Asn | Lys | Ser | Asn | Leu | Gly | Met | Gly | Ile | Asp | Val | Ser | Lys | Gly |     |  |
|     |     |     | 155 |     |     |     | 160 |     |     |     |     | 165 |     |     |     |     |  |
| GAG | CAA | GGT | TAT | AGC | GAT | CTC | TCC | TTT | TTA | AGC | CGT | AAG | CAT | TTT | AAC | 582 |  |
| Glu | Gln | Gly | Tyr | Ser | Asp | Leu | Ser | Phe | Leu | Ser | Arg | Lys | His | Phe | Asn |     |  |
|     |     | 170 |     |     |     | 175 |     |     |     |     | 180 |     |     |     |     |     |  |
| GAC | TTT | ATT | AAA | CGA | GTA | GAC | ACC | CTT | TCT | TTA | AGC | GAT | GAA | GAT | TTA | 630 |  |
| Asp | Phe | Ile | Lys | Arg | Val | Asp | Thr | Leu | Ser | Leu | Ser | Asp | Glu | Asp | Leu |     |  |
|     |     |     |     |     | 190 |     |     |     |     | 195 |     |     |     |     | 200 |     |  |
| GAG | CGC | ATT | AGA | GAA | AAG | AAA | AAC | CAA | GAA | ATA | GAA | GAC | TGC | TTA | ATG | 678 |  |
| Glu | Arg | Ile | Arg | Glu | Lys | Lys | Asn | Gln | Glu | Ile | Glu | Asp | Cys | Leu | Met |     |  |
|     |     |     |     | 205 |     |     |     |     | 210 |     |     |     |     | 215 |     |     |  |
| CGG | CTC | AAC | AAC | AAT | ATT | TAC | AAC | AAA | GAA | AAG | AAT | TTT | TTA | AGC | GAA | 726 |  |
| Arg | Leu | Asn | Asn | Asn | Ile | Tyr | Asn | Lys | Glu | Lys | Asn | Phe | Leu | Ser | Glu |     |  |
|     |     |     | 220 |     |     |     |     | 225 |     |     |     |     | 230 |     |     |     |  |
| CAC | AAT | CGG | GTA | TAT | TTA | GTG | ATT | GCG | AGC | ATT | ATC | GCT | AAT | TTA | GGC | 774 |  |
| His | Asn | Arg | Val | Tyr | Leu | Val | Ile | Ala | Ser | Ile | Ile | Ala | Asn | Leu | Gly |     |  |
|     |     |     | 235 |     |     |     | 240 |     |     |     |     | 245 |     |     |     |     |  |
| ATC | CCT | AAT | TTG | GTA | ACC | CCC | CTA | AAC | AAA | GAA | GAT | CTA | AAA | TCC | AGC | 822 |  |
| Ile | Pro | Asn | Leu | Val | Thr | Pro | Leu | Asn | Lys | Glu | Asp | Leu | Lys | Ser | Ser |     |  |
|     |     | 250 |     |     |     | 255 |     |     |     |     | 260 |     |     |     |     |     |  |
| GAT | GAG | GTC | CAT | CAA | AGA | GAT | GGC | GAC | ATC | ATG | CTC | AGA | AAA | ATC | CAA | 870 |  |
| Asp | Glu | Val | His | Gln | Arg | Asp | Gly | Asp | Ile | Met | Leu | Arg | Lys | Ile | Gln |     |  |
|     |     | 265 |     |     | 270 |     |     |     |     | 275 |     |     |     |     | 280 |     |  |
| TCC | TTT | TTA | GAG | AAT | AAG | GAT | TTG | TCT | CCA | GAG | AAA | AGG | CAA | AGC | ATT | 918 |  |
| Ser | Phe | Leu | Glu | Asn | Lys | Asp | Leu | Ser | Pro | Glu | Lys | Arg | Gln | Ser | Ile |     |  |
|     |     |     |     | 285 |     |     |     |     | 290 |     |     |     |     | 295 |     |     |  |
| ATT | TCT | TCA | TTA | GAG | ACT | TTA | TTA | AGA | AAC | GAA | AAC | AAC | AAC | AAA | GCC | 966 |  |
| Ile | Ser | Ser | Leu | Glu | Thr | Leu | Leu | Arg | Asn | Glu | Asn | Asn | Asn | Lys | Ala |     |  |
|     |     |     | 300 |     |     |     |     | 305 |     |     |     |     | 310 |     |     |     |  |





|                                                                   |     |     |      |
|-------------------------------------------------------------------|-----|-----|------|
| 540                                                               | 545 | 550 |      |
| CAA ACC CAT ATC TAT GTT TTT AGG GTC AAT GAA AAG CAT GAC GCT AAG   |     |     | 1734 |
| Gln Thr His Ile Tyr Val Phe Arg Val Asn Glu Lys His Asp Ala Lys   |     |     |      |
| 555                                                               | 560 | 565 |      |
| CAA AGG GTG AAA TTT ATT AAT TTC AGT AAC GAC GGC TAC GCT AGA GCG   |     |     | 1782 |
| Gln Arg Val Lys Phe Ile Asn Phe Ser Asn Asp Gly Tyr Ala Arg Ala   |     |     |      |
| 570                                                               | 575 | 580 |      |
| AAT CGC AAA AAA GCC AAA GCC AGC CAC AAT TTA AAA GAC ACG CAT AAC   |     |     | 1830 |
| Asn Arg Lys Lys Ala Lys Ala Ser His Asn Leu Lys Asp Thr His Asn   |     |     |      |
| 585                                                               | 590 | 595 | 600  |
| GCC AAA GAG CGC TAC AAC GAA GTC GTG GAT TTA GTC CAT ATT GGC CAA   |     |     | 1878 |
| Ala Lys Glu Arg Tyr Asn Glu Val Val Asp Leu Val His Ile Gly Gln   |     |     |      |
| 605                                                               | 610 | 615 |      |
| TCA TGT TTG AAA TTT CTA AGC GAA GAT GAC TAT TAT GAA AAC ACC ATA   |     |     | 1926 |
| Ser Cys Leu Lys Phe Leu Ser Glu Asp Asp Tyr Tyr Glu Asn Thr Ile   |     |     |      |
| 620                                                               | 625 | 630 |      |
| GAT CCC AAA AAC GGG AGC GAT TGG AAC CAA AAC AAA CCC ACT GAC ACC   |     |     | 1974 |
| Asp Pro Lys Asn Gly Ser Asp Trp Asn Gln Asn Lys Pro Thr Asp Thr   |     |     |      |
| 635                                                               | 640 | 645 |      |
| AAA CCC GAA TTA GAG GAT TTT AAA AGA ACG ATA GCC GAT TAC CTT TCT   |     |     | 2022 |
| Lys Pro Glu Leu Glu Asp Phe Lys Arg Thr Ile Ala Asp Tyr Leu Ser   |     |     |      |
| 650                                                               | 655 | 660 |      |
| TAT GAA GTA AGC TTG ATT TTA AAA AAC CAA ATG CCC CCA AAG CGA TAGGC |     |     | 2072 |
| Tyr Glu Val Ser Leu Ile Leu Lys Asn Gln Met Pro Pro Lys Arg       |     |     |      |
| 665                                                               | 670 | 675 |      |
| CCCCCTTAATA GCCAACTCAA CGCTATTAAG TGGGGCGAG                       |     |     | 2111 |

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Lys | Val | Gln | Ser | Ile | Asp | Pro | Leu | Ile | Ala | Asp | Lys | Phe | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Glu | Leu | Arg | Ser | Tyr | Asn | Leu | Glu | Tyr | Lys | Leu | Glu | Gln | Glu | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Asn | Lys | Glu | Ile | Asp | Glu | Ala | Leu | Lys | Asn | Tyr | Ala | Ser | Lys | Asn |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Gly | Leu | Gly | Gly | Asn | Arg | Pro | Asp | Val | Lys | Leu | Leu | Leu | Asn | Thr |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Asp | Pro | Asn | Arg | Arg | Val | Pro | Ile | Leu | Ile | Glu | Tyr | Lys | Gly | Leu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |



Leu Phe Ile Gly Lys Ser Ser Val Gln Thr His Ile Tyr Val Phe Arg  
 545 550 555 560  
 Val Asn Glu Lys His Asp Ala Lys Gln Arg Val Lys Phe Ile Asn Phe  
 565 570 575  
 Ser Asn Asp Gly Tyr Ala Arg Ala Asn Arg Lys Lys Ala Lys Ala Ser  
 580 585 590  
 His Asn Leu Lys Asp Thr His Asn Ala Lys Glu Arg Tyr Asn Glu Val  
 595 600 605  
 Val Asp Leu Val His Ile Gly Gln Ser Cys Leu Lys Phe Leu Ser Glu  
 610 615 620  
 Asp Asp Tyr Tyr Glu Asn Thr Ile Asp Pro Lys Asn Gly Ser Asp Trp  
 625 630 635 640  
 Asn Gln Asn Lys Pro Thr Asp Thr Lys Pro Glu Leu Glu Asp Phe Lys  
 645 650 655  
 Arg Thr Ile Ala Asp Tyr Leu Ser Tyr Glu Val Ser Leu Ile Leu Lys  
 660 665 670  
 Asn Gln Met Pro Pro Lys Arg  
 675

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...597
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATCCTTTGAT TTCAAAGGCT TAAA ATG TAT GTG GTG TTA GAA GGC GTT GAT  | 51  |
| Met Tyr Val Val Leu Glu Gly Val Asp                             |     |
| 1 5                                                             |     |
| GGC GCG GGC AAA AGC ACT CAA GTA GAA TTA TTA AAA GAC CGG TTT AAA | 99  |
| Gly Ala Gly Lys Ser Thr Gln Val Glu Leu Leu Lys Asp Arg Phe Lys |     |
| 10 15 20 25                                                     |     |
| AAC GCC CTT TTT ACC AAA GAG CCA GGG GGG ACG AGA ATG GGC GAG AGT | 147 |
| Asn Ala Leu Phe Thr Lys Glu Pro Gly Gly Thr Arg Met Gly Glu Ser |     |
| 30 35 40                                                        |     |
| TTA AGG CGT ATC GCT TTG AAT GAA AAC ATT AGC GAA TTG GCT AGA GCG | 195 |
| Leu Arg Arg Ile Ala Leu Asn Glu Asn Ile Ser Glu Leu Ala Arg Ala |     |
| 45 50 55                                                        |     |
| TTT TTA TTC TTA AGC GAT AGG GCT GAG CAT ACA GAA AGC GTG ATA AAA | 243 |
| Phe Leu Phe Leu Ser Asp Arg Ala Glu His Thr Glu Ser Val Ile Lys |     |
| 60 65 70                                                        |     |
| CCG GCA TTG AAA GAA AAA AAG CTC ATC ATT AGC GAC AGG AGC TTG ATC | 291 |







165 170 175  
 Glu Asn Asp Leu Tyr Pro Arg Trp Gly Met Asn  
 180 185

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...309
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CTCCCTGAAG CG ATG CTC GCA TGG ATG TCT TGC TCG TTG AAA AAA GTA CCA | 51  |
| Met Leu Ala Trp Met Ser Cys Ser Leu Lys Lys Val Pro               |     |
| 1 5 10                                                            |     |
| CTA GGC CGT AAA TCT TTC ATG GCG TTT TTA AGG TTA ATA TTA GAT TCT   | 99  |
| Leu Gly Arg Lys Ser Phe Met Ala Phe Leu Arg Leu Ile Leu Asp Ser   |     |
| 15 20 25                                                          |     |
| TCT AAC GCC ACG ACA TGC GCG TTT TTA GAC GCC ACG ACA AAA ACT TCA   | 147 |
| Ser Asn Ala Thr Thr Cys Ala Phe Leu Asp Ala Thr Thr Lys Thr Ser   |     |
| 30 35 40 45                                                       |     |
| ATT TCT TTG GGT AAT TTT TCT AAA AAC CGC AAG GCT AGG GGT ATC CCG   | 195 |
| Ile Ser Leu Gly Asn Phe Ser Lys Asn Arg Lys Ala Arg Gly Ile Pro   |     |
| 50 55 60                                                          |     |
| CTC GCT CCA CTG ATG CCT AAA ACC AAT TTC ATG AAT GTC CTT TAT AAG   | 243 |
| Leu Ala Pro Leu Met Pro Lys Thr Asn Phe Met Asn Val Leu Tyr Lys   |     |
| 65 70 75                                                          |     |
| ATT TGC GCT TTA GAG CTG CTC AAC ACT TTT GCT TTG AGT ATT TTA TTG   | 291 |
| Ile Cys Ala Leu Glu Leu Leu Asn Thr Phe Ala Leu Ser Ile Leu Leu   |     |
| 80 85 90                                                          |     |
| CTT TCT AAA TTT TTC GCT TGAATGATTT GATTAAGCGC GCCATTTTCT AG       | 341 |
| Leu Ser Lys Phe Phe Ala                                           |     |
| 95                                                                |     |

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

```
Met Leu Ala Trp Met Ser Cys Ser Leu Lys Lys Val Pro Leu Gly Arg
 1 5 10 15
Lys Ser Phe Met Ala Phe Leu Arg Leu Ile Leu Asp Ser Ser Asn Ala
 20 25 30
Thr Thr Cys Ala Phe Leu Asp Ala Thr Thr Lys Thr Ser Ile Ser Leu
 35 40 45
Gly Asn Phe Ser Lys Asn Arg Lys Ala Arg Gly Ile Pro Leu Ala Pro
 50 55 60
Leu Met Pro Lys Thr Asn Phe Met Asn Val Leu Tyr Lys Ile Cys Ala
 65 70 75 80
Leu Glu Leu Leu Asn Thr Phe Ala Leu Ser Ile Leu Leu Leu Ser Lys
 85 90 95
Phe Phe Ala
```

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 85...822
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

```
GGCGCCAACG ATTTTAATGA TCCTCATTGT GATTTTAGTG GTTGTCAAGC CTTTTTAAAG 60
ACAAGCCATG AAAAAAGAAA AGTC ATG AAA AAA GAA AAG CAT CTC AAG CAA 111
 Met Lys Lys Glu Lys His Leu Lys Gln
 1 5

GAA AAA ATC ATC AAC ATG TTT GAT GAT ATA GCC AGC TCT TAC GAT CAA 159
Glu Lys Ile Ile Asn Met Phe Asp Asp Ile Ala Ser Ser Tyr Asp Gln
10 15 20 25

GCC AAC CGC TTG ATG AGT TTT GGC TTA GAC GTT AAA TGG CGA GAA AGG 207
Ala Asn Arg Leu Met Ser Phe Gly Leu Asp Val Lys Trp Arg Glu Arg
 30 35 40

GCT TGC GAG CAT GCG TTT TTA TTT TTA GAA AAC AAG AAA GCG TTA AGG 255
Ala Cys Glu His Ala Phe Leu Phe Leu Glu Asn Lys Lys Ala Leu Arg
 45 50 55

CTT GTG GAT GTG GCA TGC GGG ACG GGG GAT ATG CTT GTG GCT TGG CAA 303
Leu Val Asp Val Ala Cys Gly Thr Gly Asp Met Leu Val Ala Trp Gln
 60 65 70
```

|                             |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
|-----------------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|
| AAA<br>Lys                  | AGC<br>Ser | GCT<br>Ala | CTC<br>Leu | AAT<br>Asn | TGC<br>Cys | GGT<br>Gly | ATA<br>Ile | GAG<br>Glu | TTT<br>Phe | AAG<br>Lys | GAA<br>Glu | TGT<br>Cys | TTG<br>Leu | GGG<br>Gly | ATT<br>Ile | 351 |
| 758085                      |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| GAC<br>Asp                  | CCC<br>Pro | TCT<br>Ser | AAT<br>Asn | AAC<br>Asn | ATG<br>Met | CTT<br>Leu | GAA<br>Glu | TTA<br>Leu | GCC<br>Ala | ATC<br>Ile | AAA<br>Lys | AAA<br>Lys | TGT<br>Cys | GAA<br>Glu | GAG<br>Glu | 399 |
| 9095100105                  |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| CTT<br>Leu                  | GAA<br>Glu | AAC<br>Asn | AAA<br>Lys | GCT<br>Ala | TCT<br>Ser | TTC<br>Phe | ATC<br>Ile | CAA<br>Gln | GCT<br>Ala | CAA<br>Gln | GCC<br>Ala | AAA<br>Lys | GAT<br>Asp | TTA<br>Leu | AAA<br>Lys | 447 |
| 110115120                   |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| GGC<br>Gly                  | GTT<br>Val | GAA<br>Glu | AAT<br>Asn | AAC<br>Asn | AGC<br>Ser | GTG<br>Val | GAT<br>Asp | ATC<br>Ile | CTC<br>Leu | TCT<br>Ser | ATT<br>Ile | GCG<br>Ala | TAT<br>Tyr | GGC<br>Gly | TTG<br>Leu | 495 |
| 125130135                   |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| CGT<br>Arg                  | AAT<br>Asn | GTC<br>Val | GTG<br>Val | GAA<br>Glu | AGA<br>Arg | CAA<br>Gln | GAG<br>Glu | GCC<br>Ala | TTA<br>Leu | AAA<br>Lys | GAG<br>Glu | TTT<br>Phe | TTT<br>Phe | AGG<br>Arg | GTG<br>Val | 543 |
| 140145150                   |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| TTA<br>Leu                  | AAA<br>Lys | CCC<br>Pro | AGG<br>Arg | GGC<br>Gly | GTT<br>Val | TTA<br>Leu | GTG<br>Val | ATT<br>Ile | TTA<br>Leu | GAA<br>Glu | TTT<br>Phe | TTA<br>Leu | AAA<br>Lys | AAA<br>Lys | GAC<br>Asp | 591 |
| 155160165                   |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| AAC<br>Asn                  | CCC<br>Pro | ACA<br>Thr | TGG<br>Trp | CTG<br>Leu | GAT<br>Asp | AAA<br>Lys | ATC<br>Ile | TCA<br>Ser | GGG<br>Gly | TTT<br>Phe | TAC<br>Tyr | ACG<br>Thr | AAT<br>Asn | AAG<br>Lys | GTT<br>Val | 639 |
| 170175180185                |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| TTG<br>Leu                  | CCT<br>Pro | TTA<br>Leu | GTG<br>Val | GGA<br>Gly | GGG<br>Gly | GCT<br>Ala | ATC<br>Ile | AGT<br>Ser | AAG<br>Lys | AAT<br>Asn | TAT<br>Tyr | GGT<br>Gly | GCT<br>Ala | TAT<br>Tyr | TCT<br>Ser | 687 |
| 190195200                   |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| TAT<br>Tyr                  | TTA<br>Leu | CCG<br>Pro | CAA<br>Gln | TCC<br>Ser | ATT<br>Ile | GAG<br>Glu | GGG<br>Gly | TTT<br>Phe | TTG<br>Leu | AGT<br>Ser | TTA<br>Leu | GAG<br>Glu | GGT<br>Gly | TTG<br>Leu | AAG<br>Lys | 735 |
| 205210215                   |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| CAT<br>His                  | GAA<br>Glu | TTA<br>Leu | AGA<br>Arg | AAC<br>Asn | GCA<br>Ala | GGG<br>Gly | TTT<br>Phe | GAG<br>Glu | ATT<br>Ile | TTA<br>Leu | AGG<br>Arg | ACT<br>Thr | GAA<br>Glu | GAT<br>Asp | TCT<br>Ser | 783 |
| 220225230                   |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| ATC<br>Ile                  | GCT<br>Ala | CAA<br>Gln | ATT<br>Ile | TCA<br>Ser | ACG<br>Thr | ACC<br>Thr | ATG<br>Met | CTT<br>Leu | GTT<br>Val | AAA<br>Lys | AAA<br>Lys | AAC<br>Asn | TAAAGGAATG |            | TT         | 834 |
| 235240245                   |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| ATGCAAGATG AATTATTTGA AACCG |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| 858                         |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |



|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TTG ATG GTT GCT TTT TTA TTG GTG CTG TTG AAC GCT TTT TTT GTG CTT | 155 |
| Leu Met Val Ala Phe Leu Leu Val Leu Leu Asn Ala Phe Phe Val Leu |     |
| 20 25 30                                                        |     |
| TCA GAG TTT GCC CTT GTG AAA GTG CGT AAA ACC CGC TTA GAA GAG CTG | 203 |
| Ser Glu Phe Ala Leu Val Lys Val Arg Lys Thr Arg Leu Glu Glu Leu |     |
| 35 40 45                                                        |     |
| GTT AAA ATC GGT AAT TCC AAC GCT AAA CTC GCT TTA AAG ATG AGT CAA | 251 |
| Val Lys Ile Gly Asn Ser Asn Ala Lys Leu Ala Leu Lys Met Ser Gln |     |
| 50 55 60 65                                                     |     |
| AGA CTA GAC ACT TAT TTG AGC GCG ACG CAG TTA GGC ATC ACC CTT TCT | 299 |
| Arg Leu Asp Thr Tyr Leu Ser Ala Thr Gln Leu Gly Ile Thr Leu Ser |     |
| 70 75 80                                                        |     |
| TCA TTA GCT TTA GGC TGG GTG GGT GAG CCC GCT ATC GCA AAA TTG TTA | 347 |
| Ser Leu Ala Leu Gly Trp Val Gly Glu Pro Ala Ile Ala Lys Leu Leu |     |
| 85 90 95                                                        |     |
| GCC GCG CTG TTT GAG TCT ATG GAT TTG AGA GAA AAT CCT ATT TTT ATC | 395 |
| Ala Ala Leu Phe Glu Ser Met Asp Leu Arg Glu Asn Pro Ile Phe Ile |     |
| 100 105 110                                                     |     |
| CAT TCA ATG AGC GTG GTC ATA GCG TTT TTA AGC ATC ACT TTT TTG CAT | 443 |
| His Ser Met Ser Val Val Ile Ala Phe Leu Ser Ile Thr Phe Leu His |     |
| 115 120 125                                                     |     |
| GTC GTG TTG GGC GAG ATT GTG CCT AAA TCT TTA GCG ATC GCT AAA TCT | 491 |
| Val Val Leu Gly Glu Ile Val Pro Lys Ser Leu Ala Ile Ala Lys Ser |     |
| 130 135 140 145                                                 |     |
| GAA AAA GCC ACC CTT TTT GCC GCA CGC CCT TTG CAT GTG TTT TGG GTG | 539 |
| Glu Lys Ala Thr Leu Phe Ala Ala Arg Pro Leu His Val Phe Trp Val |     |
| 150 155 160                                                     |     |
| GTG TTT TAT CCG GTG GTG CGT TTG TTT GAT GTG ATC GCT CAT TTT TTT | 587 |
| Val Phe Tyr Pro Val Val Arg Leu Phe Asp Val Ile Ala His Phe Phe |     |
| 165 170 175                                                     |     |
| TTG AAA AAG ATG GGC ATC AAT CCT AAA GAG CAT GAC GGC ACG CAT TCT | 635 |
| Leu Lys Lys Met Gly Ile Asn Pro Lys Glu His Asp Gly Thr His Ser |     |
| 180 185 190                                                     |     |
| GAA GAA GAG TTA AAA ATC ATT GTG GGC GAG AGT TTG AGA GAG GGC ATT | 683 |
| Glu Glu Glu Leu Lys Ile Ile Val Gly Glu Ser Leu Arg Glu Gly Ile |     |
| 195 200 205                                                     |     |
| ATT GAT TCA GTG GAG GGC GAA ATC ATT AAA AAC GCA GTG GAT TTT TCT | 731 |
| Ile Asp Ser Val Glu Gly Glu Ile Ile Lys Asn Ala Val Asp Phe Ser |     |
| 210 215 220 225                                                 |     |
| GAC ACG AGC GCT AAA GAA ATC ATG ACC CCA CGA AAA GAC ATG GTG TGT | 779 |
| Asp Thr Ser Ala Lys Glu Ile Met Thr Pro Arg Lys Asp Met Val Cys |     |
| 230 235 240                                                     |     |
| TTG GAT GAA GAA AAC AGC TAT GAA GAA AAT ATA GAC ATT GTT TTA AAA | 827 |
| Leu Asp Glu Glu Asn Ser Tyr Glu Glu Asn Ile Asp Ile Val Leu Lys |     |

| 245                                       |     |     |     |     |     |     |     |     |     | 250 |     |     |     |     |      |      |      |  |  | 255 |  |  |  |  |  |  |  |  |  |  |
|-------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|--|--|-----|--|--|--|--|--|--|--|--|--|--|
| GGC                                       | CAT | TTC | ACG | CGC | TAC | CCT | TAT | TGC | AAG | GGT | TCT | AAG | GAT | AAC | ATT  | 875  |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Gly                                       | His | Phe | Thr | Arg | Tyr | Pro | Tyr | Cys | Lys | Gly | Ser | Lys | Asp | Asn | Ile  |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| 260                                       |     |     |     |     |     |     |     |     |     | 270 |     |     |     |     |      |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| ATC                                       | GGC | ATG | GTG | CAT | ATT | AGG | GAT | TTG | CTT | TCG | CGC | TCT | ATT | TTT | ACC  | 923  |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Ile                                       | Gly | Met | Val | His | Ile | Arg | Asp | Leu | Leu | Ser | Arg | Ser | Ile | Phe | Thr  |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| 275                                       |     |     |     |     |     |     |     |     |     | 285 |     |     |     |     |      |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| CCC                                       | AAA | ATG | CAT | GAT | TTC | AAT | CAA | ATC | GTT | AGG | AAA | ATG | ATC | ATC | GTC  | 971  |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Pro                                       | Lys | Met | His | Asp | Phe | Asn | Gln | Ile | Val | Arg | Lys | Met | Ile | Ile | Val  |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| 290                                       |     |     |     |     |     |     |     |     |     | 305 |     |     |     |     |      |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| CCC                                       | GAA | AGC | GCT | TCC | ATT | TCT | CAA | ATC | CTT | ATT | AAA | ATG | AAA | AAA | GAG  | 1019 |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Pro                                       | Glu | Ser | Ala | Ser | Ile | Ser | Gln | Ile | Leu | Ile | Lys | Met | Lys | Lys | Glu  |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| 310                                       |     |     |     |     |     |     |     |     |     | 320 |     |     |     |     |      |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| CAA                                       | ATC | CAT | ACC | GCT | TTG | GTG | ATT | GAT | GAA | TAC | GGC | GGC | ACA | GCC | GGG  | 1067 |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Gln                                       | Ile | His | Thr | Ala | Leu | Val | Ile | Asp | Glu | Tyr | Gly | Gly | Thr | Ala | Gly  |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| 325                                       |     |     |     |     |     |     |     |     |     | 335 |     |     |     |     |      |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| TTG                                       | CTC | ACT | ATG | GAA | GAC | ATC | ATT | GAA | GAG | ATC | ATG | GGC | GAG | ATT | AGC  | 1115 |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Leu                                       | Leu | Thr | Met | Glu | Asp | Ile | Ile | Glu | Glu | Ile | Met | Gly | Glu | Ile | Ser  |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| 340                                       |     |     |     |     |     |     |     |     |     | 350 |     |     |     |     |      |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| GAC                                       | GAA | TAC | GAC | TTA | AAA | CAA | GAG | GGC | ATA | AAC | AAG | CTT | GAA | GAG | GGC  | 1163 |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Asp                                       | Glu | Tyr | Asp | Leu | Lys | Gln | Glu | Gly | Ile | Asn | Lys | Leu | Glu | Glu | Gly  |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| 355                                       |     |     |     |     |     |     |     |     |     | 365 |     |     |     |     |      |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| GTG                                       | TTT | GAA | TTA | GAG | GGC | ATG | CTG | GAT | TTA | GAG | AGC | GTA | GAA | GAA | GCG  | 1211 |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Val                                       | Phe | Glu | Leu | Glu | Gly | Met | Leu | Asp | Leu | Glu | Ser | Val | Glu | Glu | Ala  |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| 370                                       |     |     |     |     |     |     |     |     |     | 385 |     |     |     |     |      |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| CTT                                       | CAC | ATT | GAA | TTT | GAT | AAA | GAA | TGC | GAG | CAG | GTA | ACG | CTT | GGG | GGC  | 1259 |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Leu                                       | His | Ile | Glu | Phe | Asp | Lys | Glu | Cys | Glu | Gln | Val | Thr | Leu | Gly | Gly  |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| 390                                       |     |     |     |     |     |     |     |     |     | 400 |     |     |     |     |      |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| TAT                                       | GTT | TTT | AGC | TTG | TTA | GAG | CGC | ATG | CCT | ATG | GAG | GGA | GAT | ACA | ATC  | 1307 |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Tyr                                       | Val | Phe | Ser | Leu | Leu | Glu | Arg | Met | Pro | Met | Glu | Gly | Asp | Thr | Ile  |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| 405                                       |     |     |     |     |     |     |     |     |     | 415 |     |     |     |     |      |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| GTT                                       | TCG | CAT | GGG | TAT | TCT | TTT | GAA | GTC | TTA | AGC | GTG | GAT | GGG | GCT | AGG  | 1355 |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Val                                       | Ser | His | Gly | Tyr | Ser | Phe | Glu | Val | Leu | Ser | Val | Asp | Gly | Ala | Arg  |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| 420                                       |     |     |     |     |     |     |     |     |     | 430 |     |     |     |     |      |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| ATA                                       | AAA | CGC | TTA | AAA | GCG | GTT | AAA | CAA | GAT | CAG | GGA | GAA | AAT | GAA | GCA  | T    | 1404 |  |  |     |  |  |  |  |  |  |  |  |  |  |
| Ile                                       | Lys | Arg | Leu | Lys | Ala | Val | Lys | Gln | Asp | Gln | Gly | Glu | Asn | Glu | Ala  |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| 435                                       |     |     |     |     |     |     |     |     |     | 445 |     |     |     |     |      |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |
| GAAAAAACA ACCCTCTTTG TATTGGGCTT ATTATTTAA |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 1443 |      |      |  |  |     |  |  |  |  |  |  |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:372:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 449 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

Met Gly Arg Asn Gln Gly Ala Tyr Leu Asp Pro Ser Glu Ser Ile Leu  
1 5 10 15  
Met Leu Met Val Ala Phe Leu Leu Val Leu Leu Asn Ala Phe Phe Val  
20 25 30  
Leu Ser Glu Phe Ala Leu Val Lys Val Arg Lys Thr Arg Leu Glu Glu  
35 40 45  
Leu Val Lys Ile Gly Asn Ser Asn Ala Lys Leu Ala Leu Lys Met Ser  
50 55 60  
Gln Arg Leu Asp Thr Tyr Leu Ser Ala Thr Gln Leu Gly Ile Thr Leu  
65 70 75 80  
Ser Ser Leu Ala Leu Gly Trp Val Gly Glu Pro Ala Ile Ala Lys Leu  
85 90 95  
Leu Ala Ala Leu Phe Glu Ser Met Asp Leu Arg Glu Asn Pro Ile Phe  
100 105 110  
Ile His Ser Met Ser Val Val Ile Ala Phe Leu Ser Ile Thr Phe Leu  
115 120 125  
His Val Val Leu Gly Glu Ile Val Pro Lys Ser Leu Ala Ile Ala Lys  
130 135 140  
Ser Glu Lys Ala Thr Leu Phe Ala Ala Arg Pro Leu His Val Phe Trp  
145 150 155 160  
Val Val Phe Tyr Pro Val Val Arg Leu Phe Asp Val Ile Ala His Phe  
165 170 175  
Phe Leu Lys Lys Met Gly Ile Asn Pro Lys Glu His Asp Gly Thr His  
180 185 190  
Ser Glu Glu Glu Leu Lys Ile Ile Val Gly Glu Ser Leu Arg Glu Gly  
195 200 205  
Ile Ile Asp Ser Val Glu Gly Glu Ile Ile Lys Asn Ala Val Asp Phe  
210 215 220  
Ser Asp Thr Ser Ala Lys Glu Ile Met Thr Pro Arg Lys Asp Met Val  
225 230 235 240  
Cys Leu Asp Glu Glu Asn Ser Tyr Glu Glu Asn Ile Asp Ile Val Leu  
245 250 255  
Lys Gly His Phe Thr Arg Tyr Pro Tyr Cys Lys Gly Ser Lys Asp Asn  
260 265 270  
Ile Ile Gly Met Val His Ile Arg Asp Leu Leu Ser Arg Ser Ile Phe  
275 280 285  
Thr Pro Lys Met His Asp Phe Asn Gln Ile Val Arg Lys Met Ile Ile  
290 295 300  
Val Pro Glu Ser Ala Ser Ile Ser Gln Ile Leu Ile Lys Met Lys Lys  
305 310 315 320  
Glu Gln Ile His Thr Ala Leu Val Ile Asp Glu Tyr Gly Gly Thr Ala  
325 330 335  
Gly Leu Leu Thr Met Glu Asp Ile Ile Glu Glu Ile Met Gly Glu Ile  
340 345 350  
Ser Asp Glu Tyr Asp Leu Lys Gln Glu Gly Ile Asn Lys Leu Glu Glu  
355 360 365  
Gly Val Phe Glu Leu Glu Gly Met Leu Asp Leu Glu Ser Val Glu Glu  
370 375 380  
Ala Leu His Ile Glu Phe Asp Lys Glu Cys Glu Gln Val Thr Leu Gly  
385 390 395 400  
Gly Tyr Val Phe Ser Leu Leu Glu Arg Met Pro Met Glu Gly Asp Thr  
405 410 415

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Val | Ser | His | Gly | Tyr | Ser | Phe | Glu | Val | Leu | Ser | Val | Asp | Gly | Ala |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Arg | Ile | Lys | Arg | Leu | Lys | Ala | Val | Lys | Gln | Asp | Gln | Gly | Glu | Asn | Glu |
|     |     | 435 |     |     |     | 440 |     |     |     |     |     | 445 |     |     |     |
| Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 47...367
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

|            |            |            |            |        |     |     |     |            |            |         |     |     |     |     |     |     |
|------------|------------|------------|------------|--------|-----|-----|-----|------------|------------|---------|-----|-----|-----|-----|-----|-----|
| AGAAACCGGC | ACGGTTACCA | ACCAAGCGGT | AACAATCTTT | TTTAAA | ATG | GAG | CGT |            | 55         |         |     |     |     |     |     |     |
|            |            |            |            |        | Met | Glu | Arg |            |            |         |     |     |     |     |     |     |
|            |            |            |            |        | 1   |     |     |            |            |         |     |     |     |     |     |     |
| TTG        | ATC        | ACT        | TCT        | TCT    | TTA | TAC | ACT | TTT        | TTA        | AGC     | GAC | TTT | TTT | TCT | TTC | 103 |
| Leu        | Ile        | Thr        | Ser        | Ser    | Leu | Tyr | Thr | Phe        | Leu        | Ser     | Asp | Phe | Phe | Ser | Phe |     |
|            | 5          |            |            |        |     | 10  |     |            |            |         | 15  |     |     |     |     |     |
| TTT        | TTC        | AAT        | TCC        | AAA    | GCG | ATG | GCG | GTG        | TTC        | TTG     | CTT | TTT | TTT | AAG | CTC | 151 |
| Phe        | Phe        | Asn        | Ser        | Lys    | Ala | Met | Ala | Val        | Phe        | Leu     | Leu | Phe | Phe | Lys | Leu |     |
| 20         |            |            |            |        | 25  |     |     |            | 30         |         |     |     |     | 35  |     |     |
| TCT        | AGC        | ATG        | AGC        | GAT    | TTT | TCT | TTC | AAA        | TTG        | GCT     | TTA | TCA | AAG | CGC | TCT | 199 |
| Ser        | Ser        | Met        | Ser        | Asp    | Phe | Ser | Phe | Lys        | Leu        | Ala     | Leu | Ser | Lys | Arg | Ser |     |
|            |            |            | 40         |        |     |     |     | 45         |            |         |     |     |     | 50  |     |     |
| AAA        | AAG        | CCT        | TCA        | ATT    | TCT | TCT | AAA | TCT        | TCC        | CCA     | AAG | TGC | GCG | GCT | ACA | 247 |
| Lys        | Lys        | Pro        | Ser        | Ile    | Ser | Ser | Lys | Ser        | Ser        | Pro     | Lys | Cys | Ala | Ala | Thr |     |
|            |            | 55         |            |        |     |     |     | 60         |            |         |     |     | 65  |     |     |     |
| ATG        | TTG        | TCT        | CTG        | ATT    | CTA | GCA | AAA | CGC        | CTT        | CTT     | GAT | TGC | TCT | CTT | AAG | 295 |
| Met        | Leu        | Ser        | Leu        | Ile    | Leu | Ala | Lys | Arg        | Leu        | Leu     | Asp | Cys | Ser | Leu | Lys |     |
|            | 70         |            |            |        |     | 75  |     |            |            |         | 80  |     |     |     |     |     |
| CGC        | TCC        | CTT        | AAA        | AAG    | CCC | ACC | CCA | AAC        | ACC        | GCG     | CCC | ACC | ACA | ATA | TGC | 343 |
| Arg        | Ser        | Leu        | Lys        | Lys    | Pro | Thr | Pro | Asn        | Thr        | Ala     | Pro | Thr | Thr | Ile | Cys |     |
|            | 85         |            |            |        |     | 90  |     |            |            |         | 95  |     |     |     |     |     |
| GTA        | GAG        | CTT        | ACG        | GGC    | AAG | CCT | AAT | TGAGAGGCTA | AAAGCACGGT | GATGACT |     |     |     |     |     | 394 |
| Val        | Glu        | Leu        | Thr        | Gly    | Lys | Pro | Asn |            |            |         |     |     |     |     |     |     |
| 100        |            |            |            |        | 105 |     |     |            |            |         |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

Met Glu Arg Leu Ile Thr Ser Ser Leu Tyr Thr Phe Leu Ser Asp Phe  
1 5 10 15  
Phe Ser Phe Phe Phe Asn Ser Lys Ala Met Ala Val Phe Leu Leu Phe  
20 25 30  
Phe Lys Leu Ser Ser Met Ser Asp Phe Ser Phe Lys Leu Ala Leu Ser  
35 40 45  
Lys Arg Ser Lys Lys Pro Ser Ile Ser Ser Lys Ser Ser Pro Lys Cys  
50 55 60  
Ala Ala Thr Met Leu Ser Leu Ile Leu Ala Lys Arg Leu Leu Asp Cys  
65 70 75 80  
Ser Leu Lys Arg Ser Leu Lys Lys Pro Thr Pro Asn Thr Ala Pro Thr  
85 90 95  
Thr Ile Cys Val Glu Leu Thr Gly Lys Pro Asn  
100 105

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...321
- (D) OTHER INFORMATION:



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TCAAATCTCTT CATAA ATG ATT TTT TCT TTT AAA AGG ACT TCT TTT TGC GTG | 51  |
| Met Ile Phe Ser Phe Lys Arg Thr Ser Phe Cys Val                   |     |
| 1 5 10                                                            |     |
| AGC GTG CCG GTT TTG TCT ATA AAG ATT TTT TTC ACT TTA GCC AGA GTT   | 99  |
| Ser Val Pro Val Leu Ser Ile Lys Ile Phe Phe Thr Leu Ala Arg Val   |     |
| 15 20 25                                                          |     |
| TCT AAA AAC AAC GCT TCT TTA AAC ACG ATC AAA GGG TTT TTA AAC ACC   | 147 |
| Ser Lys Asn Asn Ala Ser Leu Asn Thr Ile Lys Gly Phe Leu Asn Thr   |     |
| 30 35 40                                                          |     |
| CCT ATC ACT AAC GCA ATG GGC GTA GCC AGA GCG AAC GCG CAA GGG CAG   | 195 |
| Pro Ile Thr Asn Ala Met Gly Val Ala Arg Ala Asn Ala Gln Gly Gln   |     |
| 45 50 55 60                                                       |     |
| CTG ATG ACT AGC ACG CTA ATA CAC ACC ATT AAG GCT TTT TCA AAA TTA   | 243 |
| Leu Met Thr Ser Thr Leu Ile His Thr Ile Lys Ala Phe Ser Lys Leu   |     |
| 65 70 75                                                          |     |
| CCC CCC AAA CCA AAT TGC CAT AAC AAA AAG CTT ACA AAG GCT AAA AAC   | 291 |
| Pro Pro Lys Pro Asn Cys His Asn Lys Lys Leu Thr Lys Ala Lys Asn   |     |
| 80 85 90                                                          |     |
| AAC ACC GCT TTA GAA AAA ATA TCC GCA ATT TGATTCGCGC TACTCTCAAT T   | 342 |
| Asn Thr Ala Leu Glu Lys Ile Ser Ala Ile                           |     |
| 95 100                                                            |     |

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ile Phe Ser Phe Lys Arg Thr Ser Phe Cys Val Ser Val Pro Val |  |
| 1 5 10 15                                                       |  |
| Leu Ser Ile Lys Ile Phe Phe Thr Leu Ala Arg Val Ser Lys Asn Asn |  |
| 20 25 30                                                        |  |
| Ala Ser Leu Asn Thr Ile Lys Gly Phe Leu Asn Thr Pro Ile Thr Asn |  |
| 35 40 45                                                        |  |
| Ala Met Gly Val Ala Arg Ala Asn Ala Gln Gly Gln Leu Met Thr Ser |  |
| 50 55 60                                                        |  |
| Thr Leu Ile His Thr Ile Lys Ala Phe Ser Lys Leu Pro Pro Lys Pro |  |
| 65 70 75 80                                                     |  |
| Asn Cys His Asn Lys Lys Leu Thr Lys Ala Lys Asn Asn Thr Ala Leu |  |
| 85 90 95                                                        |  |
| Glu Lys Ile Ser Ala Ile                                         |  |
| 100                                                             |  |

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...1062
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

|                                                                 |                                 |     |
|-----------------------------------------------------------------|---------------------------------|-----|
| AGGCTTTTGTG CTCTTGCCTT TTTTCCCATC                               | ATG AGA CTT TAT GAG AGT TTA TTA | 54  |
|                                                                 | Met Arg Leu Tyr Glu Ser Leu Leu |     |
|                                                                 | 1 5                             |     |
| GAA ATG TGC TTG AAT AAG GCA TGG GAG CAT CAA ACC CTA GCC TTA GAA |                                 | 102 |
| Glu Met Cys Leu Asn Lys Ala Trp Glu His Gln Thr Leu Ala Leu Glu |                                 |     |
| 10 15 20                                                        |                                 |     |
| AAC CCA AGC GTA GCT TGC ATG GTG TTG GAT AAA AAC CAT GAG ATC TTG |                                 | 150 |
| Asn Pro Ser Val Ala Cys Met Val Leu Asp Lys Asn His Glu Ile Leu |                                 |     |
| 25 30 35 40                                                     |                                 |     |
| AGT TTA GAA ACC CAC AAA AAA GCC AAA ACC CCG CAT GCA GAA GTC TTA |                                 | 198 |
| Ser Leu Glu Thr His Lys Lys Ala Lys Thr Pro His Ala Glu Val Leu |                                 |     |
| 45 50 55                                                        |                                 |     |
| GCC GCC CAA TCA GCG CTA AAG ATT TTA CGC CCC AGT TTG AAA AAC GAT |                                 | 246 |
| Ala Ala Gln Ser Ala Leu Lys Ile Leu Arg Pro Ser Leu Lys Asn Asp |                                 |     |
| 60 65 70                                                        |                                 |     |
| TTA GAA AAG TTA GAA GAC CCT AAA ACT TTA AGC GAT TTT TTA AAA ACG |                                 | 294 |
| Leu Glu Lys Leu Glu Asp Pro Lys Thr Leu Ser Asp Phe Leu Lys Thr |                                 |     |
| 75 80 85                                                        |                                 |     |
| CAC CAC GAT AAC GCT TTT ACA GAC TGC GTT TTT TTA ATC ACC TTA GAG |                                 | 342 |
| His His Asp Asn Ala Phe Thr Asp Cys Val Phe Leu Ile Thr Leu Glu |                                 |     |
| 90 95 100                                                       |                                 |     |
| CCA TGC AAT TCT TAT GGC AAA ACC CCG GCT TGT AGC GAA TTG TTA GAA |                                 | 390 |
| Pro Cys Asn Ser Tyr Gly Lys Thr Pro Ala Cys Ser Glu Leu Leu Glu |                                 |     |
| 105 110 115 120                                                 |                                 |     |
| ATT TTA AAG CCT AAA AGA GTG GTC ATT GCC ACA GAA GAA AAC GAA GCT |                                 | 438 |
| Ile Leu Lys Pro Lys Arg Val Val Ile Ala Thr Glu Glu Asn Glu Ala |                                 |     |
| 125 130 135                                                     |                                 |     |
| AAA AAA GGG GGT TTA GCA AGG CTA CAA AAG GCT CGT ATT GAA ACA ATA |                                 | 486 |
| Lys Lys Gly Gly Leu Ala Arg Leu Gln Lys Ala Arg Ile Glu Thr Ile |                                 |     |
| 140 145 150                                                     |                                 |     |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| ATT TGC CAC AAT TTA GAA AAC AAA GCT AAA GAC TTG CTC TTG CCT TTT   | 534  |
| Ile Cys His Asn Leu Glu Asn Lys Ala Lys Asp Leu Leu Leu Pro Phe   |      |
| 155 160 165                                                       |      |
| AGG GTA ATG GAA CAA AAG GGG CGT TTT AAT TTG TTC AAA CTC GCT TTA   | 582  |
| Arg Val Met Glu Gln Lys Gly Arg Phe Asn Leu Phe Lys Leu Ala Leu   |      |
| 170 175 180                                                       |      |
| AGA ATG AAT GGG GAT TAC CAT CAT GGC AAG ATC ACC GGG CAA AAA AGC   | 630  |
| Arg Met Asn Gly Asp Tyr His His Gly Lys Ile Thr Gly Gln Lys Ser   |      |
| 185 190 195 200                                                   |      |
| GTT ATT TTC ACG CAC AAC CAG CGA GCA ATA TGC GAC ACG CTT ATT GTT   | 678  |
| Val Ile Phe Thr His Asn Gln Arg Ala Ile Cys Asp Thr Leu Ile Val   |      |
| 205 210 215                                                       |      |
| TCT GGG AAA ACC ATA AGA ACG GAC AAC CCC TTA TTG GAC GCT CGC TTT   | 726  |
| Ser Gly Lys Thr Ile Arg Thr Asp Asn Pro Leu Leu Asp Ala Arg Phe   |      |
| 220 225 230                                                       |      |
| TGC GAC AGC TTT TAT CAA AAT AAA AAC CCC AAT ATC GCT ATT TTA TCC   | 774  |
| Cys Asp Ser Phe Tyr Gln Asn Lys Asn Pro Asn Ile Ala Ile Leu Ser   |      |
| 235 240 245                                                       |      |
| AAG CGC TCA ATT GAC CCT AAT TCA AAA GTT TTT TCT GCG CCT AAT CGT   | 822  |
| Lys Arg Ser Ile Asp Pro Asn Ser Lys Val Phe Ser Ala Pro Asn Arg   |      |
| 250 255 260                                                       |      |
| TTA GTT AAC ACT TTC CAT GAC CCC AAA GAT TTA CCC CTA GAG AAG GGG   | 870  |
| Leu Val Asn Thr Phe His Asp Pro Lys Asp Leu Pro Leu Glu Lys Gly   |      |
| 265 270 275 280                                                   |      |
| TTT AAT TTC ATT GAA GGG GGG TGG GAA TTG TTT GAG AGC TTG AGG GAT   | 918  |
| Phe Asn Phe Ile Glu Gly Gly Trp Glu Leu Phe Glu Ser Leu Arg Asp   |      |
| 285 290 295                                                       |      |
| AAA ATA GAC GCG TTG CTT TTG CAT TCG CAT GCG TCT ATG ATT GGC GAA   | 966  |
| Lys Ile Asp Ala Leu Leu Leu His Ser His Ala Ser Met Ile Gly Glu   |      |
| 300 305 310                                                       |      |
| GCG TTT AAG GCA CTC GCT CTA AAA ACC CCT TTT AAA GGA CGG TTG TTG   | 1014 |
| Ala Phe Lys Ala Leu Ala Leu Lys Thr Pro Phe Lys Gly Arg Leu Leu   |      |
| 315 320 325                                                       |      |
| CAT GCG CAA ATC TTA GAA AAT GAA GCC CTT TTA TGG ATA GAA AAC TCT T | 1063 |
| His Ala Gln Ile Leu Glu Asn Glu Ala Leu Leu Trp Ile Glu Asn Ser   |      |
| 330 335 340                                                       |      |
| AAGATTATAC CAGCCTTTGA ACGCTTATTC TTACAACAGC GATTC                 | 1108 |

(2) INFORMATION FOR SEQ ID NO:378:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 344 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

Met Arg Leu Tyr Glu Ser Leu Leu Glu Met Cys Leu Asn Lys Ala Trp  
1 5 10 15  
Glu His Gln Thr Leu Ala Leu Glu Asn Pro Ser Val Ala Cys Met Val  
20 25 30  
Leu Asp Lys Asn His Glu Ile Leu Ser Leu Glu Thr His Lys Lys Ala  
35 40 45  
Lys Thr Pro His Ala Glu Val Leu Ala Ala Gln Ser Ala Leu Lys Ile  
50 55 60  
Leu Arg Pro Ser Leu Lys Asn Asp Leu Glu Lys Leu Glu Asp Pro Lys  
65 70 75 80  
Thr Leu Ser Asp Phe Leu Lys Thr His His Asp Asn Ala Phe Thr Asp  
85 90 95  
Cys Val Phe Leu Ile Thr Leu Glu Pro Cys Asn Ser Tyr Gly Lys Thr  
100 105 110  
Pro Ala Cys Ser Glu Leu Leu Glu Ile Leu Lys Pro Lys Arg Val Val  
115 120 125  
Ile Ala Thr Glu Glu Asn Glu Ala Lys Lys Gly Gly Leu Ala Arg Leu  
130 135 140  
Gln Lys Ala Arg Ile Glu Thr Ile Ile Cys His Asn Leu Glu Asn Lys  
145 150 155 160  
Ala Lys Asp Leu Leu Leu Pro Phe Arg Val Met Glu Gln Lys Gly Arg  
165 170 175  
Phe Asn Leu Phe Lys Leu Ala Leu Arg Met Asn Gly Asp Tyr His His  
180 185 190  
Gly Lys Ile Thr Gly Gln Lys Ser Val Ile Phe Thr His Asn Gln Arg  
195 200 205  
Ala Ile Cys Asp Thr Leu Ile Val Ser Gly Lys Thr Ile Arg Thr Asp  
210 215 220  
Asn Pro Leu Leu Asp Ala Arg Phe Cys Asp Ser Phe Tyr Gln Asn Lys  
225 230 235 240  
Asn Pro Asn Ile Ala Ile Leu Ser Lys Arg Ser Ile Asp Pro Asn Ser  
245 250 255  
Lys Val Phe Ser Ala Pro Asn Arg Leu Val Asn Thr Phe His Asp Pro  
260 265 270  
Lys Asp Leu Pro Leu Glu Lys Gly Phe Asn Phe Ile Glu Gly Gly Trp  
275 280 285  
Glu Leu Phe Glu Ser Leu Arg Asp Lys Ile Asp Ala Leu Leu Leu His  
290 295 300  
Ser His Ala Ser Met Ile Gly Glu Ala Phe Lys Ala Leu Ala Leu Lys  
305 310 315 320  
Thr Pro Phe Lys Gly Arg Leu Leu His Ala Gln Ile Leu Glu Asn Glu  
325 330 335  
Ala Leu Leu Trp Ile Glu Asn Ser  
340

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 14...799
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

|            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ACGATTTTAA | AAA | ATG | GCT | AGA | AGT | TTC | AAG | CAT | TCT | CAA | TAT | CCT | AAA | 49  |     |
|            | Met | Ala | Arg | Ser | Phe | Lys | His | Ser | Gln | Tyr | Pro | Lys |     |     |     |
|            | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     |
| ATT        | TTT | AAG | CCA | CTA | TAC | CCT | AAC | AAC | TTA | ACG | CTT | TCA | CTT | AAA | 97  |
| Ile        | Phe | Lys | Pro | Leu | Tyr | Pro | Asn | Asn | Leu | Thr | Leu | Ser | Leu | Lys |     |
|            | 15  |     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |
| CAA        | CAT | GTT | ATA | ATG | ATC | GCT | ATT | TTA | TTT | GAA | AGG | GTA | TTT | ATG | 145 |
| Gln        | His | Val | Ile | Met | Ile | Ala | Ile | Leu | Phe | Glu | Arg | Val | Phe | Met |     |
|            | 30  |     |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     |
| AGC        | GTT | TTA | AAT | TTC | CTA | ACC | AAT | ATC | AAT | GTG | ATT | TTC | ACC | CTT | 193 |
| Ser        | Val | Leu | Asn | Phe | Leu | Thr | Asn | Ile | Asn | Val | Ile | Phe | Thr | Leu |     |
| 45         |     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |
| GGC        | TAT | TTG | ATT | GGG | GGG | ATT | CCT | TTT | GGC | TAT | GCG | TTA | ATG | AAA | 241 |
| Gly        | Tyr | Leu | Ile | Gly | Gly | Ile | Pro | Phe | Gly | Tyr | Ala | Leu | Met | Lys |     |
|            |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |
| TTT        | TAC | GGC | ATG | GAT | ATT | ACT | AAA | ATC | GGA | TCG | GGG | GGC | ATT | GGC | 289 |
| Phe        | Tyr | Gly | Met | Asp | Ile | Thr | Lys | Ile | Gly | Ser | Gly | Gly | Ile | Gly |     |
|            |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |     |     |
| ACG        | AAT | GTC | TTG | CGT | GCT | TTA | CAA | AGT | AAG | GGC | GTG | AGT | AAC | GCT | 337 |
| Thr        | Asn | Val | Leu | Arg | Ala | Leu | Gln | Ser | Lys | Gly | Val | Ser | Asn | Ala |     |
|            |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |
| CAA        | ATG | GCC | CTA | TTA | GTT | TTA | ATC | TTG | GAT | CTC | TTC | AAA | GGC | ATG | 385 |
| Gln        | Met | Ala | Leu | Leu | Val | Leu | Ile | Leu | Asp | Leu | Phe | Lys | Gly | Met |     |
|            | 110 |     |     |     |     | 115 |     |     |     |     | 120 |     |     |     |     |
| GCA        | GTA | TTT | TTG | AGC | AAA | TTG | TTT | GGG | TTG | GAT | TAT | AGT | TTG | CAA | 433 |
| Ala        | Val | Phe | Leu | Ser | Lys | Leu | Phe | Gly | Leu | Asp | Tyr | Ser | Leu | Gln |     |
| 125        |     |     |     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |
| ATG        | GTC | GCT | ATC | GCT | AGC | ATT | TTA | GGG | CAT | TGC | TAT | TCG | CCT | TTT | 481 |
| Met        | Val | Ala | Ile | Ala | Ser | Ile | Leu | Gly | His | Cys | Tyr | Ser | Pro | Phe |     |
|            |     |     |     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |
| AAT        | TTC | AAT | GGA | GGT | AAG | GGC | GTT | TCT | ACG | ATC | ATG | GGC | TCT | GTG | 529 |
| Asn        | Phe | Asn | Gly | Lys | Gly | Val | Ser | Thr | Ile | Met | Gly | Ser | Val | Val |     |
|            |     | 160 |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |
| TTG        | CTC | ATC | CCT | ATT | GAA | AGT | CTC | ATC | GGC | TTA | ACG | GTG | TGG | TTT | 577 |
| Leu        | Leu | Ile | Pro | Ile | Glu | Ser | Leu | Ile | Gly | Leu | Thr | Val | Trp | Phe |     |
|            |     | 175 |     |     |     |     | 180 |     |     |     |     | 185 |     |     |     |
| GTG        | GGT | AAG | GTG | CTT | AAA | ATC | TCT | TCA | CTC | GCT | AGC | ATT | CTA | GGG | 625 |
|            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| Val Gly Lys Val Leu Lys Ile Ser Ser Leu Ala Ser Ile Leu Gly Val   |     |
| 190 195 200                                                       |     |
| GGC ACA GCG ACT GTT CTT ATC TTT TTT GTG CCT TAT ATG CAT ATC CCA   | 673 |
| Gly Thr Ala Thr Val Leu Ile Phe Phe Val Pro Tyr Met His Ile Pro   |     |
| 205 210 215 220                                                   |     |
| GAC AGC GTC AAT ATC CTT AAA GAA GTC GGC ACG CAA ACG CCG ATG GTG   | 721 |
| Asp Ser Val Asn Ile Leu Lys Glu Val Gly Thr Gln Thr Pro Met Val   |     |
| 225 230 235                                                       |     |
| CTT ATT TTT ATT TTC ACC CTT ATC AAG CAT GCG GGT AAT ATT TTT AAT   | 769 |
| Leu Ile Phe Ile Phe Thr Leu Ile Lys His Ala Gly Asn Ile Phe Asn   |     |
| 240 245 250                                                       |     |
| TTA TTG GCC GGC AAG GAA AAG AAA GTC TTA TGAAAACTAA ACAAGGCGTT CAT | 822 |
| Leu Leu Ala Gly Lys Glu Lys Lys Val Leu                           |     |
| 255 260                                                           |     |
| A                                                                 | 823 |

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ala Arg Ser Phe Lys His Ser Gln Tyr Pro Lys Ile Phe Lys Pro |  |
| 1 5 10 15                                                       |  |
| Leu Tyr Pro Asn Asn Leu Thr Leu Ser Leu Lys Lys Gln His Val Ile |  |
| 20 25 30                                                        |  |
| Met Ile Ala Ile Leu Phe Glu Arg Val Phe Met Glu Ser Val Leu Asn |  |
| 35 40 45                                                        |  |
| Phe Leu Thr Asn Ile Asn Val Ile Phe Thr Leu Leu Gly Tyr Leu Ile |  |
| 50 55 60                                                        |  |
| Gly Gly Ile Pro Phe Gly Tyr Ala Leu Met Lys Ile Phe Tyr Gly Met |  |
| 65 70 75 80                                                     |  |
| Asp Ile Thr Lys Ile Gly Ser Gly Gly Ile Gly Ala Thr Asn Val Leu |  |
| 85 90 95                                                        |  |
| Arg Ala Leu Gln Ser Lys Gly Val Ser Asn Ala Lys Gln Met Ala Leu |  |
| 100 105 110                                                     |  |
| Leu Val Leu Ile Leu Asp Leu Phe Lys Gly Met Phe Ala Val Phe Leu |  |
| 115 120 125                                                     |  |
| Ser Lys Leu Phe Gly Leu Asp Tyr Ser Leu Gln Trp Met Val Ala Ile |  |
| 130 135 140                                                     |  |
| Ala Ser Ile Leu Gly His Cys Tyr Ser Pro Phe Leu Asn Phe Asn Gly |  |
| 145 150 155 160                                                 |  |
| Gly Lys Gly Val Ser Thr Ile Met Gly Ser Val Val Leu Leu Ile Pro |  |
| 165 170 175                                                     |  |
| Ile Glu Ser Leu Ile Gly Leu Thr Val Trp Phe Phe Val Gly Lys Val |  |
| 180 185 190                                                     |  |
| Leu Lys Ile Ser Ser Leu Ala Ser Ile Leu Gly Val Gly Thr Ala Thr |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Ile | Phe | Phe | Val | Pro | Tyr | Met | His | Ile | Pro | Asp | Ser | Val | Asn |
| 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Leu | Lys | Glu | Val | Gly | Thr | Gln | Thr | Pro | Met | Val | Leu | Ile | Phe | Ile |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Phe | Thr | Leu | Ile | Lys | His | Ala | Gly | Asn | Ile | Phe | Asn | Leu | Leu | Ala | Gly |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Lys | Glu | Lys | Lys | Val | Leu |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 260 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...381
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

|                                                                   |            |            |                                 |    |
|-------------------------------------------------------------------|------------|------------|---------------------------------|----|
| TTTATTGGCC                                                        | GGCAAGGAAA | AGAAAGTCTT | ATG AAA ACT AAA CAA GGC GTT CAT | 54 |
|                                                                   |            |            | Met Lys Thr Lys Gln Gly Val His |    |
|                                                                   |            |            | 1 5                             |    |
| ATC CAT AAC TTG GTG TTT GAG GCG ATT TTG GGG ATT TTA GAA TTT GAA   | 102        |            |                                 |    |
| Ile His Asn Leu Val Phe Glu Ala Ile Leu Gly Ile Leu Glu Phe Glu   |            |            |                                 |    |
| 10 15 20                                                          |            |            |                                 |    |
| CGC TTA AAA CCC CAA AAA ATA AGC GTG AAT TTG GAT CTT TTC TAC ACG   | 150        |            |                                 |    |
| Arg Leu Lys Pro Gln Lys Ile Ser Val Asn Leu Asp Leu Phe Tyr Thr   |            |            |                                 |    |
| 25 30 35 40                                                       |            |            |                                 |    |
| CAA TTA CCC AAT AAG GTT TAT TTA GAC TAC ATG GAA ATT CAA GAG CTT   | 198        |            |                                 |    |
| Gln Leu Pro Asn Lys Val Tyr Leu Asp Tyr Met Glu Ile Gln Glu Leu   |            |            |                                 |    |
| 45 50 55                                                          |            |            |                                 |    |
| ATT CAA AAG ATG ATG CAA GAA AAC CAA TAC CTT CTC ATT GAA GAC GCC   | 246        |            |                                 |    |
| Ile Gln Lys Met Met Gln Glu Asn Gln Tyr Leu Leu Ile Glu Asp Ala   |            |            |                                 |    |
| 60 65 70                                                          |            |            |                                 |    |
| CTG AAA GAT TTG AGC CAT GCT TTA AAA ACG CGC TAC AAG GAG ATC ACT   | 294        |            |                                 |    |
| Leu Lys Asp Leu Ser His Ala Leu Lys Thr Arg Tyr Lys Glu Ile Thr   |            |            |                                 |    |
| 75 80 85                                                          |            |            |                                 |    |
| GAA CTT TAT TTA AAA ATC AGC AAG TTA GAG ATT TCT CCC AAT TCT CAA   | 342        |            |                                 |    |
| Glu Leu Tyr Leu Lys Ile Ser Lys Leu Glu Ile Ser Pro Asn Ser Gln   |            |            |                                 |    |
| 90 95 100                                                         |            |            |                                 |    |
| GTG GGA GCG AGC GTG AAA ATC CGC TAT GAA AGC AAT CTT TAGCCTCTTT TT | 393        |            |                                 |    |
| Val Gly Ala Ser Val Lys Ile Arg Tyr Glu Ser Asn Leu               |            |            |                                 |    |

105

110

115

CCTTCTTATT G

404

## (2) INFORMATION FOR SEQ ID NO:382:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

```

Met Lys Thr Lys Gln Gly Val His Ile His Asn Leu Val Phe Glu Ala
 1 5 10 15
Ile Leu Gly Ile Leu Glu Phe Glu Arg Leu Lys Pro Gln Lys Ile Ser
 20 25 30
Val Asn Leu Asp Leu Phe Tyr Thr Gln Leu Pro Asn Lys Val Tyr Leu
 35 40 45
Asp Tyr Met Glu Ile Gln Glu Leu Ile Gln Lys Met Met Gln Glu Asn
 50 55 60
Gln Tyr Leu Leu Ile Glu Asp Ala Leu Lys Asp Leu Ser His Ala Leu
 65 70 75 80
Lys Thr Arg Tyr Lys Glu Ile Thr Glu Leu Tyr Leu Lys Ile Ser Lys
 85 90 95
Leu Glu Ile Ser Pro Asn Ser Gln Val Gly Ala Ser Val Lys Ile Arg
 100 105 110
Tyr Glu Ser Asn Leu
 115

```

## (2) INFORMATION FOR SEQ ID NO:383:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...1209
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

```

TAAATAACG CTTATTTTAA ACTCTCAAAA AAGGAATCAA ACGCACTCAT C ATG GCT 57
 Met Ala
 1

AAA GAA ACG CTT GAA ATA ACC CCG GAT CTT TTG AAA AAC CCT TAT CAA 105
Lys Glu Thr Leu Glu Ile Thr Pro Asp Leu Leu Lys Asn Pro Tyr Gln
 5 10 15

```



|              |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
|--------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|
| AAA<br>Lys   | ATC<br>Ile | ATC<br>Ile | AAT<br>Asn | GCG<br>Ala | AGC<br>Ser | GCG<br>Ala | AGC<br>Ser | GTT<br>Val | TTT<br>Phe | GAT<br>Asp | GAA<br>Glu | AAG<br>Lys | CAT<br>His | GGG<br>Gly | CGA<br>Arg | 153 |
| 202530       |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| TCG<br>Ser   | TTT<br>Phe | TTT<br>Phe | AGC<br>Ser | ACG<br>Thr | CAA<br>Gln | TTT<br>Phe | TAT<br>Tyr | GAA<br>Glu | AAA<br>Lys | ATT<br>Ile | GAA<br>Glu | CCT<br>Pro | TAT<br>Tyr | TTA<br>Leu | AAA<br>Lys | 201 |
| 354045       |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| GAA<br>Glu   | GTT<br>Val | TTA<br>Leu | ACC<br>Thr | CAT<br>His | CCC<br>Pro | ATT<br>Ile | GAT<br>Asp | TTA<br>Leu | GAA<br>Glu | TGC<br>Cys | GAT<br>Asp | CTA<br>Leu | AAC<br>Asn | ACC<br>Thr | GCT<br>Ala | 249 |
| 6065         |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| AAA<br>Lys   | AAA<br>Lys | AAG<br>Lys | AAC<br>Asn | CGC<br>Arg | TTA<br>Leu | ACC<br>Thr | CCT<br>Pro | TTA<br>Leu | AAA<br>Lys | CAG<br>Gln | CTT<br>Leu | TTT<br>Phe | AAA<br>Lys | GCG<br>Ala | TGT<br>Cys | 297 |
| 707580       |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| TTT<br>Phe   | AAC<br>Asn | ACC<br>Thr | GAA<br>Glu | GAA<br>Glu | ATT<br>Ile | TTG<br>Leu | ATT<br>Ile | GTG<br>Val | AAT<br>Asn | AAT<br>Asn | AAC<br>Asn | ACC<br>Thr | AGC<br>Ser | GCG<br>Ala | ATT<br>Ile | 345 |
| 859095       |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| TTC<br>Phe   | CTC<br>Leu | ATC<br>Ile | GCT<br>Ala | AAC<br>Asn | GCT<br>Ala | TTA<br>Leu | GCG<br>Ala | CAA<br>Gln | GAA<br>Glu | AAA<br>Lys | GAA<br>Glu | ATC<br>Ile | ATT<br>Ile | GTT<br>Val | TCT<br>Ser | 393 |
| 100105110    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| TAT<br>Tyr   | GGC<br>Gly | GAA<br>Glu | TTA<br>Leu | GTG<br>Val | GGG<br>Gly | GGG<br>Gly | GAT<br>Asp | TTT<br>Phe | AAC<br>Asn | CTT<br>Leu | AAA<br>Lys | GAT<br>Asp | ATT<br>Ile | TTA<br>Leu | TTA<br>Leu | 441 |
| 115120125130 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| AAT<br>Asn   | AGT<br>Ser | GGG<br>Gly | GCT<br>Ala | AGG<br>Arg | CTG<br>Leu | CAT<br>His | TTA<br>Leu | GTG<br>Val | GGG<br>Gly | AAT<br>Asn | ATT<br>Ile | AAT<br>Asn | CGC<br>Arg | GCT<br>Ala | TAT<br>Tyr | 489 |
| 135140145    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| TTA<br>Leu   | AGG<br>Arg | GAT<br>Asp | TAC<br>Tyr | CGC<br>Arg | TTA<br>Leu | GCC<br>Ala | TTG<br>Leu | AAT<br>Asn | GAA<br>Glu | AAC<br>Asn | AGC<br>Ser | AAA<br>Lys | ATA<br>Ile | CTC<br>Leu | TTT<br>Phe | 537 |
| 150155160    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| AAA<br>Lys   | ACC<br>Thr | CAC<br>His | AAC<br>Asn | CCC<br>Pro | CAT<br>His | TTT<br>Phe | AAA<br>Lys | AAA<br>Lys | GAC<br>Asp | ACG<br>Thr | CCC<br>Pro | TTT<br>Phe | AAA<br>Lys | GAT<br>Asp | TTA<br>Leu | 585 |
| 165170175    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| CAA<br>Gln   | ACT<br>Thr | CTT<br>Leu | GCT<br>Ala | AAA<br>Lys | GAG<br>Glu | CAT<br>His | GAT<br>Asp | CTC<br>Leu | ATT<br>Ile | GAT<br>Asp | TAT<br>Tyr | TAC<br>Tyr | AAT<br>Asn | TTA<br>Leu | GGG<br>Gly | 633 |
| 180185190    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| GAT<br>Asp   | GTG<br>Val | GAT<br>Asp | TTG<br>Leu | TCA<br>Ser | AAC<br>Asn | AGA<br>Arg | GTG<br>Val | GCT<br>Ala | TTG<br>Leu | GAA<br>Glu | GAA<br>Glu | ATT<br>Ile | TTA<br>Leu | GCC<br>Ala | CTA<br>Leu | 681 |
| 195200205210 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| AAA<br>Lys   | CCA<br>Pro | TCG<br>Ser | CTT<br>Leu | TTA<br>Leu | AGC<br>Ser | TTT<br>Phe | AGC<br>Ser | GCG<br>Ala | GAT<br>Asp | AAA<br>Lys | TTC<br>Phe | TTT<br>Phe | AAC<br>Asn | AGT<br>Ser | GCG<br>Ala | 729 |
| 215220225    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| CAA<br>Gln   | GCG<br>Ala | GGC<br>Gly | ATT<br>Ile | ATT<br>Ile | ATG<br>Met | GGG<br>Gly | CAA<br>Gln | AAA<br>Lys | GAA<br>Glu | CGG<br>Arg | GTT<br>Val | GAA<br>Glu | GCG<br>Ala | TTA<br>Leu | AAA<br>Lys | 777 |
| 230235240    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| AAC<br>Asn   | CAC<br>His | CCC<br>Pro | CTT<br>Leu | TAT<br>Tyr | AGA<br>Arg | GTT<br>Val | TTA<br>Leu | AGG<br>Arg | GTG<br>Val | GGT<br>Gly | AAA<br>Lys | ATC<br>Ile | ACG<br>Thr | CTC<br>Leu | ACC<br>Thr | 825 |

|                     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |   |      |  |  |  |
|---------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---|------|--|--|--|
| 245                 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |     |     |     |   |      |  |  |  |
| TTG                 | CTT | TTT | TGC | AGC | CTA | AAA | GCA | TGG | ATA | AAT | CAT | CAA | GAA | GAC | ATT |   | 873  |  |  |  |
| Leu                 | Leu | Phe | Cys | Ser | Leu | Lys | Ala | Trp | Ile | Asn | His | Gln | Glu | Asp | Ile |   |      |  |  |  |
| 260                 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |     |     |   |      |  |  |  |
| ACA                 | ATC | CAT | GCG | TTA | TTG | AAC | CAA | ACT | AAA | GAC | GCA | TTA | TTG | CAA | AAA |   | 921  |  |  |  |
| Thr                 | Ile | His | Ala | Leu | Leu | Asn | Gln | Thr | Lys | Asp | Ala | Leu | Leu | Gln | Lys |   |      |  |  |  |
| 275                 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     | 290 |   |      |  |  |  |
| GCC                 | CTC | AAA | CTC | TAC | GCT | CTT | TTA | AAG | CCT | TTA | GAA | TTG | AAT | GTG | AGC |   | 969  |  |  |  |
| Ala                 | Leu | Lys | Leu | Tyr | Ala | Leu | Leu | Lys | Pro | Leu | Glu | Leu | Asn | Val | Ser |   |      |  |  |  |
| 295                 |     |     |     |     | 300 |     |     |     |     | 305 |     |     |     |     |     |   |      |  |  |  |
| ATA                 | GCC | TCT | AGC | TTT | TCT | AAA | ATA | GGG | AAT | TTG | TTT | GGT | AGG | GAA | TTA |   | 1017 |  |  |  |
| Ile                 | Ala | Ser | Ser | Phe | Ser | Lys | Ile | Gly | Asn | Leu | Phe | Gly | Arg | Glu | Leu |   |      |  |  |  |
| 310                 |     |     |     |     | 315 |     |     |     |     | 320 |     |     |     |     |     |   |      |  |  |  |
| GAA                 | TCC | TTT | TGC | GTG | AAA | ATC | CAG | CCC | AAA | AAC | ACC | CGT | GCT | TTA | AAT |   | 1065 |  |  |  |
| Glu                 | Ser | Phe | Cys | Val | Lys | Ile | Gln | Pro | Lys | Asn | Thr | Arg | Ala | Leu | Asn |   |      |  |  |  |
| 325                 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |     |     |     |   |      |  |  |  |
| AGT                 | GAG | AAA | CTT | TAT | TTA | AAG | CTT | TTC | CAA | AAA | GGC | GTT | ATC | GCA | AGG |   | 1113 |  |  |  |
| Ser                 | Glu | Lys | Leu | Tyr | Leu | Lys | Leu | Phe | Gln | Lys | Gly | Val | Ile | Ala | Arg |   |      |  |  |  |
| 340                 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |     |     |   |      |  |  |  |
| ATT                 | TCA | TGC | GAA | TTC | GTG | TGC | TTT | GAA | GTC | TTT | AGC | TTG | AAT | GAA | AAA |   | 1161 |  |  |  |
| Ile                 | Ser | Cys | Glu | Phe | Val | Cys | Phe | Glu | Val | Phe | Ser | Leu | Asn | Glu | Lys |   |      |  |  |  |
| 355                 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |     | 370 |   |      |  |  |  |
| GAT                 | TTT | GAA | AAA | ATC | GCT | CTG | GTT | TTA | GAA | GAA | ATT | CTT | AAT | AAA | GCT | T | 1210 |  |  |  |
| Asp                 | Phe | Glu | Lys | Ile | Ala | Leu | Val | Leu | Glu | Glu | Ile | Leu | Asn | Lys | Ala |   |      |  |  |  |
| 375                 |     |     |     |     | 380 |     |     |     |     | 385 |     |     |     |     |     |   |      |  |  |  |
| AAAAATTTCGC TATAATA |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |   | 1227 |  |  |  |

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 386 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

|           |           |           |           |           |     |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Met<br>1  | Ala       | Lys       | Glu       | Thr<br>5  | Leu | Glu       | Ile       | Thr       | Pro<br>10 | Asp       | Leu       | Leu       | Lys       | Asn<br>15 | Pro       |
| Tyr       | Gln       | Lys       | Ile<br>20 | Ile       | Asn | Ala       | Ser       | Ala<br>25 | Ser       | Val       | Phe       | Asp       | Glu<br>30 | Lys       | His       |
| Gly       | Arg       | Ser<br>35 | Phe       | Phe       | Ser | Thr       | Gln<br>40 | Phe       | Tyr       | Glu       | Lys       | Ile<br>45 | Glu       | Pro       | Tyr       |
| Leu       | Lys<br>50 | Glu       | Val       | Leu       | Thr | His<br>55 | Pro       | Ile       | Asp       | Leu       | Glu<br>60 | Cys       | Asp       | Leu       | Asn       |
| Thr<br>65 | Ala       | Lys       | Lys       | Lys<br>70 | Asn | Arg       | Leu       | Thr       | Pro       | Leu<br>75 | Lys       | Gln       | Leu       | Phe       | Lys<br>80 |



|     |         |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AGG | AACTTAA | GA  | ATG | GAA | AAA | ATC | AGC | GAT | CTT | ATA | GAA | TGC | ATT | GCG | TAT | 51  |
|     | Met     | Glu | Lys | Ile |     |     | Ser | Asp | Leu | Ile | Glu | Cys | Ile | Ala | Tyr |     |
|     | 1       |     |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     |
| GAA | AAA     | AAT | TTG | CCT | AAA | GAG | ATG | ATT | TCA | AAA | GTG | ATT | CAA | GGC | TGT | 99  |
| Glu | Lys     | Asn | Leu | Pro | Lys | Glu | Met | Ile | Ser | Lys | Val | Ile | Gln | Gly | Cys |     |
|     | 15      |     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |
| TTG | TTA     | AAA | ATG | GCG | CAA | AAT | GAG | TTA | GAC | CCC | CTA | GCA | CGC | TAC | TTG | 147 |
| Leu | Leu     | Lys | Met | Ala | Gln | Asn | Glu | Leu | Asp | Pro | Leu | Ala | Arg | Tyr | Leu |     |
| 30  |         |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |
| GTG | GTT     | GAA | GAA | AAC | AAG | CAG | CTC | CAG | CTT | ATC | CAG | TTG | GTA | GAA | GTT | 195 |
| Val | Val     | Glu | Glu | Asn | Lys | Gln | Leu | Gln | Leu | Ile | Gln | Leu | Val | Glu | Val |     |
|     |         |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| TTA | GAA     | GAT | GGT | GAT | GAA | AGA | TTG | GTT | AAC | GAC | CCT | TCT | AAA | TAC | ATC | 243 |
| Leu | Glu     | Asp | Gly | Asp | Glu | Arg | Leu | Val | Asn | Asp | Pro | Ser | Lys | Tyr | Ile |     |
|     |         |     | 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |
| AGC | CTG     | TCT | AAA | GCC | AAA | GAA | ATG | GAT | CCA | AGC | GTT | AAG | ATT | AAA | GAC | 291 |
| Ser | Leu     | Ser | Lys | Ala | Lys | Glu | Met | Asp | Pro | Ser | Val | Lys | Ile | Lys | Asp |     |
|     | 80      |     |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |
| GAA | TTG     | TCC | TAT | AGC | TTG | AGT | TTG | GAG | AGC | ATG | AAA | CAA | GGA | GCG | ATC | 339 |
| Glu | Leu     | Ser | Tyr | Ser | Leu | Ser | Leu | Glu | Ser | Met | Lys | Gln | Gly | Ala | Ile |     |
|     | 95      |     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |
| AAC | CGC     | CTT | TTT | AAA | GAT | TTG | CAA | TAC | CAG | TTA | GAA | AAA | GCG | TTA | GAA | 387 |
| Asn | Arg     | Leu | Phe | Lys | Asp | Leu | Gln | Tyr | Gln | Leu | Glu | Lys | Ala | Leu | Glu |     |
| 110 |         |     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |
| GAC | AGC     | CAC | TTT | GAA | GCG | TTT | CAA | AAG | CGT | CTT | AAC | AGC | GTT | TTA | ATG | 435 |
| Asp | Ser     | His | Phe | Glu | Ala | Phe | Gln | Lys | Arg | Leu | Asn | Ser | Val | Leu | Met |     |
|     |         |     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |
| GGG | CAA     | GTG | ATT | TTA | GTG | GAT | CAC | AAC | CAA | AAC | ACC | TTT | ATT | GAG | ATT | 483 |
| Gly | Gln     | Val | Ile | Leu | Val | Asp | His | Asn | Gln | Asn | Thr | Phe | Ile | Glu | Ile |     |
|     |         |     | 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |
| GAG | CAG     | CAA | TTT | CAG | GGC | GTT | CTT | TCC | ATG | CGC | CAT | CGC | ATC | AAG | GGC | 531 |
| Glu | Gln     | Gln | Phe | Gln | Gly | Val | Leu | Ser | Met | Arg | His | Arg | Ile | Lys | Gly |     |
|     |         | 160 |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |
| GAG | AGT     | TTT | AAA | GTG | GGC | GAT | AGC | ATT | AAA | GCG | GTT | TTA | ACG | CAA | GTC | 579 |
| Glu | Ser     | Phe | Lys | Val | Gly | Asp | Ser | Ile | Lys | Ala | Val | Leu | Thr | Gln | Val |     |
|     | 175     |     |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     |
| AAA | CGC     | ACG | AAA | AAA | GGC | TTA | TTA | TTA | GAG | CTG | AGC | CGC | ACC | ACC | CCT | 627 |
| Lys | Arg     | Thr | Lys | Lys | Gly | Leu | Leu | Leu | Glu | Leu | Ser | Arg | Thr | Thr | Pro |     |
| 190 |         |     |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |
| AAA | ATG     | CTT | GAA | GCT | TTG | TTG |     |     |     |     |     |     |     |     |     |     |

|                                      |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |  |  |  |
|--------------------------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|--|--|--|
|                                      | 225        |            |            |            |            |            | 230        |            |            |            |            |            | 235        |            |            |      |  |  |  |
| AAA<br>Lys                           | GTG<br>Val | AGC<br>Ser | TTT<br>Phe | TTT<br>Phe | TCC<br>Ser | CAT<br>His | AAC<br>Asn | GCT<br>Ala | AGG<br>Arg | ATT<br>Ile | GAC<br>Asp | CCC<br>Pro | ATA<br>Ile | GGC<br>Gly | GCG<br>Ala | 771  |  |  |  |
|                                      |            | 240        |            |            |            |            | 245        |            |            |            |            | 250        |            |            |            |      |  |  |  |
| GCT<br>Ala                           | GTG<br>Val | GGG<br>Gly | GTT<br>Val | AAG<br>Lys | GGC<br>Gly | GTG<br>Val | CGC<br>Arg | ATT<br>Ile | AAT<br>Asn | GCG<br>Ala | ATC<br>Ile | AGT<br>Ser | AAC<br>Asn | GAA<br>Glu | TTG<br>Leu | 819  |  |  |  |
|                                      |            | 255        |            |            |            | 260        |            |            |            |            | 265        |            |            |            |            |      |  |  |  |
| AAT<br>Asn                           | AAA<br>Lys | GAA<br>Glu | AAC<br>Asn | ATT<br>Ile | GAT<br>Asp | TGC<br>Cys | ATA<br>Ile | GAA<br>Glu | TAT<br>Tyr | TCT<br>Ser | AAT<br>Asn | GTG<br>Val | CCT<br>Pro | GAA<br>Glu | ATT<br>Ile | 867  |  |  |  |
|                                      |            |            |            |            | 275        |            |            |            |            | 280        |            |            |            |            | 285        |      |  |  |  |
| TAC<br>Tyr                           | ATC<br>Ile | ACT<br>Thr | CTC<br>Leu | GCA<br>Ala | CTC<br>Leu | GCT<br>Ala | CCA<br>Pro | GCC<br>Ala | AAA<br>Lys | ATT<br>Ile | TTA<br>Leu | AGC<br>Ser | GTT<br>Val | GAA<br>Glu | ATC<br>Ile | 915  |  |  |  |
|                                      |            |            |            | 290        |            |            |            |            | 295        |            |            |            |            | 300        |            |      |  |  |  |
| AAA<br>Lys                           | AAA<br>Lys | ATC<br>Ile | CCT<br>Pro | ATA<br>Ile | GAA<br>Glu | GAA<br>Glu | TTG<br>Leu | AAT<br>Asn | GCT<br>Ala | GAA<br>Glu | GAA<br>Glu | AAA<br>Lys | GAA<br>Glu | TCC<br>Ser | ATT<br>Ile | 963  |  |  |  |
|                                      |            |            | 305        |            |            |            |            | 310        |            |            |            |            | 315        |            |            |      |  |  |  |
| CAA<br>Gln                           | GAG<br>Glu | CGT<br>Arg | TTT<br>Phe | ATC<br>Ile | GTC<br>Val | AAT<br>Asn | AAC<br>Asn | CAT<br>His | TTG<br>Leu | CAA<br>Gln | AAG<br>Lys | GCT<br>Ala | AAA<br>Lys | GTG<br>Val | CGT<br>Arg | 1011 |  |  |  |
|                                      |            | 320        |            |            |            |            | 325        |            |            |            |            | 330        |            |            |            |      |  |  |  |
| TTA<br>Leu                           | TTG<br>Leu | GAC<br>Asp | ATT<br>Ile | GAA<br>Glu | AAA<br>Lys | TCT<br>Ser | AAG<br>Lys | GCT<br>Ala | ATC<br>Ile | GGT<br>Gly | AAG<br>Lys | GGC<br>Gly | GGG<br>Gly | GTG<br>Val | AAT<br>Asn | 1059 |  |  |  |
|                                      |            | 335        |            |            |            | 340        |            |            |            |            | 345        |            |            |            |            |      |  |  |  |
| GTG<br>Val                           | TGC<br>Cys | TTA<br>Leu | GCG<br>Ala | TCC<br>Ser | ATG<br>Met | CTT<br>Leu | ACA<br>Thr | GGC<br>Gly | TAT<br>Tyr | CAC<br>His | ATA<br>Ile | GAG<br>Glu | TTT<br>Phe | GAA<br>Glu | ACC<br>Thr | 1107 |  |  |  |
|                                      |            |            |            |            | 355        |            |            |            |            | 360        |            |            |            |            | 365        |      |  |  |  |
| ATT<br>Ile                           | CCT<br>Pro | AGC<br>Ser | GTG<br>Val | AAA<br>Lys | GAA<br>Glu | AAC<br>Asn | GCA<br>Ala | GAA<br>Glu | AAT<br>Asn | GAA<br>Glu | AGC<br>Ser | GAA<br>Glu | AAA<br>Lys | GAA<br>Glu | ACG<br>Thr | 1155 |  |  |  |
|                                      |            |            |            | 370        |            |            |            |            | 375        |            |            |            |            | 380        |            |      |  |  |  |
| CCA<br>Pro                           | AAA<br>Lys | GTG<br>Val | GGG<br>Gly | GTA<br>Val | GAA<br>Glu | GCT<br>Ala | TTA<br>Leu | GAG<br>Glu | TCT<br>Ser | TTG<br>Leu | TTT<br>Phe | AAG<br>Lys | AAT<br>Asn | TAAGGGTAT  |            | 1206 |  |  |  |
|                                      |            |            | 385        |            |            |            |            | 390        |            |            |            |            | 395        |            |            |      |  |  |  |
| CTAAAAATTCA ATCTCTAAAA AAGCTTTTAA CT |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            | 1238 |  |  |  |

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 395 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

-511-



(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 21...3857
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

|                                                                 |                                         |     |
|-----------------------------------------------------------------|-----------------------------------------|-----|
| AAGCGATGTA AGGAATTAAC                                           | ATG GAT TAT AAA AAA TTA GAT TTA CCC AAC | 50  |
|                                                                 | Met Asp Tyr Lys Lys Leu Asp Leu Pro Asn |     |
|                                                                 | 1 5 10                                  |     |
| ACA AAC TAC CCA AAT CAA GAG CAA CTG AAA GCT TTT GAA ACC GCT TTT |                                         | 98  |
| Thr Asn Tyr Pro Asn Gln Glu Gln Leu Lys Ala Phe Glu Thr Ala Phe |                                         |     |
|                                                                 | 15 20 25                                |     |
| GAC GCC TTT TTA GAA ACC AAC CAA CAA GAA AAT GAA AAT CAC CAA AAC |                                         | 146 |
| Asp Ala Phe Leu Glu Thr Asn Gln Gln Glu Asn Glu Asn His Gln Asn |                                         |     |
|                                                                 | 30 35 40                                |     |
| GAC GCT TTT AAT GAT TTA TTG AAA GGC GTT TTT AAA TAC AAG GTT AAG |                                         | 194 |
| Asp Ala Phe Asn Asp Leu Leu Lys Gly Val Phe Lys Tyr Lys Val Lys |                                         |     |
|                                                                 | 45 50 55                                |     |
| CCC ACC AAA AAA ATA GAC AGC ACT ATT CTT AAT GAA AAT AAC GAA GTG |                                         | 242 |
| Pro Thr Lys Lys Ile Asp Ser Thr Ile Leu Asn Glu Asn Asn Glu Val |                                         |     |
|                                                                 | 60 65 70                                |     |
| GAG GTG ATC ATT GAA TTT AAA GCC CTT AAA AAC CCC AAC GAA TTT ATT |                                         | 290 |
| Glu Val Ile Ile Glu Phe Lys Ala Leu Lys Asn Pro Asn Glu Phe Ile |                                         |     |
|                                                                 | 75 80 85 90                             |     |
| AAA AAG GGC GAT TTG AAT GTT AAA GCC TTT CAT GAA AGC CTT TTG TCT |                                         | 338 |
| Lys Lys Gly Asp Leu Asn Val Lys Ala Phe His Glu Ser Leu Leu Ser |                                         |     |
|                                                                 | 95 100 105                              |     |
| TAT CTC ACA GAA AGA AAA GAG GGT AAT AAC AAC CTT AAG CAT CTT ATC |                                         | 386 |
| Tyr Leu Thr Glu Arg Lys Glu Gly Asn Asn Asn Leu Lys His Leu Ile |                                         |     |
|                                                                 | 110 115 120                             |     |
| TTA GCC ACT ATT AAA GAG CTT TAT ATC ATT GAT GCA AAC GAA TTT GAG |                                         | 434 |
| Leu Ala Thr Ile Lys Glu Leu Tyr Ile Ile Asp Ala Asn Glu Phe Glu |                                         |     |
|                                                                 | 125 130 135                             |     |
| GTT TTT AAT AAA GAT AAA GAA ATT GAA AAC GCC TTT AAA AAT TGC CAC |                                         | 482 |
| Val Phe Asn Lys Asp Lys Glu Ile Glu Asn Ala Phe Lys Asn Cys His |                                         |     |
|                                                                 | 140 145 150                             |     |
| GAT AGA AAG GGT AAC GAT ACA CGC ACA AAA GCG TTT TAT GAT GCT TGC |                                         | 530 |
| Asp Arg Lys Gly Asn Asp Thr Arg Thr Lys Ala Phe Tyr Asp Ala Cys |                                         |     |
|                                                                 | 155 160 165 170                         |     |
| CAA AAG CGC CTT AAT GAG TTT GAT CGT TCT TTG AAA TAC CAC TAT ATC |                                         | 578 |
| Gln Lys Arg Leu Asn Glu Phe Asp Arg Ser Leu Lys Tyr His Tyr Ile |                                         |     |
|                                                                 | 175 180 185                             |     |
| CCC CTC AAA AAA GAA AAT TTA GCC CTA ATC TAT CAA GCC CTA AGC CCT |                                         | 626 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Pro | Leu | Lys | Lys | Glu | Asn | Leu | Ala | Leu | Ile | Tyr | Gln | Ala | Leu | Ser | Pro |      |  |
|     |     |     | 190 |     |     |     |     | 195 |     |     |     |     | 200 |     |     |      |  |
| AAT | TTT | TTG | CTC | AAA | ATT | CCA | AAA | TAT | TCT | GAC | GCT | AAC | ACG | CTT | AAC | 674  |  |
| Asn | Phe | Leu | Leu | Lys | Ile | Pro | Lys | Tyr | Ser | Asp | Ala | Asn | Thr | Leu | Asn |      |  |
|     |     | 205 |     |     |     |     | 210 |     |     |     |     | 215 |     |     |     |      |  |
| AAA | GAT | TTT | TAT | GAA | GAA | TTG | CTT | TAC | ATT | TTA | GGG | TTA | GAA | GAG | CAA | 722  |  |
| Lys | Asp | Phe | Tyr | Glu | Glu | Leu | Leu | Tyr | Ile | Leu | Gly | Leu | Glu | Glu | Gln |      |  |
|     | 220 |     |     |     |     | 225 |     |     |     |     | 230 |     |     |     |     |      |  |
| AAT | GAC | AAA | GGG | AAA | ATT | TTA | ATC | AAG | CCC | AGC | CGC | ACC | CAA | AAT | TCC | 770  |  |
| Asn | Asp | Lys | Gly | Lys | Ile | Leu | Ile | Lys | Pro | Ser | Arg | Thr | Gln | Asn | Ser |      |  |
| 235 |     |     |     |     | 240 |     |     |     | 245 |     |     |     |     |     | 250 |      |  |
| CTA | AGC | GAT | GCT | TTA | AAA | AAG | GAA | TAC | AAA | AAT | TTA | GAC | GAT | GAA | GAA | 818  |  |
| Leu | Ser | Asp | Ala | Leu | Lys | Lys | Glu | Tyr | Lys | Asn | Leu | Asp | Asp | Glu | Glu |      |  |
|     |     |     |     | 255 |     |     |     |     | 260 |     |     |     |     | 265 |     |      |  |
| GTC | ATG | GCG | TTG | CTC | ATC | GCT | TGG | AAT | AAC | CGC | ATC | TTG | TTT | TTA | CGG | 866  |  |
| Val | Met | Ala | Leu | Leu | Ile | Ala | Trp | Asn | Asn | Arg | Ile | Leu | Phe | Leu | Arg |      |  |
|     |     |     | 270 |     |     |     |     | 275 |     |     |     |     | 280 |     |     |      |  |
| CTT | TTA | GAA | AGC | CTT | TTA | ATT | TCT | TTT | AAG | CAT | TTT | GAA | AAT | CCT | TTC | 914  |  |
| Leu | Leu | Glu | Ser | Leu | Leu | Ile | Ser | Phe | Lys | His | Phe | Glu | Asn | Pro | Phe |      |  |
|     |     | 285 |     |     |     |     | 290 |     |     |     |     | 295 |     |     |     |      |  |
| TTA | ACC | ACA | GAA | AAC | TTT | GAA | AAT | TTC | AAC | GAT | TTA | AAC | ACG | CTC | TTT | 962  |  |
| Leu | Thr | Thr | Glu | Asn | Phe | Glu | Asn | Phe | Asn | Asp | Leu | Asn | Thr | Leu | Phe |      |  |
|     | 300 |     |     |     |     | 305 |     |     |     |     | 310 |     |     |     |     |      |  |
| TTT | GAA | GTC | CTA | GCC | AAG | AAA | AAC | AGC | GAG | CGC | TTA | CCA | GAA | ATT | AAA | 1010 |  |
| Phe | Glu | Val | Leu | Ala | Lys | Lys | Asn | Ser | Glu | Arg | Leu | Pro | Glu | Ile | Lys |      |  |
| 315 |     |     |     |     | 320 |     |     |     | 325 |     |     |     |     |     | 330 |      |  |
| GAA | GAC | AAG | ATT | TTA | GAA | AAA | ATC | CCT | TAT | TTG | AAT | TCC | AGT | TTG | TTT | 1058 |  |
| Glu | Asp | Lys | Ile | Leu | Glu | Lys | Ile | Pro | Tyr | Leu | Asn | Ser | Ser | Leu | Phe |      |  |
|     |     |     |     | 335 |     |     |     | 340 |     |     |     |     |     | 345 |     |      |  |
| GAT | AAA | ACG | CCT | TTA | GAA | TTA | AAG | GGG | CAT | GAA | ATC | AAG | CTT | TTA | GAC | 1106 |  |
| Asp | Lys | Thr | Pro | Leu | Glu | Leu | Lys | Gly | His | Glu | Ile | Lys | Leu | Leu | Asp |      |  |
|     |     |     | 350 |     |     |     |     | 355 |     |     |     |     | 360 |     |     |      |  |
| AAT | AAA | AAG | CTA | GAA | ATC | TAT | AAA | AAT | TCC | GTT | CTC | AAA | AAA | CAT | AAA | 1154 |  |
| Asn | Lys | Lys | Leu | Glu | Ile | Tyr | Lys | Asn | Ser | Val | Leu | Lys | Lys | His | Lys |      |  |
|     |     | 365 |     |     |     |     | 370 |     |     |     |     | 375 |     |     |     |      |  |
| GAT | TAT | CAA | AAA | GAA | AAA | CCT | TTG | CCC | TTG | CTA | AAA | TAC | CTT | TTT | AAA | 1202 |  |
| Asp | Tyr | Gln | Lys | Glu | Lys | Pro | Leu | Pro | Leu | Leu | Lys | Tyr | Leu | Phe | Lys |      |  |
|     | 380 |     |     |     |     | 385 |     |     |     |     | 390 |     |     |     |     |      |  |
| TTT | TTG | CGT | CTT | TAT | AAA | TTC | ACC | ACC | ACC | CCT | AAA | GAC | ATT | AAA | GAT | 1250 |  |
| Phe | Leu | Arg | Leu | Tyr | Lys | Phe | Thr | Thr | Thr | Pro | Lys | Asp | Ile | Lys | Asp |      |  |
| 395 |     |     |     |     | 400 |     |     |     |     | 405 |     |     |     |     | 410 |      |  |
| AAT | ACC | GAT | ACC | AGC | GAA | AGC | CGT | TTG | ATT | AAC | CCT | AGC | GTT | TTA | GGG | 1298 |  |
| Asn | Thr | Asp | Thr | Ser | Glu | Ser | Arg | Leu | Ile | Asn | Pro | Ser | Val | Leu | Gly |      |  |
|     |     |     |     | 415 |     |     |     | 420 |     |     |     |     |     | 425 |     |      |  |



|                                                                 |      |
|-----------------------------------------------------------------|------|
| CTT GTT TTT GAA AAA CTC AAC GGC TAT AAA GAG GGG AGC TTT TAT ACC | 1346 |
| Leu Val Phe Glu Lys Leu Asn Gly Tyr Lys Glu Gly Ser Phe Tyr Thr |      |
| 430 435 440                                                     |      |
| CCA AGC TTT ATC ACA AGC TAC ATG TGC AAA GAG AGC ATC ACG CCC ATC | 1394 |
| Pro Ser Phe Ile Thr Ser Tyr Met Cys Lys Glu Ser Ile Thr Pro Ile |      |
| 445 450 455                                                     |      |
| GTG TTG GAT AAA TTC AAC GCC ATT TAT CAG TGG GAC TGC GAA AAT CTA | 1442 |
| Val Leu Asp Lys Phe Asn Ala Ile Tyr Gln Trp Asp Cys Glu Asn Leu |      |
| 460 465 470                                                     |      |
| AAA GCG TTG CGA GGA GAA ATA GAC AGA AAT TTT TCA AAT GAA AAA GCT | 1490 |
| Lys Ala Leu Arg Gly Glu Ile Asp Arg Asn Phe Ser Asn Glu Lys Ala |      |
| 475 480 485 490                                                 |      |
| AAA GAA TAC CTA AAC ACG CTT TTA ACC TTG CGT ATT TGC GAT CCG GCG | 1538 |
| Lys Glu Tyr Leu Asn Thr Leu Leu Thr Leu Arg Ile Cys Asp Pro Ala |      |
| 495 500 505                                                     |      |
| GTG GGG AGC GGG CAT TTC TTG GTT TCA GCG CTC AAT GAA ATG GTG CGG | 1586 |
| Val Gly Ser Gly His Phe Leu Val Ser Ala Leu Asn Glu Met Val Arg |      |
| 510 515 520                                                     |      |
| GTT GCT TAT GAG CTA GGA CTT ATT GCT TCC TTG TAT CGC TAC GAT CTT | 1634 |
| Val Ala Tyr Glu Leu Gly Leu Ile Ala Ser Leu Tyr Arg Tyr Asp Leu |      |
| 525 530 535                                                     |      |
| AAA TTA GAA AAC GAT GAA ATC ATC ATT CAC CAC ACG CCA ACG GGT GAA | 1682 |
| Lys Leu Glu Asn Asp Glu Ile Ile Ile His His Thr Pro Thr Gly Glu |      |
| 540 545 550                                                     |      |
| ATC TTT AAC TAC ATA AAA CCA GAT AGC GAA AAC GAC CCC CAC CAC CAC | 1730 |
| Ile Phe Asn Tyr Ile Lys Pro Asp Ser Glu Asn Asp Pro His His His |      |
| 555 560 565 570                                                 |      |
| ATC CAA AAA GAA CTT TTT AAT CTT AAA AAA TCC ATT ATT GAA AAC TGC | 1778 |
| Ile Gln Lys Glu Leu Phe Asn Leu Lys Lys Ser Ile Ile Glu Asn Cys |      |
| 575 580 585                                                     |      |
| CTT TTT GGC GTG GAT ATT AAC CCC AAT TCT TGC GAA ATC ACC AAG CTC | 1826 |
| Leu Phe Gly Val Asp Ile Asn Pro Asn Ser Cys Glu Ile Thr Lys Leu |      |
| 590 595 600                                                     |      |
| AGG CTA TGG ATA GAG CTT TTA AAA TAC AGC TAT TAT ATT TTT GAA AAG | 1874 |
| Arg Leu Trp Ile Glu Leu Leu Lys Tyr Ser Tyr Tyr Ile Phe Glu Lys |      |
| 605 610 615                                                     |      |
| GGC AAG AAC ACT AAC GCG CTT GAA ACC CTC CCC AAC ATT GAT ATT AAC | 1922 |
| Gly Lys Asn Thr Asn Ala Leu Glu Thr Leu Pro Asn Ile Asp Ile Asn |      |
| 620 625 630                                                     |      |
| ATT AAG TGC GCT AAT TCG CTC ATT TCT AGG TTT GCC CTC AAA GAT AAA | 1970 |
| Ile Lys Cys Ala Asn Ser Leu Ile Ser Arg Phe Ala Leu Lys Asp Lys |      |
| 635 640 645 650                                                 |      |
| GCC TTG TTA AAA AGC GAA AAA AAT AAA AAC CTA GAA TAC TCT ATC GCT | 2018 |
| Ala Leu Leu Lys Ser Glu Lys Asn Lys Asn Leu Glu Tyr Ser Ile Ala |      |













(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| TTTAAATCAT TTAAAAAAG GATAGAG ATG CAA AAT AAA GAA ATT GGT GAA GAA | 54  |
| Met Gln Asn Lys Glu Ile Gly Glu Glu                              |     |
| 1 5                                                              |     |
| AAA AGC GTT AAT GAA AAA AAT GTA GAG GTT TTT AAT CGT TAT TTT CCC  | 102 |
| Lys Ser Val Asn Glu Lys Asn Val Glu Val Phe Asn Arg Tyr Phe Pro  |     |
| 10 15 20 25                                                      |     |
| GGT TGC TTG AGT ATA GAA AAT GAT AAC AAG CTC ACG CTG GAT ACA GGA  | 150 |
| Gly Cys Leu Ser Ile Glu Asn Asp Asn Lys Leu Thr Leu Asp Thr Gly  |     |
| 30 35 40                                                         |     |
| AAA TTA AAA GCG TTA CTA GGG GAT TTT AGC GAG ATA AAA GAA GAG GGC  | 198 |
| Lys Leu Lys Ala Leu Leu Gly Asp Phe Ser Glu Ile Lys Glu Glu Gly  |     |
| 45 50 55                                                         |     |
| TAT GGG TTG GAT TTT GTG GGT AAG AAA ATC GCC TTA AAC CAA GCT TTT  | 246 |
| Tyr Gly Leu Asp Phe Val Gly Lys Lys Ile Ala Leu Asn Gln Ala Phe  |     |
| 60 65 70                                                         |     |
| AAG AAA AAT CAT AAG ATT TTA AAG CCC TTA AAC GAA TCC ACT AGC AAG  | 294 |
| Lys Lys Asn His Lys Ile Leu Lys Pro Leu Asn Glu Ser Thr Ser Lys  |     |
| 75 80 85                                                         |     |
| CAC GTT CTC ATC AAG GGC GAT AAT TTA GAC GCT CTC AAA ATC TTA AAA  | 342 |
| His Val Leu Ile Lys Gly Asp Asn Leu Asp Ala Leu Lys Ile Leu Lys  |     |
| 90 95 100 105                                                    |     |
| CAA AGC TAT AGT GAA AAA ATC AAA ATG ATT TAC ATT GAC CCG CCT TAC  | 390 |
| Gln Ser Tyr Ser Glu Lys Ile Lys Met Ile Tyr Ile Asp Pro Pro Tyr  |     |
| 110 115 120                                                      |     |
| AAC ACG AAA AAC GAG AAT TTT ATC TAT GGC GAT GAT TTC TCG CAA TCC  | 438 |
| Asn Thr Lys Asn Glu Asn Phe Ile Tyr Gly Asp Asp Phe Ser Gln Ser  |     |
| 125 130 135                                                      |     |
| AAT GAA GAG GTT TTA AAA ACA TTG GAT TAT TCT AAA GAA AAA TTG GAT  | 486 |
| Asn Glu Glu Val Leu Lys Thr Leu Asp Tyr Ser Lys Glu Lys Leu Asp  |     |
| 140 145 150                                                      |     |
| TAC ATC AAG AAC CTT TTT GGG TCA AAA TGC CAT AGC GGG TGG CTT AGT  | 534 |
| Tyr Ile Lys Asn Leu Phe Gly Ser Lys Cys His Ser Gly Trp Leu Ser  |     |
| 155 160 165                                                      |     |
| TTC ATG TAT CCC AGA TTG TTG CTC GCT AAA GAT TTG CTC AAA CAA GAC  | 582 |
| Phe Met Tyr Pro Arg Leu Leu Leu Ala Lys Asp Leu Leu Lys Gln Asp  |     |
| 170 175 180 185                                                  |     |
| GGC GTG ATT TTC ATT TCT ATT GAC GAT AAC GAA TGC GCT CAA CTC AAA  | 630 |
| Gly Val Ile Phe Ile Ser Ile Asp Asp Asn Glu Cys Ala Gln Leu Lys  |     |
| 190 195 200                                                      |     |
| CTT TTA TGC GAT GAA ATT TTT GGG GAG GGG AAT TTT GTG GCG TGT TTA  | 678 |
| Leu Leu Cys Asp Glu Ile Phe Gly Glu Gly Asn Phe Val Ala Cys Leu  |     |
| 205 210 215                                                      |     |





TCATTCTCGT C

1415

## (2) INFORMATION FOR SEQ ID NO:390:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

```

Met Gln Asn Lys Glu Ile Gly Glu Glu Lys Ser Val Asn Glu Lys Asn
 1 5 10 15
Val Glu Val Phe Asn Arg Tyr Phe Pro Gly Cys Leu Ser Ile Glu Asn
 20 25 30
Asp Asn Lys Leu Thr Leu Asp Thr Gly Lys Leu Lys Ala Leu Leu Gly
 35 40 45
Asp Phe Ser Glu Ile Lys Glu Gly Tyr Gly Leu Asp Phe Val Gly
 50 55 60
Lys Lys Ile Ala Leu Asn Gln Ala Phe Lys Lys Asn His Lys Ile Leu
 65 70 75 80
Lys Pro Leu Asn Glu Ser Thr Ser Lys His Val Leu Ile Lys Gly Asp
 85 90 95
Asn Leu Asp Ala Leu Lys Ile Leu Lys Gln Ser Tyr Ser Glu Lys Ile
 100 105 110
Lys Met Ile Tyr Ile Asp Pro Pro Tyr Asn Thr Lys Asn Glu Asn Phe
 115 120 125
Ile Tyr Gly Asp Asp Phe Ser Gln Ser Asn Glu Glu Val Leu Lys Thr
 130 135 140
Leu Asp Tyr Ser Lys Glu Lys Leu Asp Tyr Ile Lys Asn Leu Phe Gly
 145 150 155 160
Ser Lys Cys His Ser Gly Trp Leu Ser Phe Met Tyr Pro Arg Leu Leu
 165 170 175
Leu Ala Lys Asp Leu Leu Lys Gln Asp Gly Val Ile Phe Ile Ser Ile
 180 185 190
Asp Asp Asn Glu Cys Ala Gln Leu Lys Leu Leu Cys Asp Glu Ile Phe
 195 200 205
Gly Glu Gly Asn Phe Val Ala Cys Leu Lys Trp Lys Lys Lys Lys Gln
 210 215 220
Pro Ser Phe Leu Ser Lys Val Ala Val Ile Leu Glu Tyr Ile Leu Val
 225 230 235 240
Tyr Ala Lys Asp Phe Ser Leu Ile Asp Lys Leu Gly Leu Asp Asn Val
 245 250 255
Ser Asp Ser Asp Lys Pro Ile Ile Asn Thr Ser Asn Asn Leu Ser Lys
 260 265 270
Arg Tyr Phe Lys Lys Gly Ile Arg Val Lys Ser Asp Leu Asn Phe Ile
 275 280 285
Lys Ser Gly Lys Tyr Gln Asn Lys Thr Met Thr Ile Glu Phe Met Asn
 290 295 300
Asp Ile Phe Ile Glu Asn Gly Arg Thr Lys Asn Asp Phe Glu Cys Ile
 305 310 315 320
Gly Lys Phe Arg Thr Gly Gln Glu Asn Ile Asn Glu Phe Ile Glu Lys
 325 330 335

```

Asp Leu Ile Phe Ile Thr Lys Asn Leu Gly Ile Arg Arg Asp Leu Leu  
 340 345 350  
 Glu Glu Glu Gln Ser Asn Lys Lys Thr Ile Thr Asp Leu Leu Thr Glu  
 355 360 365  
 Trp Gly Gln Asn Gln Asp Ala Thr Asn Glu Leu Asn Ile Leu Phe Asn  
 370 375 380  
 Asn Ser Ser Asp Glu Ser Ile Phe Ser Asn Pro Lys Pro Thr Lys Leu  
 385 390 395 400  
 Ile Asn Arg Leu Ile Glu Leu Ser Thr Asn Glu Gly Asp Ile Ile Leu  
 405 410 415  
 Asp Phe Phe Ala Gly Ser Gly Thr Thr Ala His Ala Val Leu Glu Ser  
 420 425 430  
 Asn Lys Ser Asp Tyr Gln Lys Leu Ser Glu Gly Gly Gly Gly Tyr Leu  
 435 440 445  
 Met Val  
 450

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 55...1344
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GAAACGAATA AAAATTTTCC TTCACAACAT TTAAATGCAT TAAAATACAT TGAA ATG | 57  |
| Met                                                             |     |
| 1                                                               |     |
| CTT TTT TAT ATG AAA AAT TTA GAG CGC AAA AAA TTG CAA TTT GGC GCT | 105 |
| Leu Phe Tyr Met Lys Asn Leu Glu Arg Lys Lys Leu Gln Phe Gly Ala |     |
| 5 10 15                                                         |     |
| AAA ATC GCA TGC CCC AAT AAT AAC GAG CGC TTG AAA GCG TTT ATC GCT | 153 |
| Lys Ile Ala Cys Pro Asn Asn Asn Glu Arg Leu Lys Ala Phe Ile Ala |     |
| 20 25 30                                                        |     |
| TCT TTA CCC TTT AAA CTC ACA CGC GAT CAA CAA AAC GCC ATT AAA GAA | 201 |
| Ser Leu Pro Phe Lys Leu Thr Arg Asp Gln Gln Asn Ala Ile Lys Glu |     |
| 35 40 45                                                        |     |
| ATC CAA AAC GAT CTC ACT AGC TCC ATA GCG TGC AAG CGT TTG ATT ATA | 249 |
| Ile Gln Asn Asp Leu Thr Ser Ser Ile Ala Cys Lys Arg Leu Ile Ile |     |
| 50 55 60 65                                                     |     |
| GGC GAT GTG GGG TGC GGG AAA ACG ATG GTG ATT TTA GCG AGC ATG GTA | 297 |
| Gly Asp Val Gly Cys Gly Lys Thr Met Val Ile Leu Ala Ser Met Val |     |
| 70 75 80                                                        |     |



|                                                                   |     |     |      |
|-------------------------------------------------------------------|-----|-----|------|
| 310                                                               | 315 | 320 |      |
| GTG ATT TTA GCG CCC GAA AGG TTA GGC TTA GCG ACT TTA CAC CAG TTA   |     |     | 1065 |
| Val Ile Leu Ala Pro Glu Arg Leu Gly Leu Ala Thr Leu His Gln Leu   |     |     |      |
| 325                                                               | 330 | 335 |      |
| AGG GGG CGC GTT TCT CGT AAC GGC TTG AAA GGC TAT TGT TTT TTA TGC   |     |     | 1113 |
| Arg Gly Arg Val Ser Arg Asn Gly Leu Lys Gly Tyr Cys Phe Leu Cys   |     |     |      |
| 340                                                               | 345 | 350 |      |
| ACG ATC CAA GAA GAA AAC GAA CGA TTA GAA AAG TTT GCT GAT GAA TTG   |     |     | 1161 |
| Thr Ile Gln Glu Glu Asn Glu Arg Leu Glu Lys Phe Ala Asp Glu Leu   |     |     |      |
| 355                                                               | 360 | 365 |      |
| GAC GGC TTT AAA ATC GCT GAA TTG GAT TTA GAA TAC AGA AAA AGC GGG   |     |     | 1209 |
| Asp Gly Phe Lys Ile Ala Glu Leu Asp Leu Glu Tyr Arg Lys Ser Gly   |     |     |      |
| 370                                                               | 375 | 380 | 385  |
| GAT TTA CTC CAG GGA GGG GAG CAG AGC GGG AAT AGT TTT GAA TAC ATT   |     |     | 1257 |
| Asp Leu Leu Gln Gly Gly Glu Gln Ser Gly Asn Ser Phe Glu Tyr Ile   |     |     |      |
| 390                                                               | 395 | 400 |      |
| GAC TTA GCC AAA GAT GAA AAC ATT ATC GCT GAA GTG AAA CGG GAT TTT   |     |     | 1305 |
| Asp Leu Ala Lys Asp Glu Asn Ile Ile Ala Glu Val Lys Arg Asp Phe   |     |     |      |
| 405                                                               | 410 | 415 |      |
| TTA AAG GCC GCT AGC GTT TCA CGG GGA ACA TTT GAA AAT TGAAAATTAA GG |     |     | 1356 |
| Leu Lys Ala Ala Ser Val Ser Arg Gly Thr Phe Glu Asn               |     |     |      |
| 420                                                               | 425 | 430 |      |
| CAGAATTGGG TAATTTAAAT CATTTAAAAA AAG                              |     |     | 1389 |

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Phe | Tyr | Met | Lys | Asn | Leu | Glu | Arg | Lys | Lys | Leu | Gln | Phe | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ala | Lys | Ile | Ala | Cys | Pro | Asn | Asn | Asn | Glu | Arg | Leu | Lys | Ala | Phe | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ser | Leu | Pro | Phe | Lys | Leu | Thr | Arg | Asp | Gln | Gln | Asn | Ala | Ile | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Ile | Gln | Asn | Asp | Leu | Thr | Ser | Ser | Ile | Ala | Cys | Lys | Arg | Leu | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ile | Gly | Asp | Val | Gly | Cys | Gly | Lys | Thr | Met | Val | Ile | Leu | Ala | Ser | Met |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Val | Leu | Thr | Tyr | Pro | Asn | Lys | Thr | Leu | Leu | Met | Ala | Pro | Thr | Ser | Ile |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Ala | Lys | Gln | Leu | Tyr | Asn | Glu | Ala | Leu | Lys | Phe | Leu | Pro | Pro | Tyr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |



|                                                                          |         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |     |
|--------------------------------------------------------------------------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|-----|
| TGT TAT TCCT TTT TCA TTCA CCA CTT TAT TC ACG CTATA AT AACGCC ATG GAT ACC |         |         |         |         |         |         |         |         |         |         |         |         |         |         |         | 55  |
| Met Asp Thr                                                              |         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |     |
| 1                                                                        |         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |     |
| AAC Asn                                                                  | AAC Asn | AAT Asn | ATT Ile | GAA Glu | AAA Lys | GAA Glu | ATC Ile | TTG Leu | GCG Ala | CTA Leu | GTC Val | AAA Lys | CAA Gln | AAT Asn | CCT Pro | 103 |
| 51015                                                                    |         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |     |
| AAA Lys                                                                  | GTT Val | AGT Ser | CTC Leu | ATA Ile | GAG Glu | TAT Tyr | GAA Glu | AAT Asn | TAC Tyr | TTT Phe | AGC Ser | CAA Gln | CTC Leu | AAA Lys | TAC Tyr | 151 |
| 20253035                                                                 |         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |     |
| AAC Asn                                                                  | CCT Pro | AAC Asn | GCA Ala | AGC Ser | AAG Lys | AGC Ser | GAT Asp | ATT Ile | GCC Ala | TTT Phe | TTT Phe | TAT Tyr | GCC Ala | CCC Pro | AAC Asn | 199 |
| 404550                                                                   |         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |     |
| CAA Gln                                                                  | GTC Val | TTA Leu | TGC Cys | ACC Thr | ACG Thr | ATT Ile | ACA Thr | GCT Ala | AAA Lys | TAC Tyr | GGC Gly | GCG Ala | TTG Leu | CTT Leu | AAA Lys | 247 |
| 556065                                                                   |         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |     |
| GAA Glu                                                                  | ATT Ile | TTA Leu | AGC Ser | CAG Gln | AAT Asn | AAA Lys | GTC Val | GGC Gly | ATG Met | CAT His | TTA Leu | GCC Ala | CAC His | AGC Ser | GTG Val | 295 |
| 707580                                                                   |         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |     |
| GAT Asp                                                                  | GTG Val | CGT Arg | ATT Ile | GAA Glu | GTA Val | GCG Ala | CCT Pro | AAA Lys | ATC Ile | CAA Gln | ATT Ile | AAC Asn | GCC Ala | CAA Gln | TCT Ser | 343 |
| 859095                                                                   |         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |     |
| AAT Asn                                                                  | ATC Ile | AAT Asn | TAC Tyr | AAA Lys | GCC Ala | ATA Ile | AAA Lys | ACG Thr | AGC Ser | GTC Val | AAA Lys | GAC Asp | TCT Ser | TAC Tyr | ACT Thr | 391 |
| 100105110115                                                             |         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |     |
| TTT Phe                                                                  | GAA Glu | AAT Asn | TTT Phe | GTC Val | GTA Val | GGC Gly | TCA Ser | TGC Cys | AAT Asn | AAC Asn | ACC Thr | GTT Val | TAT Tyr | GAA Glu | ATC Ile | 439 |
| 120125130                                                                |         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |     |
| GCT Ala                                                                  | AAA Lys | AAA Lys | GTC Val | GCC Ala | CAA Gln | AGC Ser | GAT Asp | ACC Thr | CCC Pro | CCT Pro | TAT Tyr | AAC Asn | CCG Pro | GTG Val | CTT Leu | 487 |
| 135140145                                                                |         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |     |
| TTT Phe                                                                  | TAT Tyr | GGC Gly | GGC Gly | ACA Thr | GGG Gly | TTA Leu | GGC Gly | AAA Lys | ACG Thr | CAC His | ATT Ile | TTA Leu | AAC Asn | GCT Ala | ATC Ile | 535 |
| 150155160                                                                |         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |     |
| GGC Gly                                                                  | AAC Asn | CAT His | GCC Ala | CTA Leu | GAA Glu | AAG Lys | CAT His | AAA Lys | AAA Lys | GTC Val | GTG Val | TTA Leu | GTC Val | ACT Thr | TCA Ser | 583 |
| 165170175                                                                |         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |     |
| GAA Glu                                                                  | GAC Asp | TTT Phe | TTG Leu | ACA Thr | GAC Asp | TTT Phe | TTA Leu | AAG Lys | CAT His | TTA Leu | GAC Asp | AAC Asn | AAA Lys | ACC Thr | ATG Met | 631 |
| 180185190195                                                             |         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |     |
| GAT Asp                                                                  | TCT Ser | TTT Phe | AAA Lys | GCA Ala | AAA Lys | TAC Tyr | CGC Arg | CAT His | TGC Cys | GAC Asp | TTT Phe | TTC Phe | TTG Leu | TTA Leu | GAT Asp | 679 |
| 200205210                                                                |         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |     |
| GAC Asp                                                                  | GCT Ala | CAA Gln | TTT Phe | TTG Leu | CAA Gln | GGA Gly | AAA Lys | CCC Pro | AAG Lys | CTA Leu | GAA Glu | GAA Glu | GAA Glu | TTT Phe | TTC Phe | 727 |











|                                                                   |      |
|-------------------------------------------------------------------|------|
| TTC TTT AGC GCT GAT TTA GGG CTA ATG GCC TTT GGC GTG GCG CAA GTG   | 1011 |
| Phe Phe Ser Ala Asp Leu Gly Leu Met Ala Phe Gly Val Ala Gln Val   |      |
| 315 320 325                                                       |      |
| ATT TTC TTT TTG CTA CCC TTC TTG GAT CGA AGT CCA GTG GTC GCT CCT   | 1059 |
| Ile Phe Phe Leu Leu Pro Phe Leu Asp Arg Ser Pro Val Val Ala Pro   |      |
| 330 335 340 345                                                   |      |
| GCG CAC AAA CGG CCG GCG TTT ATG GTG TGG TTT TGG CTT GTA ATC ATT   | 1107 |
| Ala His Lys Arg Pro Ala Phe Met Val Trp Phe Trp Leu Val Ile Ile   |      |
| 350 355 360                                                       |      |
| GAT ATG ATT GTT TTA ACG ATC TAT GGT AAA TTG CCT CCG CTT GGG ATT   | 1155 |
| Asp Met Ile Val Leu Thr Ile Tyr Gly Lys Leu Pro Pro Leu Gly Ile   |      |
| 365 370 375                                                       |      |
| GGT AAA TAC ATT GGC TTA GCG GGT TCA ATC ACT TTT TTG GCC CTT TTC   | 1203 |
| Gly Lys Tyr Ile Gly Leu Ala Gly Ser Ile Thr Phe Leu Ala Leu Phe   |      |
| 380 385 390                                                       |      |
| TTT GTG GTA TTG CCC ATC ATC ACT ATC GCT GAG AGC AAG AAA CAA GGG   | 1251 |
| Phe Val Val Leu Pro Ile Ile Thr Ile Ala Glu Ser Lys Lys Gln Gly   |      |
| 395 400 405                                                       |      |
| GGT GTT AGA TGAAAGAGTT TAAGATTCTA ATCATCCTCA TTGTGGTGGT AGGCGTGAT | 1309 |
| Gly Val Arg                                                       |      |
| 410                                                               |      |
| TTATTATGGG GTTGA                                                  | 1324 |

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ala Glu Ile Lys Lys Ala Lys Asn Leu Gly Glu Trp Leu Asp Met |  |
| 1 5 10 15                                                       |  |
| Arg Leu Gly Thr Asn Lys Leu Val Lys Val Leu Met Thr Glu Tyr Trp |  |
| 20 25 30                                                        |  |
| Ile Pro Lys Asn Ile Asn Phe Leu Trp Ala Met Gly Val Ile Leu Leu |  |
| 35 40 45                                                        |  |
| Thr Leu Phe Gly Val Leu Val Val Ser Gly Ile Phe Leu Leu Met Tyr |  |
| 50 55 60                                                        |  |
| Tyr Lys Pro Asp Ala Lys Met Ala Phe Asp Ser Val Asn Phe Thr Ile |  |
| 65 70 75 80                                                     |  |
| Met Gln Glu Val Ala Tyr Gly Trp Leu Trp Arg His Met His Ala Thr |  |
| 85 90 95                                                        |  |
| Ala Ala Ser Met Ile Phe Val Ile Ile Tyr Ile His Met Phe Val Gly |  |
| 100 105 110                                                     |  |
| Ile Tyr Tyr Gly Ser Tyr Lys Lys Gly Arg Glu Met Ile Trp Ile Ser |  |
| 115 120 125                                                     |  |





Ile Ser Ser Gln Glu Leu Val Val Glu Arg Lys Gly Ile Leu Ile Gly  
100 105 110  
Glu Thr Arg Pro Lys Asn Ile Gln Gly Gly Ala Leu Leu Ile Asn Glu  
115 120 125  
Gln Glu Lys Lys Ile Glu Asn Lys  
130 135

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...348
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

|                                                                 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----------------------------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| TAAGGAGTTT                                                      | CT  | ATG | GAT | TGG | GGT | CGG | GTC | GTT | CAT | GTG | CTG | TTC | AGC | CTT | 51 |
|                                                                 | Met | Asp | Trp | Gly | Arg | Val | Val | His | Val | Leu | Phe | Ser | Leu |     |    |
|                                                                 | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |    |
| ATT TCT TTA ACC ACC ATT GCA GGG TTT TTG TAT GAG CCT AAT ACG GTG | 99  |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Ile Ser Leu Thr Thr Ile Ala Gly Phe Leu Tyr Glu Pro Asn Thr Val |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| 15 20 25                                                        |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| GTG TTG TTT GTA GCG TTA GCT TTA AAC CTT ATT TCT GTT ACG CTT AAA | 147 |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Val Leu Phe Val Ala Leu Ala Leu Asn Leu Ile Ser Val Thr Leu Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| 30 35 40 45                                                     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| ATT GGG GTG ATC AAG CGT TTC GCT TCA GAG CTA TTG GCC AGC TCT TTA | 195 |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Ile Gly Val Ile Lys Arg Phe Ala Ser Glu Leu Leu Ala Ser Ser Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| 50 55 60                                                        |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| GCC ACC GTA TTG CAT CTC ATA CCG GCA TTT GTG TTT TTA CAG ATT TTA | 243 |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Ala Thr Val Leu His Leu Ile Pro Ala Phe Val Phe Leu Gln Ile Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| 65 70 75                                                        |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| AAT AAT TTG GTT ACC GCT TAC ATG CTC ATG ATC GGG GCG TTG ATT AGC | 291 |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Asn Asn Leu Val Thr Ala Tyr Met Leu Met Ile Gly Ala Leu Ile Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| 80 85 90                                                        |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| AAC GCT TTC AGT CTC ATC TTT TTG TTG ATT GAA AGC GTT GTA ACG AGC | 339 |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Asn Ala Phe Ser Leu Ile Phe Leu Leu Ile Glu Ser Val Val Thr Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| 95 100 105                                                      |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| GAA ACG GAT TAAGGGGTAG TGATGGATTT TATCAATATA GAAAAAAAT GGC      | 391 |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Glu Thr Asp                                                     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| 110                                                             |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |





|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ile | Asp | Phe | Ala | Gly | Gly | Ser | Leu | Val | Gln | Val | Arg | Tyr | Thr | Gln |     |
|     |     |     | 45  |     |     |     | 50  |     |     |     |     |     |     |     |     |     |
| AAC | GCC | CCC | ATT | AAA | GAA | GTG | CGC | GAT | CTG | TTT | GAA | AAA | GAA | GCT | CGC | 243 |
| Asn | Ala | Pro | Ile | Lys | Glu | Val | Arg | Asp | Leu | Phe | Glu | Lys | Glu | Ala | Arg |     |
|     |     |     | 60  |     |     |     | 65  |     |     |     |     |     |     |     |     |     |
| TTC | AAA | GGC | GTG | CAA | GTG | AGC | GAA | TTT | GGC | TCT | AAA | GAA | GAA | ATT | TTA | 291 |
| Phe | Lys | Gly | Val | Gln | Val | Ser | Glu | Phe | Gly | Ser | Lys | Glu | Glu | Ile | Leu |     |
|     |     |     | 75  |     |     |     | 80  |     |     |     |     |     |     |     |     |     |
| ATC | AAA | TTC | CCT | TTT | GTA | GAA | ACG | GCT | GAA | AAT | GAA | GAT | CTG | AAC | GCT | 339 |
| Ile | Lys | Phe | Pro | Phe | Val | Glu | Thr | Ala | Glu | Asn | Glu | Asp | Leu | Asn | Ala |     |
|     |     |     | 90  |     |     |     | 95  |     |     |     |     |     |     |     |     |     |
| ATC | GTG | GCC | AAC | ATT | CTA | AAA | CCC | AGC | GGC | GAT | TTT | GAA | ATC | CGT | AAA | 387 |
| Ile | Val | Ala | Asn | Ile | Leu | Lys | Pro | Ser | Gly | Asp | Phe | Glu | Ile | Arg | Lys |     |
|     |     |     | 110 |     |     |     | 115 |     |     |     |     |     |     |     |     |     |
| TTT | GAC | ACC | GTG | GGC | CCT | AGA | GTG | GGG | AGC | GAA | TTG | AAA | GAG | AAA | GGC | 435 |
| Phe | Asp | Thr | Val | Gly | Pro | Arg | Val | Gly | Ser | Glu | Leu | Lys | Glu | Lys | Gly |     |
|     |     |     | 125 |     |     |     | 130 |     |     |     |     |     |     |     |     |     |
| ATT | TTG | TCG | CTG | ATT | TTA | GCA | TTA | ATA | GCG | ATC | ATG | GTT | TAT | GTG | AGT | 483 |
| Ile | Leu | Ser | Leu | Ile | Leu | Ala | Leu | Ile | Ala | Ile | Met | Val | Tyr | Val | Ser |     |
|     |     |     | 140 |     |     |     | 145 |     |     |     |     |     |     |     |     |     |
| TTC | CGC | TAT | GAA | TGG | CGT | TTT | GCT | TTA | GCG | AGC | GTC | ATT | GCG | CTT | GTG | 531 |
| Phe | Arg | Tyr | Glu | Trp | Arg | Phe | Ala | Leu | Ala | Ser | Val | Ile | Ala | Leu | Val |     |
|     |     |     | 155 |     |     |     | 160 |     |     |     |     |     |     |     |     |     |
| CAT | GAT | GTG | ATT | TTA | GTG | GCA | AGC | TCG | GTG | ATT | GTT | TTT | AAG | ATT | GAT | 579 |
| His | Asp | Val | Ile | Leu | Val | Ala | Ser | Ser | Val | Ile | Val | Phe | Lys | Ile | Asp |     |
|     |     |     | 170 |     |     |     | 175 |     |     |     |     |     |     |     |     |     |
| ATG | AAT | TTG | GAA | GTG | ATT | GCG | GCC | TTG | CTC | ACC | TTG | ATT | GGG | TAT | TCC | 627 |
| Met | Asn | Leu | Glu | Val | Ile | Ala | Ala | Leu | Leu | Thr | Leu | Ile | Gly | Tyr | Ser |     |
|     |     |     | 190 |     |     |     | 195 |     |     |     |     |     |     |     |     |     |
| ATT | AAT | GAT | ACG | ATC | ATT | ATT | TTT | GAC | AGG | ATC | AGA | GAA | GAG | ATG | CTY | 675 |
| Ile | Asn | Asp | Thr | Ile | Ile | Ile | Phe | Asp | Arg | Ile | Arg | Glu | Glu | Met | Xaa |     |
|     |     |     | 205 |     |     |     | 210 |     |     |     |     |     |     |     |     |     |
| TCT | CAA | AAA | ACC | AAA | AAC | GCC | ACT | CAA | GCC | ATT | GAT | GAA | GCC | ATT | TCT | 723 |
| Ser | Gln | Lys | Thr | Lys | Asn | Ala | Thr | Gln | Ala | Ile | Asp | Glu | Ala | Ile | Ser |     |
|     |     |     | 220 |     |     |     | 225 |     |     |     |     |     |     |     |     |     |
| AGC | ACG | CTC | ACG | CGC | ACG | CTT | TTA | ACT | TCT | TTA | ACC | GTG | TTT | TTT | GTG | 771 |
| Ser | Thr | Leu | Thr | Arg | Thr | Leu | Leu | Thr | Ser | Leu | Thr | Val | Phe | Phe | Val |     |
|     |     |     | 235 |     |     |     | 240 |     |     |     |     |     |     |     |     |     |
| GTG | TTG | ATT | TTG | TGC | GTG | TTT | GGG | AGT | AAG | ATC | ATC | ATT | GGC | TTT | TCA | 819 |
| Val | Leu | Ile | Leu | Cys | Val | Phe | Gly | Ser | Lys | Ile | Ile | Ile | Gly | Phe | Ser |     |
|     |     |     | 250 |     |     |     | 255 |     |     |     |     |     |     |     |     |     |
| TTG | CCC | ATG | TTA | ATA | GGC | ACG | ATT | GTA | GGG | ACT | TAT | AGC | TCT | ATT | TTC | 867 |
| Leu | Pro | Met | Leu | Ile | Gly | Thr | Ile | Val | Gly | Thr | Tyr | Ser | Ser | Ile | Phe |     |
|     |     |     | 270 |     |     |     | 275 |     |     |     |     |     |     |     |     |     |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ser | Lys | Ile | Ile | Ile | Gly | Phe | Ser | Leu | Pro | Met | Leu | Ile | Gly | Thr |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ile | Val | Gly | Thr | Tyr | Ser | Ser | Ile | Phe | Ile | Ala | Pro | Lys | Val | Ala | Leu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Leu | Gly | Phe | Asp | Met | Asp | Lys | Tyr | Tyr | Glu | Asn | Glu | Thr | Arg | Lys |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ile | Lys | Lys | Ala | Gln | Glu | Lys | Glu | Lys | Met | Arg | Arg | Leu | Tyr | Glu | Ser |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     | 320 |
| Gly | Gln | Val |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 56...634
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

|                                                                 |            |            |            |            |       |     |    |
|-----------------------------------------------------------------|------------|------------|------------|------------|-------|-----|----|
| TAGCTATTTTC                                                     | TTTAAAGCCG | CTCTTTTGTC | TAGCGCAAAT | AAATACAAAG | CCCCT | ATG | 58 |
|                                                                 |            |            |            |            | Met   |     |    |
|                                                                 |            |            |            |            | 1     |     |    |
| ATC CCA GAA ATC AAA GAT CCG AGT AAA ATC GCA ATT TTT GCC ACT TCC | 106        |            |            |            |       |     |    |
| Ile Pro Glu Ile Lys Asp Pro Ser Lys Ile Ala Ile Phe Ala Thr Ser |            |            |            |            |       |     |    |
|                                                                 | 5          |            | 10         |            | 15    |     |    |
| ATA GCG TCT TTA TGC TCG CTC GTG AAG GCC AGA TTA GAA ATA AAC ATA | 154        |            |            |            |       |     |    |
| Ile Ala Ser Leu Cys Ser Leu Val Lys Ala Arg Leu Glu Ile Asn Ile |            |            |            |            |       |     |    |
|                                                                 | 20         |            | 25         |            | 30    |     |    |
| GAC ATG GTA AAG CCA ATC CCT GCT AAA AGC CCA GCC CCT AAA ATA TGC | 202        |            |            |            |       |     |    |
| Asp Met Val Lys Pro Ile Pro Ala Lys Ser Pro Ala Pro Lys Ile Cys |            |            |            |            |       |     |    |
|                                                                 | 35         |            | 40         |            | 45    |     |    |
| CAC CAG CTG ATG CCT TTA GGG CGT GCG GTG ATT TTA AGC TTT TCG CTT | 250        |            |            |            |       |     |    |
| His Gln Leu Met Pro Leu Gly Arg Ala Val Ile Leu Ser Phe Ser Leu |            |            |            |            |       |     |    |
|                                                                 | 50         |            | 55         |            | 60    |     | 65 |
| ATA AAA GTG ATT AAG AAA ATC CCT AAA GGT TTG CCC AAG CAA AGC CCT | 298        |            |            |            |       |     |    |
| Ile Lys Val Ile Lys Lys Ile Pro Lys Gly Leu Pro Lys Gln Ser Pro |            |            |            |            |       |     |    |
|                                                                 | 70         |            | 75         |            | 80    |     |    |
| AAA ATA ACC CCT AAA AGC ACC TTA TCC ACT TCT AAA TTG ATG CTA GAA | 346        |            |            |            |       |     |    |
| Lys Ile Thr Pro Lys Ser Thr Leu Ser Thr Ser Lys Leu Met Leu Glu |            |            |            |            |       |     |    |
|                                                                 | 85         |            | 90         |            | 95    |     |    |
| TCA ACG CTC ACC CCA GCG TTT GCA AAC GCG AAT AAG GGC ATG ATG AAA | 394        |            |            |            |       |     |    |



|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
|     |     | 165 |     | 170 |     | 175 |
| Gly | Ile | Ile | Lys | Ala | Arg | Ile |
|     |     | 180 |     | 185 |     | 190 |
|     |     |     |     |     |     |     |
| Leu |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...1365
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

|            |          |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AAGACTGCTT | GAAAAATT | ATG | GGT | CTG | AAA | TTA | AAA | ATT | TTA | AGG | TTG | TCT | 51  |
|            |          | Met | Gly | Leu | Lys | Leu | Lys | Ile | Leu | Arg | Leu | Ser |     |
|            |          | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |
| ATG        | AAT      | CTC | AAA | AAA | ACA | GAA | AAC | GCG | CTC | AGT | TTG | ACG | 99  |
| Met        | Asn      | Leu | Lys | Lys | Thr | Glu | Asn | Ala | Leu | Ser | Leu | Thr |     |
|            |          | 15  |     |     |     |     |     | 20  |     |     |     | 25  |     |
| TTC        | ATT      | AAA | AGC | GAG | TCT | TTT | GGA | GGG | ATT | TTC | CTC | TTT | 147 |
| Phe        | Ile      | Lys | Ser | Glu | Ser | Phe | Gly | Gly | Ile | Phe | Leu | Phe |     |
|            |          | 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |
| GTT        | TTA      | GCG | ATG | GTG | GTG | GCT | AAT | TCG | TTT | TTA | AAA | GAA | 195 |
| Val        | Leu      | Ala | Met | Val | Val | Ala | Asn | Ser | Phe | Leu | Lys | Glu |     |
|            |          | 45  |     |     |     | 50  |     |     |     |     | 55  |     |     |
| GCA        | CTA      | TGG | CAC | ACC | CCT | TTT | GGG | TTT | CAA | ATA | GGG | GAT | 243 |
| Ala        | Leu      | Trp | His | Thr | Pro | Phe | Gly | Phe | Gln | Ile | Gly | Asp |     |
|            |          | 60  |     |     | 65  |     |     |     | 70  |     |     |     | 75  |
| GGC        | TTT      | AGT | TTG | CAC | AAC | TGG | ATT | GAT | GAT | GTC | TTA | ATG | 291 |
| Gly        | Phe      | Ser | Leu | His | Asn | Trp | Ile | Asp | Asp | Val | Leu | Met |     |
|            |          |     |     | 80  |     |     |     | 85  |     |     |     |     | 90  |
| TTT        | TTA      | ATG | ATA | GGC | TTA | GAA | ATC | AAA | CGA | GAA | TTG | TTG | 339 |
| Phe        | Leu      | Met | Ile | Gly | Leu | Glu | Ile | Lys | Arg | Glu | Leu | Leu |     |
|            |          |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |
| TTA        | TCC      | AGT | TTC | AAA | AAA | GCT | TCT | TTT | CCT | GTG | ATT | GCG | 387 |
| Leu        | Ser      | Ser | Phe | Lys | Lys | Ala | Ser | Phe | Pro | Val | Ile | Ala |     |
|            |          |     | 110 |     |     |     | 115 |     |     |     |     | 120 |     |
| GGC        | ATG      | ATA | GCC | CCA | GGA | TTG | ATT | TAT | TTT | TTT | CTT | AAC | 435 |
| Gly        | Met      | Ile | Ala | Pro | Gly | Leu | Ile | Tyr | Phe | Phe | Leu | Asn |     |
|            |          |     |     |     |     |     |     |     |     |     |     |     |     |

|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| 125               |                   |                   |                   | 130               |                   |                   |                   | 135               |                   |                   |                   |                   |                   |                   |                   |      |
| CCT<br>Pro<br>140 | TCC<br>Ser        | CAG<br>Gln        | CAT<br>His        | GGT<br>Gly        | TTT<br>Phe<br>145 | GGG<br>Gly        | ATC<br>Ile        | CCT<br>Pro        | ATG<br>Met        | GCG<br>Ala<br>150 | ACG<br>Thr        | GAT<br>Asp        | ATT<br>Ile        | GCG<br>Ala        | TTC<br>Phe<br>155 | 483  |
| GCT<br>Ala        | TTA<br>Leu        | GGC<br>Gly        | GTG<br>Val        | ATC<br>Ile<br>160 | ATG<br>Met        | CTT<br>Leu        | TTA<br>Leu        | GGC<br>Gly        | AAG<br>Lys<br>165 | AGG<br>Arg        | GTG<br>Val        | CCA<br>Pro        | ACC<br>Thr        | GCT<br>Ala<br>170 | TTA<br>Leu        | 531  |
| AAG<br>Lys        | GTT<br>Val        | TTT<br>Phe<br>175 | TTA<br>Leu        | ATC<br>Ile        | ACT<br>Thr        | CTA<br>Leu        | GCG<br>Ala<br>180 | GTG<br>Val        | GCT<br>Ala        | GAT<br>Asp        | GAC<br>Asp        | TTG<br>Leu        | GGG<br>Gly<br>185 | GCT<br>Ala        | ATT<br>Ile        | 579  |
| GTG<br>Val        | GTG<br>Val        | ATC<br>Ile<br>190 | GCG<br>Ala        | CTC<br>Leu        | TTT<br>Phe        | TAT<br>Tyr        | ACC<br>Thr<br>195 | ACG<br>Thr        | AAT<br>Asn        | TTA<br>Leu        | AAA<br>Lys<br>200 | TTC<br>Phe        | GCA<br>Ala        | TGG<br>Trp        | CTT<br>Leu        | 627  |
| TTA<br>Leu        | GGG<br>Gly<br>205 | GCT<br>Ala        | TTA<br>Leu        | GGG<br>Gly        | GTG<br>Val<br>210 | GTT<br>Val        | CTT<br>Leu        | GTT<br>Val        | TTA<br>Leu        | GCC<br>Ala<br>215 | GTA<br>Val<br>215 | TTA<br>Leu        | AAC<br>Asn        | CGC<br>Arg        | CTG<br>Leu        | 675  |
| AAT<br>Asn<br>220 | ATG<br>Met        | CGC<br>Arg        | TCG<br>Ser        | CTC<br>Leu        | ATC<br>Ile<br>225 | CCT<br>Pro        | TAC<br>Tyr        | TTG<br>Leu        | CTT<br>Leu        | TTA<br>Leu<br>230 | GGG<br>Gly        | GTG<br>Val        | TTG<br>Leu        | CTT<br>Leu        | TGG<br>Trp<br>235 | 723  |
| TTT<br>Phe        | TGC<br>Cys        | GTG<br>Val        | CAT<br>His<br>240 | CAA<br>Gln        | AGC<br>Ser        | GGT<br>Gly        | ATC<br>Ile        | CAT<br>His<br>245 | GCG<br>Ala        | ACG<br>Thr        | ATT<br>Ile        | GCT<br>Ala        | GCA<br>Ala        | GTG<br>Val<br>250 | ATT<br>Ile        | 771  |
| CTA<br>Leu        | GCT<br>Ala        | TTT<br>Phe<br>255 | ATG<br>Met        | ATA<br>Ile        | CCG<br>Pro        | GTG<br>Val        | AAG<br>Lys<br>260 | ATC<br>Ile        | CCT<br>Pro        | AAA<br>Lys        | GAT<br>Asp        | TCT<br>Ser        | AAA<br>Lys<br>265 | AAT<br>Asn        | GTA<br>Val        | 819  |
| GAG<br>Glu        | CTT<br>Leu        | TTG<br>Leu<br>270 | GAA<br>Glu        | CTA<br>Leu        | GGC<br>Gly        | AAA<br>Lys<br>275 | CGA<br>Arg        | TAC<br>Tyr        | GCA<br>Ala        | GAA<br>Glu        | ACG<br>Thr        | AGT<br>Ser<br>280 | TCA<br>Ser        | GGA<br>Gly        | GCG<br>Ala        | 867  |
| CTT<br>Leu<br>285 | TTG<br>Leu        | AGT<br>Ser        | AAA<br>Lys        | GAG<br>Glu        | CAG<br>Gln<br>290 | CAA<br>Gln        | GAA<br>Glu        | ATC<br>Ile        | TTG<br>Leu        | CAT<br>His<br>295 | TCT<br>Ser        | ATT<br>Ile        | GAA<br>Glu        | GAA<br>Glu        | AAA<br>Lys        | 915  |
| GCG<br>Ala<br>300 | AGC<br>Ser        | GCC<br>Ala        | TTA<br>Leu        | CAA<br>Gln<br>305 | AGC<br>Ser        | CCC<br>Pro        | TTA<br>Leu        | GAA<br>Glu        | AGA<br>Arg        | TTG<br>Leu<br>310 | GAG<br>Glu        | CAT<br>His        | TTT<br>Phe        | CTA<br>Leu        | GCC<br>Ala<br>315 | 963  |
| CCC<br>Pro        | ATT<br>Ile        | AGC<br>Ser        | GGG<br>Gly        | TAT<br>Tyr<br>320 | TTC<br>Phe        | ATC<br>Ile        | ATG<br>Met        | CCC<br>Pro<br>325 | TTA<br>Leu        | TTC<br>Phe        | GCG<br>Ala        | TTT<br>Phe        | GCA<br>Ala        | AAC<br>Asn<br>330 | GCT<br>Ala        | 1011 |
| GGG<br>Gly        | GTG<br>Val        | AGC<br>Ser<br>335 | GTT<br>Val        | GAT<br>Asp        | TCT<br>Ser        | AGC<br>Ser        | ATC<br>Ile        | AAT<br>Asn<br>340 | TTA<br>Leu        | GAA<br>Glu        | GTG<br>Val        | GAT<br>Asp        | AAG<br>Lys<br>345 | GTG<br>Val        | CTT<br>Leu        | 1059 |
| TTA<br>Leu        | GGG<br>Gly<br>350 | GTT<br>Val        | ATT<br>Ile        | TTA<br>Leu        | GGG<br>Gly        | CTT<br>Leu<br>355 | TGC<br>Cys        | TTG<br>Leu<br>355 | GGC<br>Gly        | AAA<br>Lys        | CCT<br>Pro<br>360 | TTA<br>Leu        | GGG<br>Gly        | ATT<br>Ile        | TTC<br>Phe        | 1107 |

TTA ATC ACT TTT ATA AGC GAA AAG CTT AAA ATC ACC GCA CGC CCT AAA 1155  
 Leu Ile Thr Phe Ile Ser Glu Lys Leu Lys Ile Thr Ala Arg Pro Lys  
 365 370 375

GGC ATC AGC TGG TGG CAT ATT TTA GGG GCT GGG CTT TTA GCA GGG ATT 1203  
 Gly Ile Ser Trp Trp His Ile Leu Gly Ala Gly Leu Leu Ala Gly Ile  
 380 385 390 395

GGC TTT ACC ATG TCT ATG TTT ATT TCT AAT CTG GCC TTC ACG AGC GAG 1251  
 Gly Phe Thr Met Ser Met Phe Ile Ser Asn Leu Ala Phe Thr Ser Glu  
 400 405 410

CAT AAA GAC GCT ATG GAA GTG GCA AAA ATT GCG ATT TTA CTC GGA TCT 1299  
 His Lys Asp Ala Met Glu Val Ala Lys Ile Ala Ile Leu Leu Gly Ser  
 415 420 425

TTG ATT TCT GGG ATC ATA GGG GCT TTG TAT TTA TTT GCG CTA GAC AAA 1347  
 Leu Ile Ser Gly Ile Ile Gly Ala Leu Tyr Leu Phe Ala Leu Asp Lys  
 430 435 440

AGA GCG GCT TTA AAG AAA TAGCTAAAAA TGCTATAATT TGAGATTAAA ACATCTTT 1403  
 Arg Ala Ala Leu Lys Lys  
 445

TAAGGAAATT AAATGGGACA AATT 1427

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

Met Gly Leu Lys Leu Lys Ile Leu Arg Leu Ser Met Asn Leu Lys Lys  
 1 5 10 15  
 Thr Glu Asn Ala Leu Ser Leu Thr Leu Lys Asn Phe Ile Lys Ser Glu  
 20 25 30  
 Ser Phe Gly Gly Ile Phe Leu Phe Leu Asn Ala Val Leu Ala Met Val  
 35 40 45  
 Val Ala Asn Ser Phe Leu Lys Glu Ser Tyr Phe Ala Leu Trp His Thr  
 50 55 60  
 Pro Phe Gly Phe Gln Ile Gly Asp Phe Phe Ile Gly Phe Ser Leu His  
 65 70 75 80  
 Asn Trp Ile Asp Asp Val Leu Met Ala Leu Phe Phe Leu Met Ile Gly  
 85 90 95  
 Leu Glu Ile Lys Arg Glu Leu Leu Phe Gly Glu Leu Ser Ser Phe Lys  
 100 105 110  
 Lys Ala Ser Phe Pro Val Ile Ala Ala Ile Gly Gly Met Ile Ala Pro  
 115 120 125  
 Gly Leu Ile Tyr Phe Phe Leu Asn Ala Asn Thr Pro Ser Gln His Gly  
 130 135 140  
 Phe Gly Ile Pro Met Ala Thr Asp Ile Ala Phe Ala Leu Gly Val Ile  
 145 150 155 160

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Leu | Gly | Lys | Arg | Val | Pro | Thr | Ala | Leu | Lys | Val | Phe | Leu | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Thr | Leu | Ala | Val | Ala | Asp | Asp | Leu | Gly | Ala | Ile | Val | Val | Ile | Ala | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Phe | Tyr | Thr | Thr | Asn | Leu | Lys | Phe | Ala | Trp | Leu | Leu | Gly | Ala | Leu | Gly |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Val | Val | Leu | Val | Leu | Ala | Val | Leu | Asn | Arg | Leu | Asn | Met | Arg | Ser | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Pro | Tyr | Leu | Leu | Leu | Gly | Val | Leu | Leu | Trp | Phe | Cys | Val | His | Gln |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ser | Gly | Ile | His | Ala | Thr | Ile | Ala | Ala | Val | Ile | Leu | Ala | Phe | Met | Ile |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Pro | Val | Lys | Ile | Pro | Lys | Asp | Ser | Lys | Asn | Val | Glu | Leu | Leu | Glu | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |
| Gly | Lys | Arg | Tyr | Ala | Glu | Thr | Ser | Ser | Gly | Ala | Leu | Leu | Ser | Lys | Glu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Gln | Gln | Glu | Ile | Leu | His | Ser | Ile | Glu | Glu | Lys | Ala | Ser | Ala | Leu | Gln |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ser | Pro | Leu | Glu | Arg | Leu | Glu | His | Phe | Leu | Ala | Pro | Ile | Ser | Gly | Tyr |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Phe | Ile | Met | Pro | Leu | Phe | Ala | Phe | Ala | Asn | Ala | Gly | Val | Ser | Val | Asp |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ser | Ser | Ile | Asn | Leu | Glu | Val | Asp | Lys | Val | Leu | Leu | Gly | Val | Ile | Leu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Gly | Leu | Cys | Leu | Gly | Lys | Pro | Leu | Gly | Ile | Phe | Leu | Ile | Thr | Phe | Ile |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ser | Glu | Lys | Leu | Lys | Ile | Thr | Ala | Arg | Pro | Lys | Gly | Ile | Ser | Trp | Trp |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| His | Ile | Leu | Gly | Ala | Gly | Leu | Leu | Ala | Gly | Ile | Gly | Phe | Thr | Met | Ser |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Met | Phe | Ile | Ser | Asn | Leu | Ala | Phe | Thr | Ser | Glu | His | Lys | Asp | Ala | Met |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Glu | Val | Ala | Lys | Ile | Ala | Ile | Leu | Leu | Gly | Ser | Leu | Ile | Ser | Gly | Ile |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Ile | Gly | Ala | Leu | Tyr | Leu | Phe | Ala | Leu | Asp | Lys | Arg | Ala | Ala | Leu | Lys |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1903 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...1857
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

AAGTAAGTGC TT ATG GAT AAT AGG AAT ATT GAT CCT TAC TTC AAC CCA GAG 51



| Met Asp Asn Arg Asn Ile Asp Pro Tyr Phe Asn Pro Glu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|                                                     |     | 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     |     |
| CAA                                                 | TTT | TTA | GAA | ACC | CAA | AAA | TAC | AAA | GGC | ACG | GTT | ACA | GCA | TTA | ATC | 99  |
| Gln                                                 | Phe | Leu | Glu | Thr | Gln | Lys | Tyr | Lys | Gly | Thr | Val | Thr | Ala | Leu | Ile |     |
| 15                                                  |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     |     |     |     |
| TTT                                                 | TTA | TTG | CTT | TTT | TTT | ATT | TTT | TTA | ATG | GTG | GCT | TTT | AAA | AAA | GCT | 147 |
| Phe                                                 | Leu | Leu | Leu | Phe | Phe | Ile | Phe | Leu | Met | Val | Ala | Phe | Lys | Lys | Ala |     |
| 30                                                  |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| TTT                                                 | TTT | GCC | CAA | GCC | AAC | ATG | CCT | AAT | CTA | GTG | ATG | AGC | AAA | CAA | GAC | 195 |
| Phe                                                 | Phe | Ala | Gln | Ala | Asn | Met | Pro | Asn | Leu | Val | Met | Ser | Lys | Gln | Asp |     |
|                                                     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| ACT                                                 | GCG | GCT | AGG | GGG | ACT | ATC | TAT | AGT | CAA | GAC | AAC | TAC | AGC | CTA | GCC | 243 |
| Thr                                                 | Ala | Ala | Arg | Gly | Thr | Ile | Tyr | Ser | Gln | Asp | Asn | Tyr | Ser | Leu | Ala |     |
|                                                     |     | 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     |
| ACT                                                 | TCA | CAA | ACC | CTT | TTC | AAA | CTG | GGC | TTT | GAT | ACA | AGG | TTT | TTA | AAC | 291 |
| Thr                                                 | Ser | Gln | Thr | Leu | Phe | Lys | Leu | Gly | Phe | Asp | Thr | Arg | Phe | Leu | Asn |     |
| 80                                                  |     |     |     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     |
| CCG                                                 | GAT | AAA | GAA | GAT | TTT | TTC | ATT | GAT | TTC | CTT | TCT | ATT | TAT | AGC | AAT | 339 |
| Pro                                                 | Asp | Lys | Glu | Asp | Phe | Phe | Ile | Asp | Phe | Leu | Ser | Ile | Tyr | Ser | Asn |     |
| 95                                                  |     |     |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     |     |
| ATC                                                 | CCT | AAA | AAG | TCC | TTA | AAA | GAC | GCC | ATC | AAT | ACA | AAA | GGC | TAT | ATC | 387 |
| Ile                                                 | Pro | Lys | Lys | Ser | Leu | Lys | Asp | Ala | Ile | Asn | Thr | Lys | Gly | Tyr | Ile |     |
| 110                                                 |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| ATT                                                 | CTA | GCC | TAT | GAT | CTC | ACG | CCC | AAT | ATG | GCT | GCT | AAT | ATT | AGA | GAC | 435 |
| Ile                                                 | Leu | Ala | Tyr | Asp | Leu | Thr | Pro | Asn | Met | Ala | Ala | Asn | Ile | Arg | Asp |     |
|                                                     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| TTA                                                 | AAT | AAG | AAA | TTT | TTA | GCC | TTT | GGG | GTT | TTT | CAA | AAT | TTC | AAA | GAC | 483 |
| Leu                                                 | Asn | Lys | Lys | Phe | Leu | Ala | Phe | Gly | Val | Phe | Gln | Asn | Phe | Lys | Asp |     |
|                                                     |     | 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     |
| GCG                                                 | CAC | GAT | AAG | GTG | TGG | CAA | AAG | CAA | GGG | CTA | AAC | ATT | GAA | GTG | AGC | 531 |
| Ala                                                 | His | Asp | Lys | Val | Trp | Gln | Lys | Gln | Gly | Leu | Asn | Ile | Glu | Val | Ser |     |
| 160                                                 |     |     |     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     |
| GGC                                                 | GTT | TCT | AGG | CAT | TAC | CCT | TAT | CAA | AAT | AGC | CTA | GAG | CCA | ATC | ATT | 579 |
| Gly                                                 | Val | Ser | Arg | His | Tyr | Pro | Tyr | Gln | Asn | Ser | Leu | Glu | Pro | Ile | Ile |     |
| 175                                                 |     |     |     |     |     | 180 |     |     |     | 185 |     |     |     |     |     |     |
| GGC                                                 | TAT | GTG | CAA | AAA | CAA | GAA | GAA | GAC | AAG | CTC | ACT | TTA | ACT | ACC | GGT | 627 |
| Gly                                                 | Tyr | Val | Gln | Lys | Gln | Glu | Glu | Asp | Lys | Leu | Thr | Leu | Thr | Thr | Gly |     |
| 190                                                 |     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| AAA                                                 | AAA | GGC | GTT | GAA | AAA | TCT | CAA | GAT | CAC | TTG | CTT | AAA | GCC | CAA | CAA | 675 |
| Lys                                                 | Lys | Gly | Val | Glu | Lys | Ser | Gln | Asp | His | Leu | Leu | Lys | Ala | Gln | Gln |     |
|                                                     |     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| AAT                                                 | GGC | ATA | AGA | ACA | GGC | AAA | AGA | GAC | GTG | AGT | TTT | AAC | TTT | ATC | CAA | 723 |
| Asn                                                 | Gly | Ile | Arg | Thr | Gly | Lys | Arg | Asp | Val | Ser | Phe | Asn | Phe | Ile | Gln |     |
| 225                                                 |     |     |     | 230 |     |     |     | 235 |     |     |     | 240 |     |     |     |     |

|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |            |                   |                   |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|------|
| AAC<br>Asn        | CAC<br>His        | TCT<br>Ser<br>240 | TAT<br>Tyr        | ACA<br>Thr        | GAG<br>Glu        | GTT<br>Val        | GAA<br>Glu<br>245 | CGC<br>Arg        | CTT<br>Leu        | GAT<br>Asp        | GGC<br>Gly        | TAT<br>Tyr<br>250 | GAG<br>Glu | GTG<br>Val        | TAT<br>Tyr        | 771  |
| TTG<br>Leu        | AGC<br>Ser<br>255 | GTT<br>Val        | CCT<br>Pro        | TTA<br>Leu        | AAA<br>Lys        | CTC<br>Leu<br>260 | CAA<br>Gln        | AGA<br>Arg        | GAA<br>Glu        | ATT<br>Ile        | GAA<br>Glu<br>265 | ACC<br>Thr        | CTA<br>Leu | TTG<br>Leu        | GAT<br>Asp        | 819  |
| AAA<br>Lys<br>270 | ACT<br>Thr        | AAA<br>Lys        | GAC<br>Asp        | AAA<br>Lys        | CTC<br>Leu<br>275 | AAG<br>Lys        | GCT<br>Ala        | AAA<br>Lys        | GAA<br>Glu        | ATC<br>Ile<br>280 | CTA<br>Leu        | GTG<br>Val        | GGT<br>Gly | ATC<br>Ile        | ATT<br>Ile<br>285 | 867  |
| AAC<br>Asn        | CCT<br>Pro        | AAA<br>Lys        | AGC<br>Ser        | GGG<br>Gly<br>290 | GAA<br>Glu        | ATT<br>Ile        | TTA<br>Leu        | TCG<br>Ser        | CTA<br>Leu<br>295 | GCT<br>Ala        | TCA<br>Ser        | AGC<br>Ser        | AAG<br>Lys | CGC<br>Arg<br>300 | TTC<br>Phe        | 915  |
| AAT<br>Asn        | CCT<br>Pro        | AAT<br>Asn        | GCG<br>Ala<br>305 | ATT<br>Ile        | AAA<br>Lys        | ACC<br>Thr        | AGC<br>Ser        | GAT<br>Asp<br>310 | TAT<br>Tyr        | GAA<br>Glu        | AGC<br>Ser        | TTG<br>Leu<br>315 | AAT<br>Asn | TTG<br>Leu        | AGC<br>Ser        | 963  |
| GTT<br>Val        | GCT<br>Ala<br>320 | GAA<br>Glu        | AAG<br>Lys        | GTT<br>Val        | TTT<br>Phe        | GAG<br>Glu        | CCA<br>Pro<br>325 | GGC<br>Gly        | AGC<br>Ser        | ACG<br>Thr        | ATC<br>Ile<br>330 | AAA<br>Lys        | CCC<br>Pro | ATT<br>Ile        | GTT<br>Val        | 1011 |
| TAT<br>Tyr        | TCC<br>Ser<br>335 | TTG<br>Leu        | CTG<br>Leu        | TTA<br>Leu        | GAC<br>Asp        | AAG<br>Lys<br>340 | AAT<br>Asn        | TTG<br>Leu        | ATC<br>Ile        | AAC<br>Asn        | CCC<br>Pro<br>345 | AAA<br>Lys        | GAA<br>Glu | CGC<br>Arg        | ATT<br>Ile        | 1059 |
| GAT<br>Asp<br>350 | TTA<br>Leu        | AAC<br>Asn        | CAT<br>His        | GGC<br>Gly        | TAT<br>Tyr<br>355 | TAC<br>Tyr        | CAA<br>Gln        | TTA<br>Leu        | GGA<br>Gly        | AAA<br>Lys<br>360 | TAC<br>Tyr        | ACC<br>Thr        | ATT<br>Ile | AAA<br>Lys        | GAC<br>Asp<br>365 | 1107 |
| GAC<br>Asp        | TTT<br>Phe        | ATC<br>Ile        | CCC<br>Pro        | AGT<br>Ser<br>370 | AAA<br>Lys        | AAA<br>Lys        | GCC<br>Ala        | GTT<br>Val        | GTG<br>Val<br>375 | GAA<br>Glu        | GAC<br>Asp        | ATT<br>Ile        | TTG<br>Leu | ATC<br>Ile<br>380 | CAA<br>Gln        | 1155 |
| TCT<br>Ser        | AGC<br>Ser        | AAT<br>Asn<br>385 | GTG<br>Val        | GGC<br>Gly        | ATG<br>Met        | ATA<br>Ile        | AAA<br>Lys        | ATC<br>Ile<br>390 | AGT<br>Ser        | AAA<br>Lys        | AAC<br>Asn        | TTA<br>Leu<br>395 | AAC<br>Asn | CCA<br>Pro        | AAG<br>Lys        | 1203 |
| GAT<br>Asp        | TTC<br>Phe        | TAT<br>Tyr<br>400 | AAT<br>Asn        | GGG<br>Gly        | CTT<br>Leu        | TTA<br>Leu        | GGC<br>Gly<br>405 | TAT<br>Tyr        | GGA<br>Gly        | TTT<br>Phe        | TCT<br>Ser        | CAA<br>Gln<br>410 | AAA<br>Lys | ACC<br>Thr        | GGC<br>Gly        | 1251 |
| ATT<br>Ile        | GAT<br>Asp<br>415 | TTA<br>Leu        | TCT<br>Ser        | CTA<br>Leu        | GAA<br>Glu        | GCC<br>Ala<br>420 | ACA<br>Thr        | GGA<br>Gly        | AAG<br>Lys        | ATC<br>Ile        | CCT<br>Pro<br>425 | CCT<br>Pro        | TTG<br>Leu | TCC<br>Ser        | GCT<br>Ala        | 1299 |
| TTC<br>Phe<br>430 | AAG<br>Lys        | CGT<br>Arg        | GAA<br>Glu        | GTG<br>Val        | TTA<br>Leu<br>435 | AAG<br>Lys        | GGG<br>Gly        | AGC<br>Ser        | GTT<br>Val        | TCT<br>Ser<br>440 | TAT<br>Tyr        | GGC<br>Gly        | TAT<br>Tyr | GGG<br>Gly        | CTG<br>Leu<br>445 | 1347 |
| AAC<br>Asn        | GCG<br>Ala        | ACT<br>Thr        | TTT<br>Phe        | TTG<br>Leu<br>450 | CAG<br>Gln        | CTT<br>Leu        | TTA<br>Leu        | AGG<br>Arg        | GCT<br>Ala<br>455 | TAT<br>Tyr        | GCG<br>Ala        | GTG<br>Val        | TTT<br>Phe | TCT<br>Ser<br>460 | AAT<br>Asn        | 1395 |
| GAA<br>Glu        | GGC<br>Gly        | AAA<br>Lys        | TTG<br>Leu        | ACT<br>Thr        | ACC<br>Thr        | CCC<br>Pro        | TAT<br>Tyr        | TTA<br>Leu        | GTG<br>Val        | CAA<br>Gln        | CGA<br>Arg        | GAA<br>Glu        | ACC<br>Thr | GCC<br>Ala        | CCT<br>Pro        | 1443 |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ala | Asn | Met | Pro | Asn | Leu | Val | Met | Ser | Lys | Gln | Asp | Thr | Ala | Ala |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Gly | Thr | Ile | Tyr | Ser | Gln | Asp | Asn | Tyr | Ser | Leu | Ala | Thr | Ser | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Leu | Phe | Lys | Leu | Gly | Phe | Asp | Thr | Arg | Phe | Leu | Asn | Pro | Asp | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Asp | Phe | Phe | Ile | Asp | Phe | Leu | Ser | Ile | Tyr | Ser | Asn | Ile | Pro | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Ser | Leu | Lys | Asp | Ala | Ile | Asn | Thr | Lys | Gly | Tyr | Ile | Ile | Leu | Ala |
|     |     | 115 |     |     |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Tyr | Asp | Leu | Thr | Pro | Asn | Met | Ala | Ala | Asn | Ile | Arg | Asp | Leu | Asn | Lys |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Phe | Leu | Ala | Phe | Gly | Val | Phe | Gln | Asn | Phe | Lys | Asp | Ala | His | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Val | Trp | Gln | Lys | Gln | Gly | Leu | Asn | Ile | Glu | Val | Ser | Gly | Val | Ser |
|     |     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |
| Arg | His | Tyr | Pro | Tyr | Gln | Asn | Ser | Leu | Glu | Pro | Ile | Ile | Gly | Tyr | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gln | Lys | Gln | Glu | Glu | Asp | Lys | Leu | Thr | Leu | Thr | Thr | Gly | Lys | Lys | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Glu | Lys | Ser | Gln | Asp | His | Leu | Leu | Lys | Ala | Gln | Gln | Asn | Gly | Ile |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Arg | Thr | Gly | Lys | Arg | Asp | Val | Ser | Phe | Asn | Phe | Ile | Gln | Asn | His | Ser |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     |     | 240 |
| Tyr | Thr | Glu | Val | Glu | Arg | Leu | Asp | Gly | Tyr | Glu | Val | Tyr | Leu | Ser | Val |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Pro | Leu | Lys | Leu | Gln | Arg | Glu | Ile | Glu | Thr | Leu | Leu | Asp | Lys | Thr | Lys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asp | Lys | Leu | Lys | Ala | Lys | Glu | Ile | Leu | Val | Gly | Ile | Ile | Asn | Pro | Lys |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ser | Gly | Glu | Ile | Leu | Ser | Leu | Ala | Ser | Ser | Lys | Arg | Phe | Asn | Pro | Asn |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ala | Ile | Lys | Thr | Ser | Asp | Tyr | Glu | Ser | Leu | Asn | Leu | Ser | Val | Ala | Glu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Lys | Val | Phe | Glu | Pro | Gly | Ser | Thr | Ile | Lys | Pro | Ile | Val | Tyr | Ser | Leu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Leu | Leu | Asp | Lys | Asn | Leu | Ile | Asn | Pro | Lys | Glu | Arg | Ile | Asp | Leu | Asn |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| His | Gly | Tyr | Tyr | Gln | Leu | Gly | Lys | Tyr | Thr | Ile | Lys | Asp | Asp | Phe | Ile |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Pro | Ser | Lys | Lys | Ala | Val | Val | Glu | Asp | Ile | Leu | Ile | Gln | Ser | Ser | Asn |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Val | Gly | Met | Ile | Lys | Ile | Ser | Lys | Asn | Leu | Asn | Pro | Lys | Asp | Phe | Tyr |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Asn | Gly | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |





|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Leu | Ala | Val | Gly | Thr | Leu | Val | Thr | Gln | Gly | Val | Ile | Tyr | Gly | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Gly | Ala | Phe | Ser | Asn | Ala | His | Lys | Asp | Gly | Ala | Arg | Val | Glu | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Lys | Arg | Pro | Cys | Cys | Asn | Ser | Trp | Arg | Gly | Met | Pro | Ser | Gly | His |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Gly | Gly | Val | Phe | Ser | Ala | Ala | Gly | Phe | Val | Tyr | Tyr | Arg | Tyr | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Trp | Lys | Pro | Ala | Leu | Pro | Val | Ile | Ala | Leu | Ala | Ile | Leu | Thr | Asp | Ala |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Ser | Arg | Val | Val | Ala | Arg | Gln | His | Thr | Ile | Leu | Gln | Val | Thr | Ile | Gly |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ser | Leu | Ile | Ala | Trp | Gly | Phe | Ala | Tyr | Leu | Phe | Thr | Ser | Arg | Tyr | Lys |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Pro | Lys | Gln | Trp | Met | Leu | Tyr | Pro | Glu | Ile | Ser | Ser | Asp | Phe | Lys | Gly |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ser | Ser | Arg | Tyr | Gly | Val | Ser | Phe | Ser | Tyr | Gln | Trp |     |     |     |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1087 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...1053
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

|                                                                 |             |            |     |     |     |     |     |     |     |     |    |
|-----------------------------------------------------------------|-------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|----|
| TTCAAGCAAA AACACCA                                              | CCCC        | AAATATAAAG | ATA | ATG | ATT | TTA | AGC | ATT | GAA | AGT | 54 |
|                                                                 |             |            | Met | Ile | Leu | Ser | Ile | Glu | Ser |     |    |
|                                                                 |             |            | 1   |     |     |     | 5   |     |     |     |    |
| TCT TGC GAT GAC AGC TCT TTA GCC CTT ACA AGA ATA GAG GAC GCT CAA | 102         |            |     |     |     |     |     |     |     |     |    |
| Ser Cys Asp Asp Ser Ser Leu Ala Leu Thr Arg Ile Glu Asp Ala Gln |             |            |     |     |     |     |     |     |     |     |    |
|                                                                 | 10 15 20    |            |     |     |     |     |     |     |     |     |    |
| CTC ATC GCT CAT TTT AAA ATC TCT CAA GAA AAG CAC CAT AGT TCT TAT | 150         |            |     |     |     |     |     |     |     |     |    |
| Leu Ile Ala His Phe Lys Ile Ser Gln Glu Lys His His Ser Ser Tyr |             |            |     |     |     |     |     |     |     |     |    |
|                                                                 | 25 30 35    |            |     |     |     |     |     |     |     |     |    |
| GGG GGC GTT GTG CCT GAG CTT GCA TCA CGT TTG CAT GCT GAG AAT TTG | 198         |            |     |     |     |     |     |     |     |     |    |
| Gly Gly Val Val Pro Glu Leu Ala Ser Arg Leu His Ala Glu Asn Leu |             |            |     |     |     |     |     |     |     |     |    |
|                                                                 | 40 45 50 55 |            |     |     |     |     |     |     |     |     |    |
| CCG CTT TTA TTA GAA CGC ATT AAA ATA AGC TTG AAT AAG GAT TTT TCC | 246         |            |     |     |     |     |     |     |     |     |    |
| Pro Leu Leu Leu Glu Arg Ile Lys Ile Ser Leu Asn Lys Asp Phe Ser |             |            |     |     |     |     |     |     |     |     |    |
|                                                                 | 60 65 70    |            |     |     |     |     |     |     |     |     |    |
| AAA ATT AAA GCC ATC GCT ATC ACT AAT CAG CCA GGT TTG AGC GTT ACT | 294         |            |     |     |     |     |     |     |     |     |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Lys | Ile | Lys | Ala | Ile | Ala | Ile | Thr | Asn | Gln | Pro | Gly | Leu | Ser | Val | Thr |     |  |
|     |     |     | 75  |     |     |     | 80  |     |     |     |     |     | 85  |     |     |     |  |
| TTA | ATA | GAA | GGT | TTG | ATG | ATG | GCA | AAA | GCC | TTG | AGC | TTG | TCT | TTG | AAT | 342 |  |
| Leu | Ile | Glu | Gly | Leu | Met | Met | Ala | Lys | Ala | Leu | Ser | Leu | Ser | Leu | Asn |     |  |
|     |     |     | 90  |     |     |     | 95  |     |     |     |     |     | 100 |     |     |     |  |
| TTG | CCC | TTG | ATT | TTA | GAA | GAT | CAT | TTG | AGA | GGG | CAT | GTG | TAT | TCG | CTC | 390 |  |
| Leu | Pro | Leu | Ile | Leu | Glu | Asp | His | Leu | Arg | Gly | His | Val | Tyr | Ser | Leu |     |  |
|     |     |     | 105 |     |     |     | 110 |     |     |     |     |     | 115 |     |     |     |  |
| TTT | ATC | AAT | GAA | AAA | CAA | ACC | TGC | ATG | CCT | TTA | AGC | GTG | CTC | TTA | GTC | 438 |  |
| Phe | Ile | Asn | Glu | Lys | Gln | Thr | Cys | Met | Pro | Leu | Ser | Val | Leu | Leu | Val |     |  |
|     |     |     | 120 |     |     |     | 125 |     |     |     |     |     | 130 | 135 |     |     |  |
| TCT | GGG | GGG | CAT | TCT | TTG | ATT | TTA | GAG | GCT | AGA | GAT | TAT | GAG | AAT | ATT | 486 |  |
| Ser | Gly | Gly | His | Ser | Leu | Ile | Leu | Glu | Ala | Arg | Asp | Tyr | Glu | Asn | Ile |     |  |
|     |     |     | 140 |     |     |     | 145 |     |     |     |     |     | 150 |     |     |     |  |
| AAA | ATC | GTT | GCC | ACG | AGT | TTA | GAC | GAT | AGC | TTT | GGG | GAG | AGT | TTT | GAT | 534 |  |
| Lys | Ile | Val | Ala | Thr | Ser | Leu | Asp | Asp | Ser | Phe | Gly | Glu | Ser | Phe | Asp |     |  |
|     |     |     | 155 |     |     |     | 160 |     |     |     |     |     | 165 |     |     |     |  |
| AAG | GTT | TCC | AAA | ATG | CTT | GAT | TTA | GGC | TAT | CCA | GGA | GGC | CCT | ATA | GTG | 582 |  |
| Lys | Val | Ser | Lys | Met | Leu | Asp | Leu | Gly | Tyr | Pro | Gly | Gly | Pro | Ile | Val |     |  |
|     |     |     | 170 |     |     |     | 175 |     |     |     |     |     | 180 |     |     |     |  |
| GAA | AAA | TTA | GCC | CTT | GAT | TAT | AGG | CAC | CCA | AAC | GAG | CCT | TTA | ATG | TTC | 630 |  |
| Glu | Lys | Leu | Ala | Leu | Asp | Tyr | Arg | His | Pro | Asn | Glu | Pro | Leu | Met | Phe |     |  |
|     |     |     | 185 |     |     |     | 190 |     |     |     |     |     | 195 |     |     |     |  |
| CCT | ATC | CCT | TTA | AAA | AAC | AGC | CCG | AAT | CTG | GCT | TTT | AGT | TTT | TCA | GGT | 678 |  |
| Pro | Ile | Pro | Leu | Lys | Asn | Ser | Pro | Asn | Leu | Ala | Phe | Ser | Phe | Ser | Gly |     |  |
|     |     |     | 200 |     |     |     | 205 |     |     |     |     |     | 210 | 215 |     |     |  |
| TTA | AAA | AAT | GCG | GTG | CGT | TTG | GAG | GTT | GAA | AAA | AAC | GCC | CCC | AAC | TTG | 726 |  |
| Leu | Lys | Asn | Ala | Val | Arg | Leu | Glu | Val | Glu | Lys | Asn | Ala | Pro | Asn | Leu |     |  |
|     |     |     | 220 |     |     |     | 225 |     |     |     |     |     | 230 |     |     |     |  |
| AAT | GAA | GCG | ATC | AAA | CAA | AAG | ATT | GGC | TAT | CAT | TTT | CAA | AGT | GCA | GCG | 774 |  |
| Asn | Glu | Ala | Ile | Lys | Gln | Lys | Ile | Gly | Tyr | His | Phe | Gln | Ser | Ala | Ala |     |  |
|     |     |     | 235 |     |     |     | 240 |     |     |     |     |     | 245 |     |     |     |  |
| ATT | GAG | CAT | TTA | ATC | CAG | CAG | ACT | AAA | CGC | TAT | TTT | AAA | ATC | AAA | CGC | 822 |  |
| Ile | Glu | His | Leu | Ile | Gln | Gln | Thr | Lys | Arg | Tyr | Phe | Lys | Ile | Lys | Arg |     |  |
|     |     |     | 250 |     |     |     | 255 |     |     |     |     |     | 260 |     |     |     |  |
| CCT | AAA | ATT | TTT | GGC | ATT | GTG | GGG | GGA | GCG | AGC | CAA | AAT | TTG | GCT | TTA | 870 |  |
| Pro | Lys | Ile | Phe | Gly | Ile | Val | Gly | Gly | Ala | Ser | Gln | Asn | Leu | Ala | Leu |     |  |
|     |     |     | 265 |     |     |     | 270 |     |     |     |     |     | 275 |     |     |     |  |
| AGA | AAG | GCG | TTT | GAA | AAT | TTG | TGC | GAT | GCG | TTT | GAT | TGC | AAG | CTT | GTT | 918 |  |
| Arg | Lys | Ala | Phe | Glu | Asn | Leu | Cys | Asp | Ala | Phe | Asp | Cys | Lys | Leu | Val |     |  |
|     |     |     | 280 |     |     |     | 285 |     |     |     |     |     | 290 | 295 |     |     |  |
| TTA | GCC | CCT | TTA | GAA | TTT | TGC | AGC | GAC | AAT | GCC | GCC | ATG | ATA | GGG | CGA | 966 |  |
| Leu | Ala | Pro | Leu | Glu | Phe | Cys | Ser | Asp | Asn | Ala |     |     |     |     |     |     |  |



TCC AGC CTA GAA GCT TAT CAA AAA AAG CGC TTT GTC CCT TTA GAA AAG 1014  
 Ser Ser Leu Glu Ala Tyr Gln Lys Lys Arg Phe Val Pro Leu Glu Lys  
 315 320 325

GCT AAC ATT TCG CCA AGA ACG CTG TTA AAA AGT TTT GAG TGAATGGATA CA 1065  
 Ala Asn Ile Ser Pro Arg Thr Leu Leu Lys Ser Phe Glu  
 330 335 340

AAAAGAAAGC GCATGATAAA AC 1087

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Leu | Ser | Ile | Glu | Ser | Ser | Cys | Asp | Asp | Ser | Ser | Leu | Ala | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Arg | Ile | Glu | Asp | Ala | Gln | Leu | Ile | Ala | His | Phe | Lys | Ile | Ser | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Lys | His | His | Ser | Ser | Tyr | Gly | Gly | Val | Val | Pro | Glu | Leu | Ala | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Leu | His | Ala | Glu | Asn | Leu | Pro | Leu | Leu | Leu | Glu | Arg | Ile | Lys | Ile |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Ser | Leu | Asn | Lys | Asp | Phe | Ser | Lys | Ile | Lys | Ala | Ile | Ala | Ile | Thr | Asn |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gln | Pro | Gly | Leu | Ser | Val | Thr | Leu | Ile | Glu | Gly | Leu | Met | Met | Ala | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ala | Leu | Ser | Leu | Ser | Leu | Asn | Leu | Pro | Leu | Ile | Leu | Glu | Asp | His | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Gly | His | Val | Tyr | Ser | Leu | Phe | Ile | Asn | Glu | Lys | Gln | Thr | Cys | Met |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Leu | Ser | Val | Leu | Leu | Val | Ser | Gly | Gly | His | Ser | Leu | Ile | Leu | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Arg | Asp | Tyr | Glu | Asn | Ile | Lys | Ile | Val | Ala | Thr | Ser | Leu | Asp | Asp |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Ser | Phe | Gly | Glu | Ser | Phe | Asp | Lys | Val | Ser | Lys | Met | Leu | Asp | Leu | Gly |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Tyr | Pro | Gly | Gly | Pro | Ile | Val | Glu | Lys | Leu | Ala | Leu | Asp | Tyr | Arg | His |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Pro | Asn | Glu | Pro | Leu | Met | Phe | Pro | Ile | Pro | Leu | Lys | Asn | Ser | Pro | Asn |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Leu | Ala | Phe | Ser | Phe | Ser | Gly | Leu | Lys | Asn | Ala | Val | Arg | Leu | Glu | Val |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Glu | Lys | Asn | Ala | Pro | Asn | Leu | Asn | Glu | Ala | Ile | Lys | Gln | Lys | Ile | Gly |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Tyr | His | Phe | Gln | Ser | Ala | Ala | Ile | Glu | His | Leu | Ile | Gln | Gln | Thr | Lys |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Arg | Tyr | Phe | Lys | Ile | Lys | Arg | Pro | Lys | Ile | Phe | Gly | Ile | Val | Gly | Gly |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     | 270 |     |     |     |
| Ala | Ser | Gln | Asn | Leu | Ala | Leu | Arg | Lys | Ala | Phe | Glu | Asn | Leu | Cys | Asp |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ala | Phe | Asp | Cys | Lys | Leu | Val | Leu | Ala | Pro | Leu | Glu | Phe | Cys | Ser | Asp |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Asn | Ala | Ala | Met | Ile | Gly | Arg | Ser | Ser | Leu | Glu | Ala | Tyr | Gln | Lys | Lys |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Arg | Phe | Val | Pro | Leu | Glu | Lys | Ala | Asn | Ile | Ser | Pro | Arg | Thr | Leu | Leu |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |
| Lys | Ser | Phe | Glu |     |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     | 340 |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...498
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

|            |            |            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| TGCACTTGTT | ATGATGAAGA | TGGCGCACTA | AGA | ATG | AAT | GAA | GAC | TTG | ACA | AAT |     |     |     |     |     | 54  |
|            |            |            |     | Met | Asn | Glu | Asp | Leu | Thr | Asn |     |     |     |     |     |     |
|            |            |            |     | 1   |     |     |     | 5   |     |     |     |     |     |     |     |     |
| TCA        | ACA        | GAA        | TAT | AAA | AGA | TAT | GGC | CAT | GAT | TAC | GCC | AAA | TAC | CCA | AGA | 102 |
| Ser        | Thr        | Glu        | Tyr | Lys | Arg | Tyr | Gly | His | Asp | Tyr | Ala | Lys | Tyr | Pro | Arg |     |
|            |            | 10         |     |     |     |     | 15  |     |     |     |     | 20  |     |     |     |     |
| AGA        | ATC        | GCT        | GAA | GAA | TTG | CAA | CAT | TAT | GGG | GGC | AAT | AGT | TTT | GCG | AAT | 150 |
| Arg        | Ile        | Ala        | Glu | Glu | Leu | Gln | His | Tyr | Gly | Gly | Asn | Ser | Phe | Ala | Asn |     |
|            | 25         |            |     |     |     | 30  |     |     |     |     | 35  |     |     |     |     |     |
| TTT        | TTT        | AGA        | GAT | GAA | GGG | GTC | TTA | TAC | AAA | GAG | ATT | TTG | TGC | GAT | GCG | 198 |
| Phe        | Phe        | Arg        | Asp | Glu | Gly | Val | Leu | Tyr | Lys | Glu | Ile | Leu | Cys | Asp | Ala |     |
| 40         |            |            |     | 45  |     |     |     |     | 50  |     |     |     |     | 55  |     |     |
| TGC        | GAT        | CAT        | TTA | AAG | GTT | AAT | TAC | AAT | GAA | GAA | TCT | GCA | ACC | TCT | TTG | 246 |
| Cys        | Asp        | His        | Leu | Lys | Val | Asn | Tyr | Asn | Glu | Glu | Ser | Ala | Thr | Ser | Leu |     |
|            |            |            |     | 60  |     |     |     |     | 65  |     |     |     |     | 70  |     |     |
| ATT        | GAG        | CAA        | AAC | ATG | CTT | TCT | AAA | CTC | TTG | AAA | GAT | AGT | TTA | GAA | AAA | 294 |
| Ile        | Glu        | Gln        | Asn | Met | Leu | Ser | Lys | Leu | Leu | Lys | Asp | Ser | Leu | Glu | Lys |     |
|            |            |            | 75  |     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |
| ATG        | AGT        | AGG        | AGA | GAG | ATT | AAA | GAA | CTT | TGC | AAT | GAA | TTG | GGC | ATG | ACA | 342 |
| Met        | Ser        | Arg        | Arg | Glu | Ile | Lys | Glu | Leu | Cys | Asn | Glu | Leu | Gly | Met | Thr |     |
|            |            | 90         |     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     |
| AAT        | ATT        | GAT        | AAA | GTG | ATT | GGT | GAA | AAC | AAA | CAA | GTC | CTA | ATC | GCA | TCT | 390 |
| Asn        | Ile        | Asp        | Lys | Val | Ile | Gly | Glu | Asn | Lys | Gln | Val | Leu | Ile | Ala | Ser |     |
|            | 105        |            |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     |     |

ACT TTA ACG CTG TTT AAA GCG GGT GGC TCT CAT TCT TAT GCG TTG GCT 438  
 Thr Leu Thr Leu Phe Lys Ala Gly Gly Ser His Ser Tyr Ala Leu Ala  
 120 125 130 135

GTA TCT GTT GCA GAT GCA ATG GTA AGA CAA ACT CTA GGG CAT GTT ATG 486  
 Val Ser Val Ala Asp Ala Met Val Arg Gln Thr Leu Gly His Val Met  
 140 145 150

TGG TGG GTA AAG TAGCACTTAA AAAAAGTTTG GCGGTTTTGG CTGGCCCTAT TGGTT 543  
 Trp Trp Val Lys  
 155

GGGT 547

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

Met Asn Glu Asp Leu Thr Asn Ser Thr Glu Tyr Lys Arg Tyr Gly His  
 1 5 10 15  
 Asp Tyr Ala Lys Tyr Pro Arg Arg Ile Ala Glu Glu Leu Gln His Tyr  
 20 25 30  
 Gly Gly Asn Ser Phe Ala Asn Phe Arg Asp Glu Gly Val Leu Tyr  
 35 40 45  
 Lys Glu Ile Leu Cys Asp Ala Cys Asp His Leu Lys Val Asn Tyr Asn  
 50 55 60  
 Glu Glu Ser Ala Thr Ser Leu Ile Glu Gln Asn Met Leu Ser Lys Leu  
 65 70 75 80  
 Leu Lys Asp Ser Leu Glu Lys Met Ser Arg Arg Glu Ile Lys Glu Leu  
 85 90 95  
 Cys Asn Glu Leu Gly Met Thr Asn Ile Asp Lys Val Ile Gly Glu Asn  
 100 105 110  
 Lys Gln Val Leu Ile Ala Ser Thr Leu Thr Leu Phe Lys Ala Gly Gly  
 115 120 125  
 Ser His Ser Tyr Ala Leu Ala Val Ser Val Ala Asp Ala Met Val Arg  
 130 135 140  
 Gln Thr Leu Gly His Val Met Trp Trp Val Lys  
 145 150 155

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 19...486  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| TTATTTTAAA GGAATTTTC ATG CAA ATC ATA GAA GGG AAA TTG CAA TTA CAA | 51  |
| Met Gln Ile Ile Glu Gly Lys Leu Gln Leu Gln                      |     |
| 1 5 10                                                           |     |
| GGG AAT GAA AGA GTC GCT ATT TTA ACA TCG CGC TTC AAT CAT ATC ATC  | 99  |
| Gly Asn Glu Arg Val Ala Ile Leu Thr Ser Arg Phe Asn His Ile Ile  |     |
| 15 20 25                                                         |     |
| ACA GAC AGA TTG CAA GAA GGG GCG ATG GAC TGC TTT AAA AGG CAT GGG  | 147 |
| Thr Asp Arg Leu Gln Glu Gly Ala Met Asp Cys Phe Lys Arg His Gly  |     |
| 30 35 40                                                         |     |
| GGC GAT GAG GAT CTT TTA GAC ATC GTG CTG GTG CCT GGG GCT TAT GAA  | 195 |
| Gly Asp Glu Asp Leu Leu Asp Ile Val Leu Val Pro Gly Ala Tyr Glu  |     |
| 45 50 55                                                         |     |
| TTG CCT TTT ATT TTA GAC AAA TTA TTA GAG AGC GAA AAA TAC GAT GGC  | 243 |
| Leu Pro Phe Ile Leu Asp Lys Leu Leu Glu Ser Glu Lys Tyr Asp Gly  |     |
| 60 65 70 75                                                      |     |
| GTG TGC GTT TTG GGA GCG ATC ATT AGA GGG GGG ACT CCG CAT TTT GAT  | 291 |
| Val Cys Val Leu Gly Ala Ile Ile Arg Gly Gly Thr Pro His Phe Asp  |     |
| 80 85 90                                                         |     |
| TAT GTG AGC GCG GAA GCG ACT AAG GGT ATT GCC CAT GCG ATG CTT AAA  | 339 |
| Tyr Val Ser Ala Glu Ala Thr Lys Gly Ile Ala His Ala Met Leu Lys  |     |
| 95 100 105                                                       |     |
| TAC AGC ATG CCG GTA AGC TTT GGC GTG CTG ACC ACG GAC AAT ATT GAA  | 387 |
| Tyr Ser Met Pro Val Ser Phe Gly Val Leu Thr Thr Asp Asn Ile Glu  |     |
| 110 115 120                                                      |     |
| CAA GCG ATT GAA AGA GCG GGC AGT AAA GCC GGC AAT AAG GGC TTT GAA  | 435 |
| Gln Ala Ile Glu Arg Ala Gly Ser Lys Ala Gly Asn Lys Gly Phe Glu  |     |
| 125 130 135                                                      |     |
| GCG ATG AGC ACC CTC ATT GAA TTG TTG AGC TTG TGC CAA ACT CTC AAG  | 483 |
| Ala Met Ser Thr Leu Ile Glu Leu Leu Ser Leu Cys Gln Thr Leu Lys  |     |
| 140 145 150 155                                                  |     |
| GGT TAAAATGGCG ACACGAACTC AAGCCAGGGG GGCTGTG                     | 523 |
| Gly                                                              |     |

(2) INFORMATION FOR SEQ ID NO:416:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 156 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

Met Gln Ile Ile Glu Gly Lys Leu Gln Leu Gln Gly Asn Glu Arg Val  
1 5 10 15  
Ala Ile Leu Thr Ser Arg Phe Asn His Ile Ile Thr Asp Arg Leu Gln  
20 25 30  
Glu Gly Ala Met Asp Cys Phe Lys Arg His Gly Gly Asp Glu Asp Leu  
35 40 45  
Leu Asp Ile Val Leu Val Pro Gly Ala Tyr Glu Leu Pro Phe Ile Leu  
50 55 60  
Asp Lys Leu Leu Glu Ser Glu Lys Tyr Asp Gly Val Cys Val Leu Gly  
65 70 75 80  
Ala Ile Ile Arg Gly Gly Thr Pro His Phe Asp Tyr Val Ser Ala Glu  
85 90 95  
Ala Thr Lys Gly Ile Ala His Ala Met Leu Lys Tyr Ser Met Pro Val  
100 105 110  
Ser Phe Gly Val Leu Thr Thr Asp Asn Ile Glu Gln Ala Ile Glu Arg  
115 120 125  
Ala Gly Ser Lys Ala Gly Asn Lys Gly Phe Glu Ala Met Ser Thr Leu  
130 135 140  
Ile Glu Leu Leu Ser Leu Cys Gln Thr Leu Lys Gly  
145 150 155

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...1656
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

TATTATTAAAG GATACAAA ATG GCA AAA GAA ATC AAA TTT TCA GAT AGC GCG 51  
Met Ala Lys Glu Ile Lys Phe Ser Asp Ser Ala  
1 5 10  
AGA AAC CTT TTA TTT GAA GGC GTG AGA CAA CTC CAT GAC GCT GTT AAA 99  
Arg Asn Leu Leu Phe Glu Gly Val Arg Gln Leu His Asp Ala Val Lys  
15 20 25  
GTA ACC ATG GGG CCA AGA GGC AGG AAC GTG TTG ATC CAA AAA AGC TAT 147  
Val Thr Met Gly Pro Arg Gly Arg Asn Val Leu Ile Gln Lys Ser Tyr  
30 35 40  
GGC GCT CCA AGC ATC ACT AAA GAT GGC GTG AGC GTG GCT AAA GAG ATT 195



|              |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
|--------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| AGA<br>Arg   | AAA<br>Lys | GAA<br>Glu | ATG<br>Met | CTC<br>Leu | AAA<br>Lys | GAC<br>Asp | ATC<br>Ile | GCT<br>Ala | ATT<br>Ile | TTA<br>Leu | ACC<br>Thr | GGC<br>Gly | GGT<br>Gly | CAA<br>Gln | GTT<br>Val | 915  |
| 285290295    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| ATT<br>Ile   | AGC<br>Ser | GAA<br>Glu | GAA<br>Glu | TTG<br>Leu | GGC<br>Gly | TTG<br>Leu | AGT<br>Ser | CTA<br>Leu | GAA<br>Glu | AAC<br>Asn | GCT<br>Ala | GAA<br>Glu | GTG<br>Val | GAG<br>Glu | TTT<br>Phe | 963  |
| 300305310315 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| TTA<br>Leu   | GGC<br>Gly | AAA<br>Lys | GCC<br>Ala | GGA<br>Gly | AGG<br>Arg | ATT<br>Ile | GTG<br>Val | ATT<br>Ile | GAC<br>Asp | AAA<br>Lys | GAC<br>Asp | AAC<br>Asn | ACC<br>Thr | ACG<br>Thr | ATC<br>Ile | 1011 |
| 320325330    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GTA<br>Val   | GAT<br>Asp | GGC<br>Gly | AAA<br>Lys | GGC<br>Gly | CAT<br>His | AGC<br>Ser | CAT<br>His | GAT<br>Asp | GTC<br>Val | AAA<br>Lys | GAC<br>Asp | AGA<br>Arg | GTC<br>Val | GCG<br>Ala | CAA<br>Gln | 1059 |
| 335340345    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| ATC<br>Ile   | AAA<br>Lys | ACC<br>Thr | CAA<br>Gln | ATT<br>Ile | GCA<br>Ala | AGC<br>Ser | ACG<br>Thr | ACA<br>Thr | AGC<br>Ser | GAT<br>Asp | TAT<br>Tyr | GAC<br>Asp | AAA<br>Lys | GAA<br>Glu | AAA<br>Lys | 1107 |
| 350355360    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| TTG<br>Leu   | CAA<br>Gln | GAA<br>Glu | AGG<br>Arg | TTG<br>Leu | GCT<br>Ala | AAA<br>Lys | CTC<br>Leu | TCT<br>Ser | GGC<br>Gly | GGT<br>Gly | GTG<br>Val | GCT<br>Ala | GTG<br>Val | ATT<br>Ile | AAA<br>Lys | 1155 |
| 365370375    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GTG<br>Val   | GGC<br>Gly | GCT<br>Ala | GCG<br>Ala | AGT<br>Ser | GAA<br>Glu | GTG<br>Val | GAA<br>Glu | ATG<br>Met | AAA<br>Lys | GAG<br>Glu | AAA<br>Lys | AAA<br>Lys | GAC<br>Asp | CGG<br>Arg | GTT<br>Val | 1203 |
| 380385390395 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GAT<br>Asp   | GAT<br>Asp | GCG<br>Ala | TTG<br>Leu | AGC<br>Ser | GCG<br>Ala | ACT<br>Thr | AAA<br>Lys | GCG<br>Ala | GCT<br>Ala | GTT<br>Val | GAA<br>Glu | GAA<br>Glu | GGT<br>Gly | ATT<br>Ile | GTG<br>Val | 1251 |
| 400405410    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| ATT<br>Ile   | GGC<br>Gly | GGC<br>Gly | GGT<br>Gly | GCG<br>Ala | GCT<br>Ala | CTC<br>Leu | ATT<br>Ile | CGC<br>Arg | GCG<br>Ala | GCT<br>Ala | CAA<br>Gln | AAA<br>Lys | GTG<br>Val | CAT<br>His | TTG<br>Leu | 1299 |
| 415420425    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| AAT<br>Asn   | TTG<br>Leu | CAC<br>His | GAT<br>Asp | GAT<br>Asp | GAA<br>Glu | AAA<br>Lys | GTG<br>Val | GGC<br>Gly | TAT<br>Tyr | GAA<br>Glu | ATC<br>Ile | ATC<br>Ile | ATG<br>Met | CGC<br>Arg | GCC<br>Ala | 1347 |
| 430435440    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| ATT<br>Ile   | AAA<br>Lys | GCC<br>Ala | CCA<br>Pro | TTA<br>Leu | GCT<br>Ala | CAA<br>Gln | ATC<br>Ile | GCT<br>Ala | ATC<br>Ile | AAT<br>Asn | GCC<br>Ala | GGT<br>Gly | TAT<br>Tyr | GAT<br>Asp | GGC<br>Gly | 1395 |
| 445450455    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GGT<br>Gly   | GTG<br>Val | GTC<br>Val | GTG<br>Val | AAT<br>Asn | GAA<br>Glu | GTA<br>Val | GAA<br>Glu | AAA<br>Lys | CAC<br>His | GAA<br>Glu | GGG<br>Gly | CAT<br>His | TTT<br>Phe | GGT<br>Gly | TTT<br>Phe | 1443 |
| 460465470475 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| AAC<br>Asn   | GCT<br>Ala | AGC<br>Ser | AAT<br>Asn | GGC<br>Gly | AAG<br>Lys | TAT<br>Tyr | GTG<br>Val | GAT<br>Asp | ATG<br>Met | TTT<br>Phe | AAA<br>Lys | GAA<br>Glu | GGC<br>Gly | ATT<br>Ile | ATT<br>Ile | 1491 |
| 480485490    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GAC<br>Asp   | CCC<br>Pro | TTA<br>Leu | AAA<br>Lys | GTA<br>Val | GAA<br>Glu | AGG<br>Arg | ATC<br>Ile | GCT<br>Ala | TTA<br>Leu | CAA<br>Gln | AAT<br>Asn | GCG<br>Ala | GTT<br>Val | TCG<br>Ser | GTT<br>Val | 1539 |
| 495500505    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| TCA<br>Ser   | AGC<br>Ser | CTG<br>Leu | CTT<br>Leu | TTA<br>Leu | ACC<br>Thr | ACA<br>Thr | GAA<br>Glu | GCC<br>Ala | ACC<br>Thr | GTG<br>Val | CAT<br>His | GAA<br>Glu | ATC<br>Ile | AAA<br>Lys | GAA<br>Glu | 1587 |











Ile Val Glu  
275

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 40...300
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AGCTCCGAGT TTAGCGAATT GGTTCATGGG AATTTTATA ATG ATT ATC CTG TCA  | 54  |
| Met Ile Ile Leu Ser                                             |     |
| 1 5                                                             |     |
| GCG AGC GTG AAG AAT TTG CGT GAA ATT TCG GTT AAA GAA AAA TTT TTA | 102 |
| Ala Ser Val Lys Asn Leu Arg Glu Ile Ser Val Lys Glu Lys Phe Leu |     |
| 10 15 20                                                        |     |
| TGG CTG AAC GCT AAG TCT TAT TTG ATT TCT GTT TTT GCG CCT TTT ATC | 150 |
| Trp Leu Asn Ala Lys Ser Tyr Leu Ile Ser Val Phe Ala Pro Phe Ile |     |
| 25 30 35                                                        |     |
| TTG CTC CCT TGG ATT GAT TTG TTG AGC GCT TTT TTA TTG TAT TTA GGG | 198 |
| Leu Leu Pro Trp Ile Asp Leu Leu Ser Ala Phe Leu Leu Tyr Leu Gly |     |
| 40 45 50                                                        |     |
| TTT TTA GCG CTC TTT AGC GTG CTG GAA TTT TTT GAT GAA GAC ATT GCA | 246 |
| Phe Leu Ala Leu Phe Ser Val Leu Glu Phe Phe Asp Glu Asp Ile Ala |     |
| 55 60 65                                                        |     |
| GAT ATT ATC GTG GCT AAA AGC AAA ATA AAG ACT AAA ACC AAA TGT TAT | 294 |
| Asp Ile Ile Val Ala Lys Ser Lys Ile Lys Thr Lys Thr Lys Cys Tyr |     |
| 70 75 80 85                                                     |     |
| AGA GCG TAGAATGTTA GAAAAGCTTT TAAGCGCTAT CAAACAA                | 337 |
| Arg Ala                                                         |     |

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

```
Met Ile Ile Leu Ser Ala Ser Val Lys Asn Leu Arg Glu Ile Ser Val
 1 5 10 15
Lys Glu Lys Phe Leu Trp Leu Asn Ala Lys Ser Tyr Leu Ile Ser Val
 20 25 30
Phe Ala Pro Phe Ile Leu Leu Pro Trp Ile Asp Leu Leu Ser Ala Phe
 35 40 45
Leu Leu Tyr Leu Gly Phe Leu Ala Leu Phe Ser Val Leu Glu Phe Phe
 50 55 60
Asp Glu Asp Ile Ala Asp Ile Ile Val Ala Lys Ser Lys Ile Lys Thr
65 70 75 80
Lys Thr Lys Cys Tyr Arg Ala
 85
```

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1044 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 15...977
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

```
ATTAAGGGGA AGTC ATG GCT GAT AGT TTA GCG GGC ATT GAT CAA GTT ACG 50
 Met Ala Asp Ser Leu Ala Gly Ile Asp Gln Val Thr
 1 5 10

AGT TTG CAT AAA AAT AAC GAG TTA CAA TTG TTG TGT TTC AGG CTG GGT 98
Ser Leu His Lys Asn Asn Glu Leu Gln Leu Leu Cys Phe Arg Leu Gly
 15 20 25

AAA AAC AAG GAT TTG TAT GCG GTC AAT GTT TTT AAG ATC CGT GAA GTG 146
Lys Asn Lys Asp Leu Tyr Ala Val Asn Val Phe Lys Ile Arg Glu Val
 30 35 40

GTG AAA TAC CAT GGC AAT CTC ACC ATC ATT AGC CAC GAA AAC AAT TCG 194
Val Lys Tyr His Gly Asn Leu Thr Ile Ile Ser His Glu Asn Asn Ser
45 50 55 60

CTC GTT GAG GGG CTA ATC ATT ATA AGA GAA CTC ACC ATT CCC TTG ATT 242
Leu Val Glu Gly Leu Ile Ile Ile Arg Glu Leu Thr Ile Pro Leu Ile
 65 70 75

GAT ATG AAA AAA TGG TTT TAT TAT GAC AGC CAA AAC AAA AAC AAG GAT 290
Asp Met Lys Lys Trp Phe Tyr Tyr Asp Ser Gln Asn Lys Asn Lys Asp
 80 85 90
```



GAGAGCGAAC GCTTAGAAAA AAACGC

1044

## (2) INFORMATION FOR SEQ ID NO:424:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

```

Met Ala Asp Ser Leu Ala Gly Ile Asp Gln Val Thr Ser Leu His Lys
 1 5 10 15
Asn Asn Glu Leu Gln Leu Leu Cys Phe Arg Leu Gly Lys Asn Lys Asp
 20 25 30
Leu Tyr Ala Val Asn Val Phe Lys Ile Arg Glu Val Val Lys Tyr His
 35 40 45
Gly Asn Leu Thr Ile Ile Ser His Glu Asn Asn Ser Leu Val Glu Gly
 50 55 60
Leu Ile Ile Ile Arg Glu Leu Thr Ile Pro Leu Ile Asp Met Lys Lys
 65 70 75 80
Trp Phe Tyr Tyr Asp Ser Gln Asn Lys Asn Lys Asp Leu Arg Pro Tyr
 85 90 95
Arg Ile Glu Lys Glu Lys Gly Glu Asp Asp Ile Val Met Ile Cys Glu
 100 105 110
Phe Ser Arg Trp Thr Ile Gly Val Arg Ile Tyr Glu Ala Asp Arg Ile
 115 120 125
Leu Ser Lys Lys Trp Thr Glu Met Glu Gln Ser Ala Gly Leu Gly Gly
 130 135 140
Ser Ala Gly Asn Asn Lys Leu Val Ser Arg Thr Arg Tyr Phe Asp Gly
 145 150 155 160
Arg Leu Val Gln Val Val Asp Ile Glu Lys Met Leu Ile Asp Val Phe
 165 170 175
Pro Trp Ile Glu Asp Glu Lys His Asn Asp Leu Glu Thr Leu Ser Lys
 180 185 190
Ile His Ser Asn Gln Cys Val Leu Ala Asp Asp Ser Pro Ser Val
 195 200 205
Leu Lys Thr Met Gln Met Ile Leu Asp Lys Leu Gly Val Lys His Ile
 210 215 220
Asp Phe Ile Asn Gly Lys Thr Leu Leu Glu His Leu Phe Asn Pro Thr
 225 230 235 240
Thr Asp Val Ser Asn Ile Gly Leu Ile Ile Thr Asp Leu Glu Met Pro
 245 250 255
Glu Ala Ser Gly Phe Glu Val Ile Lys Gln Val Lys Asn Asn Pro Leu
 260 265 270
Thr Ser Lys Ile Pro Ile Val Val Asn Ser Ser Met Ser Gly Ser Ser
 275 280 285
Asn Glu Asp Met Ala Arg Ser Leu Lys Ala Asp Asp Phe Ile Ser Lys
 290 295 300
Ser Asn Pro Lys Asp Ile Gln Arg Val Val Lys Gln Phe Leu Glu Leu
 305 310 315 320
Ala

```

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 37...618
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

|             |                                                     |            |        |     |     |     |     |     |     |    |
|-------------|-----------------------------------------------------|------------|--------|-----|-----|-----|-----|-----|-----|----|
| ATCTGCTTAA  | ACACAAAAAA                                          | GAGTAAAATA | ACACGC | ATG | AAA | AAA | TTC | TTA | TTT | 54 |
|             |                                                     |            |        | Met | Lys | Lys | Phe | Leu | Phe |    |
|             |                                                     |            |        | 1   |     |     |     | 5   |     |    |
| AAA CAA AAA | TTT TGT GAA AGC CTG CCC AAA AGC TTT TCT AAA ACT TTG | 102        |        |     |     |     |     |     |     |    |
| Lys Gln Lys | Phe Cys Glu Ser Leu Pro Lys Ser Phe Ser Lys Thr Leu |            |        |     |     |     |     |     |     |    |
|             | 10                                                  | 15         |        |     |     |     |     |     |     |    |
| TTA GCG CTC | AGT TTG GGC TTG ATT TTA TTA GGC ATT TTT GCG CCT TTC | 150        |        |     |     |     |     |     |     |    |
| Leu Ala Leu | Ser Leu Gly Leu Ile Leu Leu Gly Ile Phe Ala Pro Phe |            |        |     |     |     |     |     |     |    |
|             | 25                                                  | 30         |        |     |     |     |     |     |     |    |
| CCT AAA GTC | CCT AAA CAG CCT AGC GTG CCT TTA ATG TTT CAT TTC ACC | 198        |        |     |     |     |     |     |     |    |
| Pro Lys Val | Pro Lys Gln Pro Ser Val Pro Leu Met Phe His Phe Thr |            |        |     |     |     |     |     |     |    |
|             | 40                                                  | 45         |        |     |     |     |     |     |     |    |
| GAG CAT TAT | GCG CGC TTT ATC CCT ACG ATT TTA TCT GTG GCG ATT CCC | 246        |        |     |     |     |     |     |     |    |
| Glu His Tyr | Ala Arg Phe Ile Pro Thr Ile Leu Ser Val Ala Ile Pro |            |        |     |     |     |     |     |     |    |
|             | 55                                                  | 60         |        |     |     |     |     |     |     |    |
| TTA ATC CAA | AGA GAT GCG GTA GGG CTT TTT CAA GTC GCT AAC GCT TCT | 294        |        |     |     |     |     |     |     |    |
| Leu Ile Gln | Arg Asp Ala Val Gly Leu Phe Gln Val Ala Asn Ala Ser |            |        |     |     |     |     |     |     |    |
|             | 75                                                  | 80         |        |     |     |     |     |     |     |    |
| ATC GCT ACA | ACC CTT CTC ACG CAC ACC ACC AAA AGA GCC TTA AAC CAT | 342        |        |     |     |     |     |     |     |    |
| Ile Ala Thr | Thr Leu Leu Thr His Thr Thr Lys Arg Ala Leu Asn His |            |        |     |     |     |     |     |     |    |
|             | 90                                                  | 95         |        |     |     |     |     |     |     |    |
| GTA ACA ATC | AAC GAT CAG CGT TTG GGC GAG CGC CCT TAT GGA GGT AAT | 390        |        |     |     |     |     |     |     |    |
| Val Thr Ile | Asn Asp Gln Arg Leu Gly Glu Arg Pro Tyr Gly Gly Asn |            |        |     |     |     |     |     |     |    |
|             | 105                                                 | 110        |        |     |     |     |     |     |     |    |
| TTC AAC ATG | CCA AGC GGG CAT TCG TCT ATG GTG GGT TTG GCG GTG GCG | 438        |        |     |     |     |     |     |     |    |
| Phe Asn Met | Pro Ser Gly His Ser Ser Met Val Gly Leu Ala Val Ala |            |        |     |     |     |     |     |     |    |
|             | 120                                                 | 125        |        |     |     |     |     |     |     |    |
| TTT TTA ATG | CGC CGC TAT TCT TTT AAA AAA TAC TTT TGG CTC TTG CCC | 486        |        |     |     |     |     |     |     |    |
| Phe Leu Met | Arg Arg Tyr Ser Phe Lys Lys Tyr Phe Trp Leu Leu Pro |            |        |     |     |     |     |     |     |    |
|             | 135                                                 | 140        |        |     |     |     |     |     |     |    |





(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 57...1040

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATTTCCCTTT GTTCGTTTAT GTTTATAAAG AAAGCAACCA GGTCAGTTTT ATCGCC ATG | 59  |
| Met                                                               |     |
| 1                                                                 |     |
| ATG GTT GTG GTG CTT TTT TGC GTT AAT GGC GCT CTT TTT TTG GCG TTA   | 107 |
| Met Val Val Val Leu Phe Cys Val Asn Gly Ala Leu Phe Leu Ala Leu   |     |
| 5 10 15                                                           |     |
| GGC TTG ATC TCT GCT TCT TTG ATG CGT TGG AGT GCG ATA GTT TTT AGC   | 155 |
| Gly Leu Ile Ser Ala Ser Leu Met Arg Trp Ser Ala Ile Val Phe Ser   |     |
| 20 25 30                                                          |     |
| CTG CTC AAT TCC GTT GCT TTC TAT TTC ATT AGC GCT TAT AAG GTG TTT   | 203 |
| Leu Leu Asn Ser Val Ala Phe Tyr Phe Ile Ser Ala Tyr Lys Val Phe   |     |
| 35 40 45                                                          |     |
| TTA AAT AAG AGC ATG ATG GGT AAT GTC TTA AAC ACC AAC ACG CAT GAA   | 251 |
| Leu Asn Lys Ser Met Met Gly Asn Val Leu Asn Thr Asn Thr His Glu   |     |
| 50 55 60 65                                                       |     |
| GTT TTA GGC TTT TTG AGC GTC AAA TTA TTC GTT TTT ATC GTT GTT TTT   | 299 |
| Val Leu Gly Phe Leu Ser Val Lys Leu Phe Val Phe Ile Val Val Phe   |     |
| 70 75 80                                                          |     |
| GGG GTG TTG CCT GGC TAT GTC ATC TAT AAA ATC CCC CTT AAA AAT TCT   | 347 |
| Gly Val Leu Pro Gly Tyr Val Ile Tyr Lys Ile Pro Leu Lys Asn Ser   |     |
| 85 90 95                                                          |     |
| TCT AAA AAA GCG CCC TTT TTA GCG ATC TTG GCG TTA GTG TTT ATC TTT   | 395 |
| Ser Lys Lys Ala Pro Phe Leu Ala Ile Leu Ala Leu Val Phe Ile Phe   |     |
| 100 105 110                                                       |     |
| ATC GCT AGC GCT TTA GCT AAC ACT AAA AAT TGG CTG TGG TTT GAC AAG   | 443 |
| Ile Ala Ser Ala Leu Ala Asn Thr Lys Asn Trp Leu Trp Phe Asp Lys   |     |
| 115 120 125                                                       |     |
| CAT GCG AAA TTC ATA GGG GGC TTA ATT TTG CCC TTC GCT TAT AGC GTG   | 491 |
| His Ala Lys Phe Ile Gly Gly Leu Ile Leu Pro Phe Ala Tyr Ser Val   |     |
| 130 135 140 145                                                   |     |
| AAC GCT TTT AGA GTG AGC GCT CTC AAA TTT TTC GCC CCC ACC ATC AAG   | 539 |
| Asn Ala Phe Arg Val Ser Ala Leu Lys Phe Phe Ala Pro Thr Ile Lys   |     |
| 150 155 160                                                       |     |
| CCG CTC CCT CTT TTT TCA CCC AAT CAT TCC CAT TCG TTT GTG GTG CTA   | 587 |
| Pro Leu Pro Leu Phe Ser Pro Asn His Ser His Ser Phe Val Val Leu   |     |







| 215 |     |     |     |     |     |     | 220 |     |     |     |     |     |     | 225 |     |      |  |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|--|--|--|--|
| GCA | AGG | ACA | CAA | GCA | TTA | AAA | GAC | ATA | ATG | AAT | ATT | GAC | AGA | GAT | TTC | 777  |  |  |  |  |  |
| Ala | Arg | Thr | Gln | Ala | Leu | Lys | Asp | Ile | Met | Asn | Ile | Asp | Arg | Asp | Phe |      |  |  |  |  |  |
|     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |     |     |      |  |  |  |  |  |
| ATT | GGT | TAT | ATT | GAA | GTG | TTA | GGG | TAT | TGG | AAA | GAC | AAC | CCT | AAA | GAC | 825  |  |  |  |  |  |
| Ile | Gly | Tyr | Ile | Glu | Val | Leu | Gly | Tyr | Trp | Lys | Asp | Asn | Pro | Lys | Asp |      |  |  |  |  |  |
|     |     | 245 |     |     |     | 250 |     |     |     |     | 255 |     |     |     |     |      |  |  |  |  |  |
| AAT | ATC | TTA | CCA | GAC | AAA | GAG | GTT | AGC | TTT | TTT | GTA | TTC | CAA | AAC | GAA | 873  |  |  |  |  |  |
| Asn | Ile | Leu | Pro | Asp | Lys | Glu | Val | Ser | Phe | Phe | Val | Phe | Gln | Asn | Glu |      |  |  |  |  |  |
| 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |     | 275 |      |  |  |  |  |  |
| CCT | AGT | AGC | ACA | TTT | GAT | TTG | AAA | AAC | CAC | TTA | TTG | ATA | TGG | GGT | AAA | 921  |  |  |  |  |  |
| Pro | Ser | Ser | Thr | Phe | Asp | Leu | Lys | Asn | His | Leu | Leu | Ile | Trp | Gly | Lys |      |  |  |  |  |  |
|     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     | 290 |     |      |  |  |  |  |  |
| CAA | TTC | AGA | CAA | GTA | GCG | ATT | TGC | TAT | GGC | GGA | CAA | TTG | ATT | GCT | AAT | 969  |  |  |  |  |  |
| Gln | Phe | Arg | Gln | Val | Ala | Ile | Cys | Tyr | Gly | Gly | Gln | Leu | Ile | Ala | Asn |      |  |  |  |  |  |
|     |     |     | 295 |     |     |     | 300 |     |     |     |     |     | 305 |     |     |      |  |  |  |  |  |
| AAG | AAT | AAG | ACT | TAT | AGG | ATA | GAT | TTG | ATA | AGT | TGC | AGA | CCT | GAT | AAT | 1017 |  |  |  |  |  |
| Lys | Asn | Lys | Thr | Tyr | Arg | Ile | Asp | Leu | Ile | Ser | Cys | Arg | Pro | Asp | Asn |      |  |  |  |  |  |
|     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |     |     |      |  |  |  |  |  |
| TTT | GGT | GAG | GTT | TGG | GCT | AAA | TTC | ACA | GGG | ATT | AAA | TTT | TCA | GTT | CCT | 1065 |  |  |  |  |  |
| Phe | Gly | Glu | Val | Trp | Ala | Lys | Phe | Thr | Gly | Ile | Lys | Phe | Ser | Val | Pro |      |  |  |  |  |  |
|     |     | 325 |     |     |     | 330 |     |     |     |     | 335 |     |     |     |     |      |  |  |  |  |  |
| AGC | GAC | TTA | CCA | CAA | GCT | CTC | ACA | CGC | ATA | AAT | GAC | AGC | GTT | TAT | ACT | 1113 |  |  |  |  |  |
| Ser | Asp | Leu | Pro | Gln | Ala | Leu | Thr | Arg | Ile | Asn | Asp | Ser | Val | Tyr | Thr |      |  |  |  |  |  |
| 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |     | 355 |      |  |  |  |  |  |
| TTT | CTC | TCT | AGG | AAT | AAA | GAG | GGT | ATC | GGT | CTT | AAT | AAA | CTC | GCT | CTC | 1161 |  |  |  |  |  |
| Phe | Leu | Ser | Arg | Asn | Lys | Glu | Gly | Ile | Gly | Leu | Asn | Lys | Leu | Ala | Leu |      |  |  |  |  |  |
|     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |     | 370 |     |      |  |  |  |  |  |
| AAT | AAA | GTC | GTT | AAG | ACA | GAA | TTA | AAA | GCG | ACT | TGT | ATG | CCC | TAT | GAT | 1209 |  |  |  |  |  |
| Asn | Lys | Val | Val | Lys | Thr | Glu | Leu | Lys | Ala | Thr | Cys | Met | Pro | Tyr | Asp |      |  |  |  |  |  |
|     |     |     | 375 |     |     |     |     | 380 |     |     |     |     | 385 |     |     |      |  |  |  |  |  |
| TAC | TCT | AAA | TTG | GGT | ATA | GAG | ACT | ATT | GGC | GAG | GAC | ATT | AGA | AGC | AAT | 1257 |  |  |  |  |  |
| Tyr | Ser | Lys | Leu | Gly | Ile | Glu | Thr | Ile | Gly | Glu | Asp | Ile | Arg | Ser | Asn |      |  |  |  |  |  |
|     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |     |     |     |      |  |  |  |  |  |
| ATT | AAA | GCA | TTA | CAG | AAA | ATG | TCT | CGT | GGG | TAT | GGA | CAC | CCT | AAA | GAG | 1305 |  |  |  |  |  |
| Ile | Lys | Ala | Leu | Gln | Lys | Met | Ser | Arg | Gly | Tyr | Gly | His | Pro | Lys | Glu |      |  |  |  |  |  |
|     |     | 405 |     |     |     | 410 |     |     |     |     | 415 |     |     |     |     |      |  |  |  |  |  |
| TTC | TTT | TTG | GAC | GCA | ATG | ATA | AAA | AAA | CAG | GAA | AAT | GCG | ATT | AAA | CGC | 1353 |  |  |  |  |  |
| Phe | Phe | Leu | Asp | Ala | Met | Ile | Lys | Lys | Gln | Glu | Asn | Ala | Ile | Lys | Arg |      |  |  |  |  |  |
| 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |     |     | 435 |      |  |  |  |  |  |
| ATA | GAA | GCA | CGA | AAA | TGT | GCG | GTA | AGC | GAT | GAC | TTC | AAA | CAA | GGT | ATG | 1401 |  |  |  |  |  |
| Ile | Glu | Ala | Arg | Lys | Cys | Ala | Val | Ser | Asp | Asp | Phe | Lys | Gln | Gly | Met |      |  |  |  |  |  |
|     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |     | 450 |     |      |  |  |  |  |  |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| AAA CGA AAC ATT AAA GTT AAT AAC CTT GTT AAA GCT ATG CGA CAA GGC   | 1449 |
| Lys Arg Asn Ile Lys Val Asn Asn Leu Val Lys Ala Met Arg Gln Gly   |      |
| 455 460 465                                                       |      |
| AAA AAA GTG AGT AGG ACA TTG ATT GCT AAA GTG CTT GCT AAC ACC ATA   | 1497 |
| Lys Lys Val Ser Arg Thr Leu Ile Ala Lys Val Leu Ala Asn Thr Ile   |      |
| 470 475 480                                                       |      |
| GAC ACC GAT GCG GGT TAT TGC TTC ATT TCG CCG ACA GAT TTA GCG ACA   | 1545 |
| Asp Thr Asp Ala Gly Tyr Cys Phe Ile Ser Pro Thr Asp Leu Ala Thr   |      |
| 485 490 495                                                       |      |
| CAA CTT GGC AAC ATC AGC CCT AGA CTA TCT AAA AGC ATA GTT ACC GCC   | 1593 |
| Gln Leu Gly Asn Ile Ser Pro Arg Leu Ser Lys Ser Ile Val Thr Ala   |      |
| 500 505 510 515                                                   |      |
| ATA GAG CAA GCA GAG GGC GTG AGA CTG AAT TAT GCG TTG ATT GAC AAA   | 1641 |
| Ile Glu Gln Ala Glu Gly Val Arg Leu Asn Tyr Ala Leu Ile Asp Lys   |      |
| 520 525 530                                                       |      |
| ATC ACC TAT AAC TCA CTC CAC AAT ATC TTA AGT TTC ATT TTT GAT ATT   | 1689 |
| Ile Thr Tyr Asn Ser Leu His Asn Ile Leu Ser Phe Ile Phe Asp Ile   |      |
| 535 540 545                                                       |      |
| GAT AAC CCT TTA AGC GAC CAA GTG TTT GAG AGA TTA GTC ATT GAA GTC   | 1737 |
| Asp Asn Pro Leu Ser Asp Gln Val Phe Glu Arg Leu Val Ile Glu Val   |      |
| 550 555 560                                                       |      |
| CCA AGA GAA GCA CTT AAA AAT GTG AAG TTG CCA CAA ATC AAA AAT GTA   | 1785 |
| Pro Arg Glu Ala Leu Lys Asn Val Lys Leu Pro Gln Ile Lys Asn Val   |      |
| 565 570 575                                                       |      |
| TTG ACT TCT CAA ATC TTT GAT GGC GCT TAC CAC TTT AAA AGT TAAACCATG | 1836 |
| Leu Thr Ser Gln Ile Phe Asp Gly Ala Tyr His Phe Lys Ser           |      |
| 580 585 590                                                       |      |
| CTCTTTATCA GCGCAACTAA CACGAATGCC GGAAAAACCA CAT                   | 1879 |

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Leu Leu Asn Tyr Asp Phe Leu Glu Phe Val Asp Glu Pro Lys Arg |  |
| 1 5 10 15                                                       |  |
| Asn Thr Ser Leu Thr Ala Ser Ile Asp Lys Ala Leu Ala Asp Arg Lys |  |
| 20 25 30                                                        |  |
| Leu Ala Arg Gln Asn Lys Pro Ser Val Arg Val Leu Gly Lys Ala Met |  |
| 35 40 45                                                        |  |
| Pro Leu Ser Lys Phe Leu Asp Ala Val Gly Asp Glu Ile Ser Arg Leu |  |
| 50 55 60                                                        |  |





Ile Asp Lys Ile Thr Tyr Asn Ser Leu His Asn Ile Leu Ser Phe Ile  
530 535 540  
Phe Asp Ile Asp Asn Pro Leu Ser Asp Gln Val Phe Glu Arg Leu Val  
545 550 555 560  
Ile Glu Val Pro Arg Glu Ala Leu Lys Asn Val Lys Leu Pro Gln Ile  
565 570 575  
Lys Asn Val Leu Thr Ser Gln Ile Phe Asp Gly Ala Tyr His Phe Lys  
580 585 590  
Ser

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1063 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...1014
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TGCTAAATTG TG ATG TTT CAC AAA GCC CTT ATT ACC TTT ATC GTT CTA TGG | 51  |
| Met Phe His Lys Ala Leu Ile Thr Phe Ile Val Leu Trp               |     |
| 1 5 10                                                            |     |
| TTT TTT TTG AAT GGC TTA GGG GCT TAT GAT TTC AAG CAT TGT CAA GCG   | 99  |
| Phe Phe Leu Asn Gly Leu Gly Ala Tyr Asp Phe Lys His Cys Gln Ala   |     |
| 15 20 25                                                          |     |
| TTT TTT AAA AAA GCG AGC CTT CAA AAA GGA GGC GTG GCT TTA AAA GAA   | 147 |
| Phe Phe Lys Lys Ala Ser Leu Gln Lys Gly Gly Val Ala Leu Lys Glu   |     |
| 30 35 40 45                                                       |     |
| TTG CCT AAA GGC GTG TAT TTG TAT TAT TCC AAA ACC TAT CCC AAA CAC   | 195 |
| Leu Pro Lys Gly Val Tyr Leu Tyr Tyr Ser Lys Thr Tyr Pro Lys His   |     |
| 50 55 60                                                          |     |
| GCC AAA GTC ATC AAA TCC GAT CCC TTT GTA GGG TTG TAT TTG TTG CAA   | 243 |
| Ala Lys Val Ile Lys Ser Asp Pro Phe Val Gly Leu Tyr Leu Leu Gln   |     |
| 65 70 75                                                          |     |
| AGC GCA CCA AGC GAG TAT GTT TAT ACC TTA AGG GAT TTA GAC AAA GAC   | 291 |
| Ser Ala Pro Ser Glu Tyr Val Tyr Thr Leu Arg Asp Leu Asp Lys Asp   |     |
| 80 85 90                                                          |     |
| GCC CTT ATA AGG CCA ATG GCT AGC ATA GGG GAT AAA GAA GCC CTA GAA   | 339 |
| Ala Leu Ile Arg Pro Met Ala Ser Ile Gly Asp Lys Glu Ala Leu Glu   |     |
| 95 100 105                                                        |     |
| ACG CGA TTA TTG GTG GGG CAA AGA GGC TAT GAG CGC TAC GCT CAA ATT   | 387 |

|     |     |     |       |     |       |     |     |     |       |      |     |      |     |     |     |
|-----|-----|-----|-------|-----|-------|-----|-----|-----|-------|------|-----|------|-----|-----|-----|
| Thr | Arg | Leu | Val   | Gly | Gln   | Arg | Gly | Tyr | Glu   | Arg  | Tyr | Ala  | Gln | Ile |     |
| 110 |     |     |       | 115 |       |     |     |     | 120   |      |     |      |     | 125 |     |
| TCG | CAA | AAG | ACT   | CAA | AAA   | AAT | GGC | GTT | ATC   | AGC  | AAT | ATT  | TGC | TAT | CAA |
| Ser | Gln | Lys | Thr   | Gln | Lys   | Asn | Gly | Val | Ile   | Ser  | Asn | Ile  | Cys | Tyr | Gln |
|     |     |     |       | 130 |       |     |     |     | 135   |      |     |      |     | 140 |     |
| ATG | TTA | GGG | CTA   | GGG | GTA   | GGG | GGG | AAT | GGC   | TTT  | ATA | GAA  | ACG | AAA | TTT |
| Met | Leu | Gly | Leu   | Gly | Val   | Gly | Gly | Asn | Gly   | Phe  | Ile | Glu  | Thr | Lys | Phe |
|     |     |     |       | 145 |       |     |     |     | 150   |      |     |      | 155 |     |     |
| ATC | AAG | CGC | TTT   | TTA | AAC   | CAG | CAA | GAG | CCT   | TAT  | TAT | GGG  | GAT | ATT | GGG |
| Ile | Lys | Arg | Phe   | Leu | Asn   | Gln | Gln | Glu | Pro   | Tyr  | Tyr | Gly  | Asp | Ile | Gly |
|     |     |     |       | 160 |       |     |     | 165 |       |      |     | 170  |     |     |     |
| GTG | CGT | TTA | GAA   | GAA | CAT   | CAT | AAG | CGT | TTA   | GTG  | GTA | GTG  | CAA | TTT | GAT |
| Val | Arg | Leu | Glu   | Glu | His   | His | Lys | Arg | Leu   | Val  | Val | Val  | Gln | Phe | Asp |
|     |     |     |       | 175 |       |     | 180 |     |       |      | 185 |      |     |     |     |
| CCA | TTT | TTC | CCT   | AAA | AAC   | CCT | TTT | TTA | AAA   | AAC  | GAT | GAA  | ATC | CTA | GCG |
| Pro | Phe | Phe | Pro   | Lys | Asn   | Pro | Phe | Leu | Lys   | Asn  | Asp | Glu  | Ile | Leu | Ala |
|     |     |     |       |     | 195   |     |     |     |       | 200  |     |      |     |     | 205 |
| ATC | AAC | CAT | CAA   | AAG | ATC   | CAC | TCA | TTA | GCG   | GAG  | TTT | GAA  | TGG | GTG | GTG |
| Ile | Asn | His | Gln   | Lys | Ile   | His | Ser | Leu | Ala   | Glu  | Phe | Glu  | Trp | Val | Val |
|     |     |     |       | 210 |       |     |     |     | 215   |      |     |      |     | 220 |     |
| AGC | AAT | CTT | AAA   | TAC | CAA   | AGC | CTT | GCA | AAA   | GTG  | GAA | ATC  | AAA | CGA | AAC |
| Ser | Asn | Leu | Lys   | Tyr | Gln   | Ser | Leu | Ala | Lys   | Val  | Glu | Ile  | Lys | Arg | Asn |
|     |     |     |       | 225 |       |     |     | 230 |       |      |     |      | 235 |     |     |
| CAT | AAA | GTC | AAA   | GAA | GTA   | ACG | CTC | AAA | GTC   | AAT  | AAG | CGT  | TAT | GGG | GGG |
| His | Lys | Val | Lys   | Glu | Val   | Thr | Leu | Lys | Val   | Asn  | Lys | Arg  | Tyr | Gly | Gly |
|     |     |     |       | 240 |       |     |     | 245 |       |      |     | 250  |     |     |     |
| TTT | TTA | CTC | AAA   | GAC | ACT   | TTT | TTA | GAG | CGC   | TAT  | GGC | ATC  | GCT | TTA | GAT |
| Phe | Leu | Leu | Lys   | Asp | Thr   | Phe | Leu | Glu | Arg   | Tyr  | Gly | Ile  | Ala | Leu | Asp |
|     |     |     |       | 255 |       |     | 260 |     |       |      | 265 |      |     |     |     |
| GAG | CGT | TTT | ATT   | ATC | ACT   | AAA | ATA | GGC | GCT   | CAT  | TTG | CCC  | AAA | GGC | TTG |
| Glu | Arg | Phe | Ile   | Ile | Thr   | Lys | Ile | Gly | Ala   | His  | Leu | Pro  | Lys | Gly | Leu |
|     |     |     |       |     | 275   |     |     |     |       | 280  |     |      |     |     | 285 |
| GAT | TTT | TTA | AAG   | CTT | GGG   | GAT | AGG | ATT | TTA   | TGG  | GTG | AAT  | TAT | AAA | AGC |
| Asp | Phe | Leu | Lys   | Leu | Gly   | Asp | Arg | Ile | Leu   | Trp  | Val | Asn  | Tyr | Lys | Ser |
|     |     |     |       | 290 |       |     |     |     | 295   |      |     |      |     | 300 |     |
| GTG | GCG | TCC | AAC   | CCA | AAG   | GCT | TTA | AGA | GAA   | GCG  | TTA | AGC  | GCG | CCT | AAA |
| Val | Ala | Ser | Asn   | Pro | Lys   | Ala | Leu | Arg | Glu   | Ala  | Leu | Ser  | Ala | Pro | Lys |
|     |     |     |       | 305 |       |     |     | 310 |       |      |     |      | 315 |     |     |
| ATT | GAA | TTA | TTA   | GTC | TTG   | CGT | AAA | GGC | TTT   | GAA  | TTT | TAC  | ATT | AAA | GTC |
| Ile | Glu | Leu | Leu   | Val | Leu   | Arg | Lys | Gly | Phe   | Glu  | Phe | Tyr  | Ile | Lys | Val |
|     |     |     |       | 320 |       |     | 325 |     |       |      |     | 330  |     |     |     |
| CGT | TGA | AGT | TATTG | ATG | AAAAA | ATG | ACG | CTT | TATGA | AATT | ATT | CCTT |     |     |     |

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | His | Lys | Ala | Leu | Ile | Thr | Phe | Ile | Val | Leu | Trp | Phe | Phe | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Gly | Leu | Gly | Ala | Tyr | Asp | Phe | Lys | His | Cys | Gln | Ala | Phe | Phe | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Ala | Ser | Leu | Gln | Lys | Gly | Gly | Val | Ala | Leu | Lys | Glu | Leu | Pro | Lys |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Gly | Val | Tyr | Leu | Tyr | Tyr | Ser | Lys | Thr | Tyr | Pro | Lys | His | Ala | Lys | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Lys | Ser | Asp | Pro | Phe | Val | Gly | Leu | Tyr | Leu | Leu | Gln | Ser | Ala | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Glu | Tyr | Val | Tyr | Thr | Leu | Arg | Asp | Leu | Asp | Lys | Asp | Ala | Leu | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Pro | Met | Ala | Ser | Ile | Gly | Asp | Lys | Glu | Ala | Leu | Glu | Thr | Arg | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Val | Gly | Gln | Arg | Gly | Tyr | Glu | Arg | Tyr | Ala | Gln | Ile | Ser | Gln | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Gln | Lys | Asn | Gly | Val | Ile | Ser | Asn | Ile | Cys | Tyr | Gln | Met | Leu | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Gly | Val | Gly | Gly | Asn | Gly | Phe | Ile | Glu | Thr | Lys | Phe | Ile | Lys | Arg |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Phe | Leu | Asn | Gln | Gln | Glu | Pro | Tyr | Tyr | Gly | Asp | Ile | Gly | Val | Arg | Leu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Glu | His | His | Lys | Arg | Leu | Val | Val | Val | Gln | Phe | Asp | Pro | Phe | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Pro | Lys | Asn | Pro | Phe | Leu | Lys | Asn | Asp | Glu | Ile | Leu | Ala | Ile | Asn | His |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gln | Lys | Ile | His | Ser | Leu | Ala | Glu | Phe | Glu | Trp | Val | Val | Ser | Asn | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Tyr | Gln | Ser | Leu | Ala | Lys | Val | Glu | Ile | Lys | Arg | Asn | His | Lys | Val |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Lys | Glu | Val | Thr | Leu | Lys | Val | Asn | Lys | Arg | Tyr | Gly | Gly | Phe | Leu | Leu |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Lys | Asp | Thr | Phe | Leu | Glu | Arg | Tyr | Gly | Ile | Ala | Leu | Asp | Glu | Arg | Phe |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ile | Ile | Thr | Lys | Ile | Gly | Ala | His | Leu | Pro | Lys | Gly | Leu | Asp | Phe | Leu |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Lys | Leu | Gly | Asp | Arg | Ile | Leu | Trp | Val | Asn | Tyr | Lys | Ser | Val | Ala | Ser |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asn | Pro | Lys | Ala | Leu | Arg | Glu | Ala | Leu | Ser | Ala | Pro | Lys | Ile | Glu | Leu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Leu | Val | Leu | Arg | Lys | Gly | Phe | Glu | Phe | Tyr | Ile | Lys | Val | Arg |     |     |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:433:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1133 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:  
 (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 52...1104  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| TAGTCTTGCG TAAAGGCTTT GAATTTTACA TTAAAGTCCG TTGAAGTATT G ATG AAA | 57  |
| Met Lys                                                          |     |
| 1                                                                |     |
| AAT GAC GCT TAT GAA ATT ATT CTT TCT TGG TTT ATC ACG CCT CTC ACG  | 105 |
| Asn Asp Ala Tyr Glu Ile Ile Leu Ser Trp Phe Ile Thr Pro Leu Thr  |     |
| 5 10 15                                                          |     |
| GCG ATT TTA GGG CGT TTC GCT GAA TTT TTT CTC TAC ACT TTG CAT GCG  | 153 |
| Ala Ile Leu Gly Arg Phe Ala Glu Phe Phe Leu Tyr Thr Leu His Ala  |     |
| 20 25 30                                                         |     |
| CAA TTG GTG TTT AAT AGC GTG GTC GCT TTG GCG TTC ATG CTC TTT GCT  | 201 |
| Gln Leu Val Phe Asn Ser Val Val Ala Leu Ala Phe Met Leu Phe Ala  |     |
| 35 40 45 50                                                      |     |
| TAT AGG AGT TTG AAA GAA CAG AAT TTC TTC AGC GCT AGC GCG CTA ACA  | 249 |
| Tyr Arg Ser Leu Lys Glu Gln Asn Phe Phe Ser Ala Ser Ala Leu Thr  |     |
| 55 60 65                                                         |     |
| GAA GCG TTA TTG TTT GTG GGG TTT TTT GCA CTT TTC AAC TAC GCT TTA  | 297 |
| Glu Ala Leu Leu Phe Val Gly Phe Phe Ala Leu Phe Asn Tyr Ala Leu  |     |
| 70 75 80                                                         |     |
| AAA AAT CCC ATG CAT TTT TAT GAA TTT TTC CAA AAC GCT ATT TTT ATT  | 345 |
| Lys Asn Pro Met His Phe Tyr Glu Phe Phe Gln Asn Ala Ile Phe Ile  |     |
| 85 90 95                                                         |     |
| GCG CCT AAC ATG ATC GCG CAA AGC CTC TCT CAA AGC TTG AGT AAC TTT  | 393 |
| Ala Pro Asn Met Ile Ala Gln Ser Leu Ser Gln Ser Leu Ser Asn Phe  |     |
| 100 105 110                                                      |     |
| TCT GAC CAT GCG CTT TCT TTA GAT TTT ATC TTT AAT CAT GGT TTT TAT  | 441 |
| Ser Asp His Ala Leu Ser Leu Asp Phe Ile Phe Asn His Gly Phe Tyr  |     |
| 115 120 125 130                                                  |     |
| GCC CTT AGT TTC ATC AGC GAT TTG AGC CAT AAT GAA ATG TCT GTG TGG  | 489 |
| Ala Leu Ser Phe Ile Ser Asp Leu Ser His Asn Glu Met Ser Val Trp  |     |
| 135 140 145                                                      |     |
| CTT TTT TTA AGC GTT TTG CAA GGG CTT TTT TTG AGC GTG CTG TTT GCA  | 537 |
| Leu Phe Leu Ser Val Leu Gln Gly Leu Phe Leu Ser Val Leu Phe Ala  |     |

| 150                |     |     |     |     |     |     |     |     |     | 155 |     |     |            |     |      |      |  |  |  | 160 |  |  |  |  |  |  |  |  |  |
|--------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------------|-----|------|------|--|--|--|-----|--|--|--|--|--|--|--|--|--|
| ATC                | ATC | ATT | TTA | GTG | TAT | TTA | GAA | GTG | CAT | GTG | TGG | TGC | TCT        | TTA | GGG  | 585  |  |  |  |     |  |  |  |  |  |  |  |  |  |
| Ile                | Ile | Ile | Leu | Val | Tyr | Leu | Glu | Val | His | Val | Trp | Cys | Ser        | Leu | Gly  |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
| 165                |     |     |     |     |     |     | 170 |     |     |     |     |     |            | 175 |      |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
| GTG                | CTG | TTT | TTA | GCG | TTT | GGG | TTT | TTT | AAA | ACC | TGG | AGG | AGC        | GTT | GTG  | 633  |  |  |  |     |  |  |  |  |  |  |  |  |  |
| Val                | Leu | Phe | Leu | Ala | Phe | Gly | Phe | Phe | Lys | Thr | Trp | Arg | Ser        | Val | Val  |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
| 180                |     |     |     |     |     |     | 185 |     |     |     |     |     |            | 190 |      |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
| GTT                | ATA | TGC | CTA | AAA | AAG | TGC | TTC | GCT | CTT | GGG | TTT | TAC | AAG        | CCT | TTT  | 681  |  |  |  |     |  |  |  |  |  |  |  |  |  |
| Val                | Ile | Cys | Leu | Lys | Lys | Cys | Phe | Ala | Leu | Gly | Phe | Tyr | Lys        | Pro | Phe  |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
| 195                |     |     |     |     |     |     | 200 |     |     |     |     |     |            | 205 |      |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
| TTG                | TTG | TTG | GTA | GGG | TTT | TTG | AAT | GTG | TCG | GTT | ACT | AAG | GCT        | TTA | ATA  | 729  |  |  |  |     |  |  |  |  |  |  |  |  |  |
| Leu                | Leu | Leu | Val | Gly | Phe | Leu | Asn | Val | Ser | Val | Thr | Lys | Ala        | Leu | Ile  |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
|                    |     |     |     |     |     |     | 215 |     |     |     |     |     |            | 225 |      |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
| GAC                | GCT | CAT | ATG | CAA | GAA | AAA | CAA | GAC | TTA | AGC | CTT | TTA | TTG        | GTG | GTA  | 777  |  |  |  |     |  |  |  |  |  |  |  |  |  |
| Asp                | Ala | His | Met | Gln | Glu | Lys | Gln | Asp | Leu | Ser | Leu | Leu | Val        | Val |      |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
| 230                |     |     |     |     |     |     | 235 |     |     |     |     |     |            | 240 |      |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
| GCG                | TTA | TTT | TTG | TGT | TGC | GTT | TTT | ATC | ATC | GGC | GTG | CCT | TTT        | TTC | ATC  | 825  |  |  |  |     |  |  |  |  |  |  |  |  |  |
| Ala                | Leu | Phe | Leu | Cys | Cys | Val | Phe | Ile | Ile | Gly | Val | Pro | Phe        | Phe | Ile  |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
| 245                |     |     |     |     |     |     | 250 |     |     |     |     |     |            | 255 |      |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
| AAC                | GCT | TTG | TTT | AGG | GTG | CAA | AAC | AGC | CTT | AAA | GAA | ACT | TAC        | AAA | CTC  | 873  |  |  |  |     |  |  |  |  |  |  |  |  |  |
| Asn                | Ala | Leu | Phe | Arg | Val | Gln | Asn | Ser | Leu | Lys | Glu | Thr | Tyr        | Lys | Leu  |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
| 260                |     |     |     |     |     |     | 265 |     |     |     |     |     |            | 270 |      |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
| GCC                | ACC | AAT | TTG | AGT | GCC | AAC | CTC | AGC | CAA | AAC | GCC | CTT | AAT        | TCC | TTA  | 921  |  |  |  |     |  |  |  |  |  |  |  |  |  |
| Ala                | Thr | Asn | Leu | Ser | Ala | Asn | Leu | Ser | Gln | Asn | Ala | Leu | Asn        | Ser | Leu  |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
| 275                |     |     |     |     |     |     | 280 |     |     |     |     |     |            | 285 |      |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
| CAA                | TAC | ATC | ACG | ACC | CCA | CCC | GCT | TCT | TCT | AGC | GTT | TCT | TCT        | TCT | ATG  | 969  |  |  |  |     |  |  |  |  |  |  |  |  |  |
| Gln                | Tyr | Ile | Thr | Thr | Pro | Pro | Ala | Ser | Ser | Ser | Val | Ser | Ser        | Ser | Met  |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
| 295                |     |     |     |     |     |     | 300 |     |     |     |     |     |            | 305 |      |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
| AGT                | GAA | AGC | GTC | TCT | AAA | GAA | AAA | GAA | ACG | CAT | TCC | CCC | ACA        | TTT | AAG  | 1017 |  |  |  |     |  |  |  |  |  |  |  |  |  |
| Ser                | Glu | Ser | Val | Ser | Lys | Glu | Lys | Glu | Thr | His | Ser | Pro | Thr        | Phe | Lys  |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
| 310                |     |     |     |     |     |     | 315 |     |     |     |     |     |            | 320 |      |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
| GTA                | GAA | ACC | ACT | CAA | TTA | GAT | GTA | AAA | ATC | CCA | AAT | TTC | AAG        | CAA | AAA  | 1065 |  |  |  |     |  |  |  |  |  |  |  |  |  |
| Val                | Glu | Thr | Thr | Gln | Leu | Asp | Val | Lys | Ile | Pro | Asn | Phe | Lys        | Gln | Lys  |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
| 325                |     |     |     |     |     |     | 330 |     |     |     |     |     |            | 335 |      |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
| AAG                | GTT | AAA | AAG | GAT | ACA | ATA | AAT | ACA | AAA | AAT | GAA | ATT | TAAATAAATA | GG  | 1116 |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
| Lys                | Val | Lys | Lys | Asp | Thr | Ile | Asn | Thr | Lys | Asn | Glu | Ile |            |     |      |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
| 340                |     |     |     |     |     |     | 345 |     |     |     |     |     |            | 350 |      |      |  |  |  |     |  |  |  |  |  |  |  |  |  |
| AATTTAATGA GAATTTT |     |     |     |     |     |     |     |     |     |     |     |     |            |     |      | 1133 |  |  |  |     |  |  |  |  |  |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

Met Lys Asn Asp Ala Tyr Glu Ile Ile Leu Ser Trp Phe Ile Thr Pro  
1 5 10 15  
Leu Thr Ala Ile Leu Gly Arg Phe Ala Glu Phe Phe Leu Tyr Thr Leu  
20 25 30  
His Ala Gln Leu Val Phe Asn Ser Val Val Ala Leu Ala Phe Met Leu  
35 40 45  
Phe Ala Tyr Arg Ser Leu Lys Glu Gln Asn Phe Phe Ser Ala Ser Ala  
50 55 60  
Leu Thr Glu Ala Leu Leu Phe Val Gly Phe Phe Ala Leu Phe Asn Tyr  
65 70 75 80  
Ala Leu Lys Asn Pro Met His Phe Tyr Glu Phe Phe Gln Asn Ala Ile  
85 90 95  
Phe Ile Ala Pro Asn Met Ile Ala Gln Ser Leu Ser Gln Ser Leu Ser  
100 105 110  
Asn Phe Ser Asp His Ala Leu Ser Leu Asp Phe Ile Phe Asn His Gly  
115 120 125  
Phe Tyr Ala Leu Ser Phe Ile Ser Asp Leu Ser His Asn Glu Met Ser  
130 135 140  
Val Trp Leu Phe Leu Ser Val Leu Gln Gly Leu Phe Leu Ser Val Leu  
145 150 155 160  
Phe Ala Ile Ile Ile Leu Val Tyr Leu Glu Val His Val Trp Cys Ser  
165 170 175  
Leu Gly Val Leu Phe Leu Ala Phe Gly Phe Phe Lys Thr Trp Arg Ser  
180 185 190  
Val Val Val Ile Cys Leu Lys Lys Cys Phe Ala Leu Gly Phe Tyr Lys  
195 200 205  
Pro Phe Leu Leu Leu Val Gly Phe Leu Asn Val Ser Val Thr Lys Ala  
210 215 220  
Leu Ile Asp Ala His Met Gln Glu Lys Gln Asp Leu Ser Leu Leu Leu  
225 230 235 240  
Val Val Ala Leu Phe Leu Cys Cys Val Phe Ile Ile Gly Val Pro Phe  
245 250 255  
Phe Ile Asn Ala Leu Phe Arg Val Gln Asn Ser Leu Lys Glu Thr Tyr  
260 265 270  
Lys Leu Ala Thr Asn Leu Ser Ala Asn Leu Ser Gln Asn Ala Leu Asn  
275 280 285  
Ser Leu Gln Tyr Ile Thr Thr Pro Pro Ala Ser Ser Ser Val Ser Ser  
290 295 300  
Ser Met Ser Glu Ser Val Ser Lys Glu Lys Glu Thr His Ser Pro Thr  
305 310 315 320  
Phe Lys Val Glu Thr Thr Gln Leu Asp Val Lys Ile Pro Asn Phe Lys  
325 330 335  
Gln Lys Lys Val Lys Lys Asp Thr Ile Asn Thr Lys Asn Glu Ile  
340 345 350

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 777 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 50...748  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

|                                                                 |             |     |
|-----------------------------------------------------------------|-------------|-----|
| CCCTTTCAAA CAAGGCCCTA AAAATTACGA AGAAAACCTG ATTTTCCCC           | ATG GAT AAC | 58  |
|                                                                 | Met Asp Asn |     |
|                                                                 | 1           |     |
| CCT AAA GGC ATT GAT GGT TTT ACT AAC CTT AAA GAA AAA GAC ATC GCC |             | 106 |
| Pro Lys Gly Ile Asp Gly Phe Thr Asn Leu Lys Glu Lys Asp Ile Ala |             |     |
| 5 10 15                                                         |             |     |
| ACT AAT GAA AAT AAG CTT TTA CGC ACC ATT ACA GCG GAT AAA ATG ATA |             | 154 |
| Thr Asn Glu Asn Lys Leu Leu Arg Thr Ile Thr Ala Asp Lys Met Ile |             |     |
| 20 25 30 35                                                     |             |     |
| CCC GCC TTT CTC ATC ACG CCT ATT TCT AGC CAG ATC GCT GGT AAA GTC |             | 202 |
| Pro Ala Phe Leu Ile Thr Pro Ile Ser Ser Gln Ile Ala Gly Lys Val |             |     |
| 40 45 50                                                        |             |     |
| ATC GCG CAG GTG GAG AGC GAT ATT TTT GCT CAC ATG GGC AAG GCC GTC |             | 250 |
| Ile Ala Gln Val Glu Ser Asp Ile Phe Ala His Met Gly Lys Ala Val |             |     |
| 55 60 65                                                        |             |     |
| TTA ATC CCC AAA GGC TCT AAA GTC ATA GGT TAT TAC AGC AAC AAT AAC |             | 298 |
| Leu Ile Pro Lys Gly Ser Lys Val Ile Gly Tyr Tyr Ser Asn Asn Asn |             |     |
| 70 75 80                                                        |             |     |
| AAA ATG GGC GAA TAC CGC TTG GAT ATT GTA TGG AGC CGC ATC ATC ACT |             | 346 |
| Lys Met Gly Glu Tyr Arg Leu Asp Ile Val Trp Ser Arg Ile Ile Thr |             |     |
| 85 90 95                                                        |             |     |
| CCC CAT GGC ATC AAT ATC ATG CTC ACT AAC GCT AAA GGG GCG GAC ATT |             | 394 |
| Pro His Gly Ile Asn Ile Met Leu Thr Asn Ala Lys Gly Ala Asp Ile |             |     |
| 100 105 110 115                                                 |             |     |
| AAA GGC TAT AAC GGC TTG GTG GGG GAA TTG ATT GAA AGG AAT TTC CAG |             | 442 |
| Lys Gly Tyr Asn Gly Leu Val Gly Glu Leu Ile Glu Arg Asn Phe Gln |             |     |
| 120 125 130                                                     |             |     |
| CGC TAT GGC GTG CCG TTA CTG CTT TCT ACT CTC ACT AAC GGC CTA TTG |             | 490 |
| Arg Tyr Gly Val Pro Leu Leu Leu Ser Thr Leu Thr Asn Gly Leu Leu |             |     |
| 135 140 145                                                     |             |     |
| ATT GGG ATC ACT TCG GCT TTA AAC AAC AGA GGC AAT AAA GAA GGA GCC |             | 538 |
| Ile Gly Ile Thr Ser Ala Leu Asn Asn Arg Gly Asn Lys Glu Gly Ala |             |     |
| 150 155 160                                                     |             |     |
| ACC AAT TTC TTT GGG GAT TAT CTT TTA ATG CAA TTG ATG AGG CAA AGC |             | 586 |
| Thr Asn Phe Phe Gly Asp Tyr Leu Leu Met Gln Leu Met Arg Gln Ser |             |     |
| 165 170 175                                                     |             |     |

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GGC ATG GGG ATC AAT CAA GTA GTC AAT CAA ATT TTA AGA GAT AAG AGC | 634 |
| Gly Met Gly Ile Asn Gln Val Val Asn Gln Ile Leu Arg Asp Lys Ser |     |
| 180 185 190 195                                                 |     |
|                                                                 |     |
| AAA ATC GCT CCT ATT GTG GTG ATT AGA GAA GGG AGT AGG GTC TTC ATT | 682 |
| Lys Ile Ala Pro Ile Val Val Ile Arg Glu Gly Ser Arg Val Phe Ile |     |
| 200 205 210                                                     |     |
|                                                                 |     |
| TCG CCC AAT ACT GAC ATC TTT TTC CCT ATA CCC AGA GAG AAT GAA GTC | 730 |
| Ser Pro Asn Thr Asp Ile Phe Phe Pro Ile Pro Arg Glu Asn Glu Val |     |
| 215 220 225                                                     |     |
|                                                                 |     |
| ATC GCT GAG TTT TTG AAG TGACTCAAAA ATCCCCAATT AAAAACGCT         | 777 |
| Ile Ala Glu Phe Leu Lys                                         |     |
| 230                                                             |     |

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Asn | Pro | Lys | Gly | Ile | Asp | Gly | Phe | Thr | Asn | Leu | Lys | Glu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Ile | Ala | Thr | Asn | Glu | Asn | Lys | Leu | Leu | Arg | Thr | Ile | Thr | Ala | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Met | Ile | Pro | Ala | Phe | Leu | Ile | Thr | Pro | Ile | Ser | Ser | Gln | Ile | Ala |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Gly | Lys | Val | Ile | Ala | Gln | Val | Glu | Ser | Asp | Ile | Phe | Ala | His | Met | Gly |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Ala | Val | Leu | Ile | Pro | Lys | Gly | Ser | Lys | Val | Ile | Gly | Tyr | Tyr | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asn | Asn | Asn | Lys | Met | Gly | Glu | Tyr | Arg | Leu | Asp | Ile | Val | Trp | Ser | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Ile | Thr | Pro | His | Gly | Ile | Asn | Ile | Met | Leu | Thr | Asn | Ala | Lys | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Asp | Ile | Lys | Gly | Tyr | Asn | Gly | Leu | Val | Gly | Glu | Leu | Ile | Glu | Arg |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Phe | Gln | Arg | Tyr | Gly | Val | Pro | Leu | Leu | Leu | Ser | Thr | Leu | Thr | Asn |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Leu | Leu | Ile | Gly | Ile | Thr | Ser | Ala | Leu | Asn | Asn | Arg | Gly | Asn | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Glu | Gly | Ala | Thr | Asn | Phe | Phe | Gly | Asp | Tyr | Leu | Leu | Met | Gln | Leu | Met |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Arg | Gln | Ser | Gly | Met | Gly | Ile | Asn | Gln | Val | Val | Asn | Gln | Ile | Leu | Arg |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asp | Lys | Ser | Lys | Ile | Ala | Pro | Ile | Val | Val | Ile | Arg | Glu | Gly | Ser | Arg |
|     |     |     | 195 |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Val | Phe | Ile | Ser | Pro | Asn | Thr | Asp | Ile | Phe | Phe | Pro | Ile | Pro | Arg | Glu |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asn | Glu | Val | Ile | Ala | Glu | Phe | Leu | Lys |     |     |     |     |     |     |     |



## (2) INFORMATION FOR SEQ ID NO:437:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1229 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 27...1169  
 (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| AAATAAAATT CAATAAAGGA AAAATA ATG AAA GAA AAA ATC GCT TTA ATC ACC | 53  |
| Met Lys Glu Lys Ile Ala Leu Ile Thr                              |     |
| 1 5                                                              |     |
| GGG GTT ACC GGG CAA GAC GGG AGC TAT CTG GCT GAA TAC TTG CTG AAT  | 101 |
| Gly Val Thr Gly Gln Asp Gly Ser Tyr Leu Ala Glu Tyr Leu Leu Asn  |     |
| 10 15 20 25                                                      |     |
| TTG GGT TAT GAA GTG CAT GGG TTA AAA AGG CGC TCT TCT AGC ATC AAC  | 149 |
| Leu Gly Tyr Glu Val His Gly Leu Lys Arg Arg Ser Ser Ser Ile Asn  |     |
| 30 35 40                                                         |     |
| ACT TCT AGG ATC GAT CAT CTG TAT GAA GAT TTG CAT AGC GAT CAT AAA  | 197 |
| Thr Ser Arg Ile Asp His Leu Tyr Glu Asp Leu His Ser Asp His Lys  |     |
| 45 50 55                                                         |     |
| AGG CGT TTT TTC TTA CAC TAT GGG GAT ATG ACC GAT AGC TCT AAT CTT  | 245 |
| Arg Arg Phe Phe Leu His Tyr Gly Asp Met Thr Asp Ser Ser Asn Leu  |     |
| 60 65 70                                                         |     |
| ATC CAT TTA ATC GCT ACC ACT AAG CCT ACA GAG ATT TAT AAT TTA GCC  | 293 |
| Ile His Leu Ile Ala Thr Thr Lys Pro Thr Glu Ile Tyr Asn Leu Ala  |     |
| 75 80 85                                                         |     |
| GCT CAA AGC CAT GTA AAA GTC TCT TTT GAA ACC CCC GAA TAC ACC GCT  | 341 |
| Ala Gln Ser His Val Lys Val Ser Phe Glu Thr Pro Glu Tyr Thr Ala  |     |
| 90 95 100 105                                                    |     |
| AAC GCT GAT GGT ATT GGC ACG CTA AGG ATT TTA GAA GCC ATG CGG ATT  | 389 |
| Asn Ala Asp Gly Ile Gly Thr Leu Arg Ile Leu Glu Ala Met Arg Ile  |     |
| 110 115 120                                                      |     |
| TTA GGA TTA GAA AAG AAA ACG CGC TTT TAT CAA GCC AGC ACG AGC GAA  | 437 |
| Leu Gly Leu Glu Lys Lys Thr Arg Phe Tyr Gln Ala Ser Thr Ser Glu  |     |
| 125 130 135                                                      |     |
| TTG TAT GGC GAA GTC TTA GAA ACC CCG CAA AAT GAA AAC ACC CCC TTT  | 485 |
| Leu Tyr Gly Glu Val Leu Glu Thr Pro Gln Asn Glu Asn Thr Pro Phe  |     |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
|            | 140        |            |            |            |            | 145        |            |            |            |            | 150        |            |            |            |            |      |
| AAC<br>Asn | CCA<br>Pro | CGA<br>Arg | AGC<br>Ser | CCC<br>Pro | TAT<br>Tyr | GCG<br>Ala | GTC<br>Val | GCT<br>Ala | AAA<br>Lys | ATG<br>Met | TAT<br>Tyr | GCC<br>Ala | TTT<br>Phe | TAC<br>Tyr | ATC<br>Ile | 533  |
|            | 155        |            |            |            |            | 160        |            |            |            |            | 165        |            |            |            |            |      |
| ACC<br>Thr | AAA<br>Lys | AAT<br>Asn | TAC<br>Tyr | AGA<br>Arg | GAG<br>Glu | GCC<br>Ala | TAT<br>Tyr | AAC<br>Asn | TTG<br>Leu | TTT<br>Phe | GCG<br>Ala | GTT<br>Val | AAT<br>Asn | GGC<br>Gly | ATT<br>Ile | 581  |
| 170        |            |            |            |            | 175        |            |            |            |            | 180        |            |            |            |            | 185        |      |
| CTT<br>Leu | TTT<br>Phe | AAC<br>Asn | CAT<br>His | GAG<br>Glu | AGC<br>Ser | AGG<br>Arg | GTA<br>Val | AGG<br>Arg | GGC<br>Gly | GAA<br>Glu | ACT<br>Thr | TTT<br>Phe | GTA<br>Val | ACC<br>Thr | CGT<br>Arg | 629  |
|            |            |            |            | 190        |            |            |            |            | 195        |            |            |            |            | 200        |            |      |
| AAA<br>Lys | ATC<br>Ile | ACA<br>Thr | CGA<br>Arg | GCC<br>Ala | GCT<br>Ala | AGC<br>Ser | GCG<br>Ala | ATA<br>Ile | GCG<br>Ala | TAT<br>Tyr | AAC<br>Asn | TTA<br>Leu | ACG<br>Thr | GAT<br>Asp | TGC<br>Cys | 677  |
|            |            |            | 205        |            |            |            |            | 210        |            |            |            |            | 215        |            |            |      |
| TTG<br>Leu | TAT<br>Tyr | TTA<br>Leu | GGG<br>Gly | AAT<br>Asn | TTA<br>Leu | GAC<br>Asp | GCT<br>Ala | AAA<br>Lys | AGA<br>Arg | GAC<br>Asp | TGG<br>Trp | GGG<br>Gly | CAT<br>His | GCC<br>Ala | AAA<br>Lys | 725  |
|            |            | 220        |            |            |            | 225        |            |            |            |            |            | 230        |            |            |            |      |
| GAT<br>Asp | TAC<br>Tyr | GTG<br>Val | AAA<br>Lys | ATG<br>Met | ATG<br>Met | CAT<br>His | TTA<br>Leu | ATG<br>Met | CTC<br>Leu | CAA<br>Gln | GCG<br>Ala | CCC<br>Pro | ATC<br>Ile | CCA<br>Pro | CAA<br>Gln | 773  |
|            | 235        |            |            |            |            | 240        |            |            |            |            | 245        |            |            |            |            |      |
| GAT<br>Asp | TAT<br>Tyr | GTG<br>Val | ATC<br>Ile | GCC<br>Ala | ACA<br>Thr | GGA<br>Gly | AAG<br>Lys | ACC<br>Thr | ACA<br>Thr | AGC<br>Ser | GTG<br>Val | CGC<br>Arg | GAT<br>Asp | TTT<br>Phe | GTG<br>Val | 821  |
| 250        |            |            |            |            | 255        |            |            |            |            | 260        |            |            |            |            | 265        |      |
| AAA<br>Lys | ATG<br>Met | AGC<br>Ser | TTT<br>Phe | GAA<br>Glu | TTT<br>Phe | ATC<br>Ile | GGT<br>Gly | ATC<br>Ile | AAT<br>Asn | TTA<br>Leu | GAA<br>Glu | TTT<br>Phe | CAA<br>Gln | AAT<br>Asn | ACA<br>Thr | 869  |
|            |            |            |            | 270        |            |            |            |            | 275        |            |            |            |            | 280        |            |      |
| GGG<br>Gly | ATT<br>Ile | AAA<br>Lys | GAA<br>Glu | ATC<br>Ile | GGT<br>Gly | TTG<br>Leu | ATT<br>Ile | AAA<br>Lys | AGC<br>Ser | GTT<br>Val | GAT<br>Asp | GAA<br>Glu | AAA<br>Lys | AGA<br>Arg | GCG<br>Ala | 917  |
|            |            |            | 285        |            |            |            |            | 290        |            |            |            |            | 295        |            |            |      |
| AAC<br>Asn | GCT<br>Ala | TTA<br>Leu | AAA<br>Lys | TTG<br>Leu | AAC<br>Asn | TTA<br>Leu | AGC<br>Ser | CAT<br>His | TTA<br>Leu | AAA<br>Lys | AAA<br>Lys | GGC<br>Gly | CAA<br>Gln | ATC<br>Ile | GTG<br>Val | 965  |
|            |            | 300        |            |            |            |            | 305        |            |            |            |            | 310        |            |            |            |      |
| GTG<br>Val | CGC<br>Arg | ATA<br>Ile | GAC<br>Asp | GAG<br>Glu | CGT<br>Arg | TAT<br>Tyr | TTC<br>Phe | AGG<br>Arg | CCT<br>Pro | ACC<br>Thr | GAA<br>Glu | GTG<br>Val | GAT<br>Asp | TTG<br>Leu | CTT<br>Leu | 1013 |
|            | 315        |            |            |            |            | 320        |            |            |            |            | 325        |            |            |            |            |      |
| TTA<br>Leu | GGC<br>Gly | GAT<br>Asp | CCC<br>Pro | ACT<br>Thr | AAG<br>Lys | GCA<br>Ala | GAG<br>Glu | AAA<br>Lys | GAG<br>Glu | CTA<br>Leu | GAC<br>Asp | TGG<br>Trp | GTT<br>Val | AGG<br>Arg | GAA<br>Glu | 1061 |
| 330        |            |            |            |            | 335        |            |            |            |            | 340        |            |            |            |            | 345        |      |
| TAC<br>Tyr | GAT<br>Asp | TTA<br>Leu | AAA<br>Lys | GAG<br>Glu | TTG<br>Leu | GTT<br>Val | AAG<br>Lys | GAC<br>Asp | ATG<br>Met | TTA<br>Leu | GAA<br>Glu | TAC<br>Tyr | GAT<br>Asp | TTA<br>Leu | AAA<br>Lys | 1109 |
|            |            |            |            | 350        |            |            |            |            | 355        |            |            |            |            | 360        |            |      |
| GAA<br>Glu | TGC<br>Cys | CAA<br>Gln | AAA<br>Lys | AAC<br>Asn | CTT<br>Leu | TAC<br>Tyr | TTG<br>Leu | CAA<br>Gln | GAT<br>Asp | GGG<br>Gly | GGT<br>Gly | TAT<br>Tyr | ATT<br>Ile | TTA<br>Leu | AGG<br>Arg | 1157 |
|            |            |            | 365        |            |            |            |            | 370        |            |            |            |            | 375        |            |            |      |

AAT TTT TAT GAA TGAGATTATT TTAATCACTG GTGCCTATGG CATGGTGGGG CAGAA 1214  
Asn Phe Tyr Glu  
380

CACGGCGTTG TATTT 1229

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

```

Met Lys Glu Lys Ile Ala Leu Ile Thr Gly Val Thr Gly Gln Asp Gly
 1 5 10 15
Ser Tyr Leu Ala Glu Tyr Leu Leu Asn Leu Gly Tyr Glu Val His Gly
 20 25 30
Leu Lys Arg Arg Ser Ser Ser Ile Asn Thr Ser Arg Ile Asp His Leu
 35 40 45
Tyr Glu Asp Leu His Ser Asp His Lys Arg Arg Phe Phe Leu His Tyr
 50 55 60
Gly Asp Met Thr Asp Ser Ser Asn Leu Ile His Leu Ile Ala Thr Thr
65 70 75 80
Lys Pro Thr Glu Ile Tyr Asn Leu Ala Ala Gln Ser His Val Lys Val
 85 90 95
Ser Phe Glu Thr Pro Glu Tyr Thr Ala Asn Ala Asp Gly Ile Gly Thr
 100 105 110
Leu Arg Ile Leu Glu Ala Met Arg Ile Leu Gly Leu Glu Lys Lys Thr
 115 120 125
Arg Phe Tyr Gln Ala Ser Thr Ser Glu Leu Tyr Gly Glu Val Leu Glu
 130 135 140
Thr Pro Gln Asn Glu Asn Thr Pro Phe Asn Pro Arg Ser Pro Tyr Ala
145 150 155 160
Val Ala Lys Met Tyr Ala Phe Tyr Ile Thr Lys Asn Tyr Arg Glu Ala
 165 170 175
Tyr Asn Leu Phe Ala Val Asn Gly Ile Leu Phe Asn His Glu Ser Arg
 180 185 190
Val Arg Gly Glu Thr Phe Val Thr Arg Lys Ile Thr Arg Ala Ala Ser
 195 200 205
Ala Ile Ala Tyr Asn Leu Thr Asp Cys Leu Tyr Leu Gly Asn Leu Asp
 210 215 220
Ala Lys Arg Asp Trp Gly His Ala Lys Asp Tyr Val Lys Met Met His
225 230 235 240
Leu Met Leu Gln Ala Pro Ile Pro Gln Asp Tyr Val Ile Ala Thr Gly
 245 250 255
Lys Thr Thr Ser Val Arg Asp Phe Val Lys Met Ser Phe Glu Phe Ile
 260 265 270
Gly Ile Asn Leu Glu Phe Gln Asn Thr Gly Ile Lys Glu Ile Gly Leu
 275 280 285
Ile Lys Ser Val Asp Glu Lys Arg Ala Asn Ala Leu Lys Leu Asn Leu
 290 295 300
Ser His Leu Lys Lys Gly Gln Ile Val Val Arg Ile Asp Glu Arg Tyr
305 310 315 320
Phe Arg Pro Thr Glu Val Asp Leu Leu Leu Gly Asp Pro Thr Lys Ala
 325 330 335
Glu Lys Glu Leu Asp Trp Val Arg Glu Tyr Asp Leu Lys Glu Leu Val
 340 345 350
Lys Asp Met Leu Glu Tyr Asp Leu Lys Glu Cys Gln Lys Asn Leu Tyr
 355 360 365

```

Leu Gln Asp Gly Gly Tyr Ile Leu Arg Asn Phe Tyr Glu  
 370 375 380

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 70...1065
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CAGCAGTATC CCTATCGGTC AAGCCTTAAT GCGTATTTTC AACCTACAA TCATCAAAAA  | 60  |
| AGGATAAAA ATG GAT AGC GTA ACT CTA GCA TGC GGG AAC GGA GGG AAA GAA | 111 |
| Met Asp Ser Val Thr Leu Ala Cys Gly Asn Gly Gly Lys Glu           |     |
| 1 5 10                                                            |     |
| ACA AAC GCT TTG ATT GAG CGA GTC TTT ATG CCC TAT TTA AAA GAA TGG   | 159 |
| Thr Asn Ala Leu Ile Glu Arg Val Phe Met Pro Tyr Leu Lys Glu Trp   |     |
| 15 20 25 30                                                       |     |
| ATT GTT GCA TTT GAT GAA GAC GCC CCT AAA TTT GAA GCT AGT GGG GAA   | 207 |
| Ile Val Ala Phe Asp Glu Asp Ala Pro Lys Phe Glu Ala Ser Gly Glu   |     |
| 35 40 45                                                          |     |
| TAT TGC GTG AGC ACG GAT AGT TTT GTC ATC ACG CCC TTA ATT TTT AAT   | 255 |
| Tyr Cys Val Ser Thr Asp Ser Phe Val Ile Thr Pro Leu Ile Phe Asn   |     |
| 50 55 60                                                          |     |
| GGG GGC GAT ATA GGC AAG CTT TGC GTT TGC GGG AGT GCG AAT GAT GTG   | 303 |
| Gly Gly Asp Ile Gly Lys Leu Cys Val Cys Gly Ser Ala Asn Asp Val   |     |
| 65 70 75                                                          |     |
| AGC GTG CAA GGG GGC GAA CCT TTG TAT TTG AAT ATG GGT TTT ATT TTA   | 351 |
| Ser Val Gln Gly Gly Glu Pro Leu Tyr Leu Asn Met Gly Phe Ile Leu   |     |
| 80 85 90                                                          |     |
| GAA GAA GGC TTA GAA ATT TCT CTT TTA AAA CAA ATT TTA CAA TCC ATA   | 399 |
| Glu Glu Gly Leu Glu Ile Ser Leu Leu Lys Gln Ile Leu Gln Ser Ile   |     |
| 95 100 105 110                                                    |     |
| CAA AAA GAA TTG TTT AAA GCC AAC CTG AAA CTC CTC TCC CTA GAC ACT   | 447 |
| Gln Lys Glu Leu Phe Lys Ala Asn Leu Lys Leu Leu Ser Leu Asp Thr   |     |
| 115 120 125                                                       |     |
| AAA GTC GTG CCA AAG GGG AGC GTG GAT AAG CTT TTT ATC AAC ACA ACC   | 495 |
| Lys Val Val Pro Lys Gly Ser Val Asp Lys Leu Phe Ile Asn Thr Thr   |     |
| 130 135 140                                                       |     |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| TGC ATT GGT AAA ATC ATC AAG CCA GGG ATT TCT TCG TAC CAT TTA CAA   | 543  |
| Cys Ile Gly Lys Ile Ile Lys Pro Gly Ile Ser Ser Tyr His Leu Gln   |      |
| 145 150 155                                                       |      |
| CAA GGG CAA GCC ATT ATC CTA AGC GAC ACT ATC GCC AAT CAT GGG GCA   | 591  |
| Gln Gly Gln Ala Ile Ile Leu Ser Asp Thr Ile Ala Asn His Gly Ala   |      |
| 160 165 170                                                       |      |
| AGC TTA TTT GCG ATG CGT AAT GAA ATC AAG CTT AAA ACG AAT CTA GAA   | 639  |
| Ser Leu Phe Ala Met Arg Asn Glu Ile Lys Leu Lys Thr Asn Leu Glu   |      |
| 175 180 185 190                                                   |      |
| AGC GAT TGC CAA CTG CTC TAT CCC TTA TTA AAA CCC CTA TTT TTA AGC   | 687  |
| Ser Asp Cys Gln Leu Leu Tyr Pro Leu Leu Lys Pro Leu Phe Leu Ser   |      |
| 195 200 205                                                       |      |
| GAT CTC AAA ATT GAT GCT TTA AGA GAT GCG ACT AGG GGC GGG TTA GCG   | 735  |
| Asp Leu Lys Ile Asp Ala Leu Arg Asp Ala Thr Arg Gly Gly Leu Ala   |      |
| 210 215 220                                                       |      |
| AGC GTG CTG AAC GAA TGG GCG AAC AGC TCT AGA GTG AAA ATC GTT ATA   | 783  |
| Ser Val Leu Asn Glu Trp Ala Asn Ser Ser Arg Val Lys Ile Val Ile   |      |
| 225 230 235                                                       |      |
| GAA GAA GAA AAA ATC CCC TTA AAA GAA GAA ACG AAA GGG ATT TGT GAG   | 831  |
| Glu Glu Glu Lys Ile Pro Leu Lys Glu Glu Thr Lys Gly Ile Cys Glu   |      |
| 240 245 250                                                       |      |
| ATT TTA GGG TTA GAA CCC TAC GCG CTA GCC AAT GAG GGG GTG TTT GTT   | 879  |
| Ile Leu Gly Leu Glu Pro Tyr Ala Leu Ala Asn Glu Gly Val Phe Val   |      |
| 255 260 265 270                                                   |      |
| TTA GCG CTC AAT CAA AAA GAC GCC CCT AAA GCC TTA GAA ATT TTA AAA   | 927  |
| Leu Ala Leu Asn Gln Lys Asp Ala Pro Lys Ala Leu Glu Ile Leu Lys   |      |
| 275 280 285                                                       |      |
| AGT AAC GAA AAA GCT AAA AAC GCT TGC GTG ATT GGC AAA GTG TTT GAA   | 975  |
| Ser Asn Glu Lys Ala Lys Asn Ala Cys Val Ile Gly Lys Val Phe Glu   |      |
| 290 295 300                                                       |      |
| AAC CCT TAT CCT AGC GTG GTT TTA AAG AAC GCA TGG GGT TTT GAA AGG   | 1023 |
| Asn Pro Tyr Pro Ser Val Val Leu Lys Asn Ala Trp Gly Phe Glu Arg   |      |
| 305 310 315                                                       |      |
| ATT TTA GAG GTG CCA GAG GGC GAA TTA TTG CCT AGG ATT TGT TAACACGCC | 1074 |
| Ile Leu Glu Val Pro Glu Gly Glu Leu Leu Pro Arg Ile Cys           |      |
| 320 325 330                                                       |      |
| GTCATTTTTT AATCGTTTTA AGCCTGCCCT AAAAATGGTT TA                    | 1116 |

(2) INFORMATION FOR SEQ ID NO:440:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

Met Asp Ser Val Thr Leu Ala Cys Gly Asn Gly Gly Lys Glu Thr Asn  
1 5 10 15  
Ala Leu Ile Glu Arg Val Phe Met Pro Tyr Leu Lys Glu Trp Ile Val  
20 25 30  
Ala Phe Asp Glu Asp Ala Pro Lys Phe Glu Ala Ser Gly Glu Tyr Cys  
35 40 45  
Val Ser Thr Asp Ser Phe Val Ile Thr Pro Leu Ile Phe Asn Gly Gly  
50 55 60  
Asp Ile Gly Lys Leu Cys Val Cys Gly Ser Ala Asn Asp Val Ser Val  
65 70 75 80  
Gln Gly Gly Glu Pro Leu Tyr Leu Asn Met Gly Phe Ile Leu Glu Glu  
85 90 95  
Gly Leu Glu Ile Ser Leu Leu Lys Gln Ile Leu Gln Ser Ile Gln Lys  
100 105 110  
Glu Leu Phe Lys Ala Asn Leu Lys Leu Leu Ser Leu Asp Thr Lys Val  
115 120 125  
Val Pro Lys Gly Ser Val Asp Lys Leu Phe Ile Asn Thr Thr Cys Ile  
130 135 140  
Gly Lys Ile Ile Lys Pro Gly Ile Ser Ser Tyr His Leu Gln Gln Gly  
145 150 155 160  
Gln Ala Ile Ile Leu Ser Asp Thr Ile Ala Asn His Gly Ala Ser Leu  
165 170 175  
Phe Ala Met Arg Asn Glu Ile Lys Leu Lys Thr Asn Leu Glu Ser Asp  
180 185 190  
Cys Gln Leu Leu Tyr Pro Leu Leu Lys Pro Leu Phe Leu Ser Asp Leu  
195 200 205  
Lys Ile Asp Ala Leu Arg Asp Ala Thr Arg Gly Gly Leu Ala Ser Val  
210 215 220  
Leu Asn Glu Trp Ala Asn Ser Ser Arg Val Lys Ile Val Ile Glu Glu  
225 230 235 240  
Glu Lys Ile Pro Leu Lys Glu Glu Thr Lys Gly Ile Cys Glu Ile Leu  
245 250 255  
Gly Leu Glu Pro Tyr Ala Leu Ala Asn Glu Gly Val Phe Val Leu Ala  
260 265 270  
Leu Asn Gln Lys Asp Ala Pro Lys Ala Leu Glu Ile Leu Lys Ser Asn  
275 280 285  
Glu Lys Ala Lys Asn Ala Cys Val Ile Gly Lys Val Phe Glu Asn Pro  
290 295 300  
Tyr Pro Ser Val Val Leu Lys Asn Ala Trp Gly Phe Glu Arg Ile Leu  
305 310 315 320  
Glu Val Pro Glu Gly Glu Leu Leu Pro Arg Ile Cys  
325 330

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1033 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 16...1005  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| AAAAGGATAT TTTGA ATG AAA AGA ATG TTA GCG GAG TTT GAA AAA ATC CAA | 51  |
| Met Lys Arg Met Leu Ala Glu Phe Glu Lys Ile Gln                  |     |
| 1 5 10                                                           |     |
| GCG ATT CTA ATG GCT TTC CCC CAT GAG TTT AGC GAC TGG GCG TAT TGT  | 99  |
| Ala Ile Leu Met Ala Phe Pro His Glu Phe Ser Asp Trp Ala Tyr Cys  |     |
| 15 20 25                                                         |     |
| ATC AAA GAG GCT AGG GAA AGT TTT TTA AAC ATC ATT CAA ACC ATA GCC  | 147 |
| Ile Lys Glu Ala Arg Glu Ser Phe Leu Asn Ile Ile Gln Thr Ile Ala  |     |
| 30 35 40                                                         |     |
| AAA CAC GCT AAA GTG CTA GTG TGC GTC CAC ACT AAC GAT ATT ATC GGT  | 195 |
| Lys His Ala Lys Val Leu Val Cys Val His Thr Asn Asp Ile Ile Gly  |     |
| 45 50 55 60                                                      |     |
| TAT GAA ACG CTT AAA AAC TTA CCC GGT GTA GAG ATC GCA AGG ATT GAC  | 243 |
| Tyr Glu Thr Leu Lys Asn Leu Pro Gly Val Glu Ile Ala Arg Ile Asp  |     |
| 65 70 75                                                         |     |
| ACT AAC GAC ACA TGG GCT AGG GAT TTT GGA GCG ATC AGC GTT GAA AAT  | 291 |
| Thr Asn Asp Thr Trp Ala Arg Asp Phe Gly Ala Ile Ser Val Glu Asn  |     |
| 80 85 90                                                         |     |
| CAT GGC GTT TTA GAG TGC TTG GAT TTT GGC TTT AAT GGC TGG GGG TTA  | 339 |
| His Gly Val Leu Glu Cys Leu Asp Phe Gly Phe Asn Gly Trp Gly Leu  |     |
| 95 100 105                                                       |     |
| AAA TAC CCG TCC AAT TTA GAC AAT CAA GTG AAT TTC AAA CTC AAA AGT  | 387 |
| Lys Tyr Pro Ser Asn Leu Asp Asn Gln Val Asn Phe Lys Leu Lys Ser  |     |
| 110 115 120                                                      |     |
| TTA GGG TTT TTA AAA CAC CCT TTA AAA ACG ATG CCC TAT ATT TTA GAG  | 435 |
| Leu Gly Phe Leu Lys His Pro Leu Lys Thr Met Pro Tyr Ile Leu Glu  |     |
| 125 130 135 140                                                  |     |
| GGC GGG AGT ATA GAA AGC GAT GGG GCT GGG AGC GTT TTA ACC AAC ACC  | 483 |
| Gly Gly Ser Ile Glu Ser Asp Gly Ala Gly Ser Val Leu Thr Asn Thr  |     |
| 145 150 155                                                      |     |
| CAA TGC CTG TTA GAA AAA AAT CGT AAC CCC CAT TTG AAT CAA AAT GGA  | 531 |
| Gln Cys Leu Leu Glu Lys Asn Arg Asn Pro His Leu Asn Gln Asn Gly  |     |
| 160 165 170                                                      |     |
| ATA GAA AAC ATG CTT AAA AAG GAA TTA GGG GCT AAA CAA GTG CTG TGG  | 579 |
| Ile Glu Asn Met Leu Lys Lys Glu Leu Gly Ala Lys Gln Val Leu Trp  |     |
| 175 180 185                                                      |     |
| TAT TCT TAT GGC TAT CTC AAA GGC GAT GAT ACC GAT AGC CAT ACC GAC  | 627 |
| Tyr Ser Tyr Gly Tyr Leu Lys Gly Asp Asp Thr Asp Ser His Thr Asp  |     |
| 190 195 200                                                      |     |









(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 25...375

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AAAAACTGGA ATCAAGGGGT TAAA ATG TTT TCT CAT GAA GTT TAT TTG GAG    | 51  |
| Met Phe Ser His Glu Val Tyr Leu Glu                               |     |
| 1 5                                                               |     |
| GGT TGC ACC CTT GAA TTA AGA AAG ATT TGC GAT GAT TTT GAA AAA AAT   | 99  |
| Gly Cys Thr Leu Glu Leu Arg Lys Ile Cys Asp Asp Phe Glu Lys Asn   |     |
| 10 15 20 25                                                       |     |
| GCC ATG CAA GAT GAT TTA GGG CAG AAA CTC AGG AGT GAT GTG CTA GAG   | 147 |
| Ala Met Gln Asp Asp Leu Gly Gln Lys Leu Arg Ser Asp Val Leu Glu   |     |
| 30 35 40                                                          |     |
| GAC ATG CTA AAA ATC GCG CAT GAT TTA GAA AAT TTA GAA GAT GAC ACC   | 195 |
| Asp Met Leu Lys Ile Ala His Asp Leu Glu Asn Leu Glu Asp Asp Thr   |     |
| 45 50 55                                                          |     |
| CAA TAC CAA AGA AGA ATA ATT GAC GAG CAA ATT GAA GAA GCC AAA TCT   | 243 |
| Gln Tyr Gln Arg Arg Ile Ile Asp Glu Gln Ile Glu Glu Ala Lys Ser   |     |
| 60 65 70                                                          |     |
| TTG ATG AGG CAA ATT GAT ATG AAT TTC CAT CCA TCA AGC GAG ATC GAT   | 291 |
| Leu Met Arg Gln Ile Asp Met Asn Phe His Pro Ser Ser Glu Ile Asp   |     |
| 75 80 85                                                          |     |
| AGG CTT ATG CGT GAA GCC AAA GAG CAT GAA AGA GAA GCT AGT AAA AGA   | 339 |
| Arg Leu Met Arg Glu Ala Lys Glu His Glu Arg Glu Ala Ser Lys Arg   |     |
| 90 95 100 105                                                     |     |
| TAT GAT GAG TAT CTT AAA TCT AAG GAT AAA AAT GAT TGATGTGAAT GGTTTA | 391 |
| Tyr Asp Glu Tyr Leu Lys Ser Lys Asp Lys Asn Asp                   |     |
| 110 115                                                           |     |
| TTAAAAGAAC TGGATGATGC CTTAGATAA                                   | 420 |

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:



[illegible]

(2) INFORMATION FOR SEQ ID NO:448:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Asp | His | Lys | Val | Leu | Gly | Ile | Thr | Glu | Gly | Asp | Trp | Trp | Ala | Ile |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Trp | Leu | Ala | Trp | Gly | Val | Leu | Trp | Leu | Thr | Ala | Phe | Ile | Glu | Asn |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | Leu | Lys | Ile | Pro | Leu | Gly | Lys | Phe | Thr | Pro | Trp | Leu | Ala | Ile | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Gly | Ile | Leu | Thr | Ala | Trp | Ile | Pro | Ala | Trp | Leu | Leu | Phe | Ile | Gln |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| His | Trp | Val |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 195 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 48...482
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

|                                                                 |             |     |
|-----------------------------------------------------------------|-------------|-----|
| GAAGGGCATT TGTGCTAAAA ACCACTAAAA AAAGCCTGTT GGTTTTT             | ATG GGG GTT | 56  |
|                                                                 | Met Gly Val |     |
|                                                                 | 1           |     |
| TTT TTC CTT ATT TTT GGC GTG GAT CAA GCG ATT AAA TAC GCT ATT TTA |             | 104 |
| Phe Phe Leu Ile Phe Gly Val Asp Gln Ala Ile Lys Tyr Ala Ile Leu |             |     |
| 5 10 15                                                         |             |     |
| GAA GGG TTT CGC TAT GAA AGT TTG ATG ATA GAT ATT GTT TTA GTG TTC |             | 152 |
| Glu Gly Phe Arg Tyr Glu Ser Leu Met Ile Asp Ile Val Leu Val Phe |             |     |
| 20 25 30 35                                                     |             |     |
| AAT AAA GGC GTG GCG TTT TCC TTG CTC AGT TTT TTA GAG GGG GGT TTG |             | 200 |
| Asn Lys Gly Val Ala Phe Ser Leu Leu Ser Phe Leu Glu Gly Gly Leu |             |     |
| 40 45 50                                                        |             |     |
| AAA TAC TTG CAA ATC CTT TTG ATT TTA GGG CTT TTT ATC TTT TTA ATG |             | 248 |
| Lys Tyr Leu Gln Ile Leu Leu Ile Leu Gly Leu Phe Ile Phe Leu Met |             |     |
| 55 60 65                                                        |             |     |
| CGC CAA AGG GAG CTT TTT AAA AAC CAT GCG ATA GAG TTT GGC ATG GTG |             | 296 |
| Arg Gln Arg Glu Leu Phe Lys Asn His Ala Ile Glu Phe Gly Met Val |             |     |
| 70 75 80                                                        |             |     |
| TTT GGC GCC GGG GTT TCT AAT GTT TTA GAC CGG TTT GTG CAT GGG GGC |             | 344 |
| Phe Gly Ala Gly Val Ser Asn Val Leu Asp Arg Phe Val His Gly Gly |             |     |
| 85 90 95                                                        |             |     |
| GTG GTG GAT TAT GTG TAT TAT CAT TAT GGC TTT GAT TTT GCC ATT TTT |             | 392 |

Val Val Asp Tyr Val Tyr Tyr His Tyr Gly Phe Asp Phe Ala Ile Phe  
100 105 110 115

AAT TTC GCT GAT GTC ATG ATA GAT GTG GGC GTG GGC GTT TTA TTG TTG 440  
Asn Phe Ala Asp Val Met Ile Asp Val Gly Val Gly Val Leu Leu Leu  
120 125 130

AAA CAA TTC TTT TTT AAG CAA AAA CAA AAC AAA ATT AAG GCA TAATCACTC 491  
Lys Gln Phe Phe Phe Lys Gln Lys Gln Asn Lys Ile Lys Ala  
135 140 145

TTTTTAAAAT GAAAGGTCGC GTAGCTCAGT TGGTA 526

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

Met Gly Val Phe Phe Leu Ile Phe Gly Val Asp Gln Ala Ile Lys Tyr  
1 5 10 15  
Ala Ile Leu Glu Gly Phe Arg Tyr Glu Ser Leu Met Ile Asp Ile Val  
20 25 30  
Leu Val Phe Asn Lys Gly Val Ala Phe Ser Leu Leu Ser Phe Leu Glu  
35 40 45  
Gly Gly Leu Lys Tyr Leu Gln Ile Leu Leu Ile Leu Gly Leu Phe Ile  
50 55 60  
Phe Leu Met Arg Gln Arg Glu Leu Phe Lys Asn His Ala Ile Glu Phe  
65 70 75 80  
Gly Met Val Phe Gly Ala Gly Val Ser Asn Val Leu Asp Arg Phe Val  
85 90 95  
His Gly Gly Val Val Asp Tyr Val Tyr Tyr His Tyr Gly Phe Asp Phe  
100 105 110  
Ala Ile Phe Asn Phe Ala Asp Val Met Ile Asp Val Gly Val Gly Val  
115 120 125  
Leu Leu Leu Lys Gln Phe Phe Phe Lys Gln Lys Gln Asn Lys Ile Lys  
130 135 140  
Ala  
145

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence



(B) LOCATION: 22...1356  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TTTAAAAGGT ATTTTATAAC G ATG AAA ATT TTT GGG ACT GAT GGC GTG AGG | 51  |
| Met Lys Ile Phe Gly Thr Asp Gly Val Arg                         |     |
| 1 5 10                                                          |     |
| GGT AAA GCA GGG GTG AAA CTC ACC CCC ATG TTT GTG ATG CGT TTA GGC | 99  |
| Gly Lys Ala Gly Val Lys Leu Thr Pro Met Phe Val Met Arg Leu Gly |     |
| 15 20 25                                                        |     |
| ATT GCT GCC GGA TTG TAT TTT AAA AAA CAT TCT CAA ACG AAT AAA ATT | 147 |
| Ile Ala Ala Gly Leu Tyr Phe Lys Lys His Ser Gln Thr Asn Lys Ile |     |
| 30 35 40                                                        |     |
| CTA ATC GGT AAA GAC ACC AGA AAA AGC GGC TAT ATG GTA GAA AAC GCT | 195 |
| Leu Ile Gly Lys Asp Thr Arg Lys Ser Gly Tyr Met Val Glu Asn Ala |     |
| 45 50 55                                                        |     |
| TTA GTG AGC GCT CTA ACT TCC ATA GGC TAT AAT GTG ATT CAA ATA GGG | 243 |
| Leu Val Ser Ala Leu Thr Ser Ile Gly Tyr Asn Val Ile Gln Ile Gly |     |
| 60 65 70                                                        |     |
| CCT ATG CCC ACC CCT GCG ATT GCG TTT TTA ACT GAA GAC ATG CGC TGT | 291 |
| Pro Met Pro Thr Pro Ala Ile Ala Phe Leu Thr Glu Asp Met Arg Cys |     |
| 75 80 85 90                                                     |     |
| GAT GCG GGT ATT ATG ATA AGC GCG AGC CAC AAC CCT TTT GAA GAT AAT | 339 |
| Asp Ala Gly Ile Met Ile Ser Ala Ser His Asn Pro Phe Glu Asp Asn |     |
| 95 100 105                                                      |     |
| GGC ATT AAG TTT TTC AAT TCT TAT GGC TAT AAG CTT AAA GAA GAA GAA | 387 |
| Gly Ile Lys Phe Phe Asn Ser Tyr Gly Tyr Lys Leu Lys Glu Glu Glu |     |
| 110 115 120                                                     |     |
| GAA AAA GCG ATT GAA GAA ATC TTT CAT GAT GAA GAA TTA CTG CAT TCT | 435 |
| Glu Lys Ala Ile Glu Glu Ile Phe His Asp Glu Glu Leu Leu His Ser |     |
| 125 130 135                                                     |     |
| AGC TAT AAA GTG GGT GAG AGC GTC GGT AGC GCT AAA AGG ATA GAC GAT | 483 |
| Ser Tyr Lys Val Gly Glu Ser Val Gly Ser Ala Lys Arg Ile Asp Asp |     |
| 140 145 150                                                     |     |
| GTC ATA GGG CGC TAT ATT GCA CAT TTA AAA CAC TCT TTC CCC AAA CAT | 531 |
| Val Ile Gly Arg Tyr Ile Ala His Leu Lys His Ser Phe Pro Lys His |     |
| 155 160 165 170                                                 |     |
| TTG AAT TTA CAG AGT TTA AGG ATC GTG CTA GAT ACG GCT AAT GGC GCG | 579 |
| Leu Asn Leu Gln Ser Leu Arg Ile Val Leu Asp Thr Ala Asn Gly Ala |     |
| 175 180 185                                                     |     |
| GCT TAT AAG GTG GCT CCG GTC GTT TTT AGC GAG CTT GGG GCT GAT GTG | 627 |
| Ala Tyr Lys Val Ala Pro Val Val Phe Ser Glu Leu Gly Ala Asp Val |     |
| 190 195 200                                                     |     |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| TTA GTG ATT AAT GAT GAG CCT AAC GGG TGT AAC ATT AAT GAT CAA TGC<br>Leu Val Ile Asn Asp Glu Pro Asn Gly Cys Asn Ile Asn Asp Gln Cys<br>205 210 215     | 675  |
| GGG GCT TTA CAC CCC AAC CAA TTA AGC CAG GAA GTG AAA AAA TAC CGC<br>Gly Ala Leu His Pro Asn Gln Leu Ser Gln Glu Val Lys Lys Tyr Arg<br>220 225 230     | 723  |
| GCA GAT TTA GGC TTT GCT TTT GAT GGC GAT GCT GAC AGG CTA GTG GTG<br>Ala Asp Leu Gly Phe Ala Phe Asp Gly Asp Ala Asp Arg Leu Val Val<br>235 240 245 250 | 771  |
| GTG GAT AAT TTA GGG AAT ATC GTG CAT GGG GAT AAG CTT TTA GGG GTG<br>Val Asp Asn Leu Gly Asn Ile Val His Gly Asp Lys Leu Leu Gly Val<br>255 260 265     | 819  |
| TTA GGG GTT TAT CAA AAA TCT AAA AAC GCC CTT TCT TCT CAA GCG GTT<br>Leu Gly Val Tyr Gln Lys Ser Lys Asn Ala Leu Ser Ser Gln Ala Val<br>270 275 280     | 867  |
| GTC GCC ACA AAC ATG AGC AAT TTA GCC CTT AAA GAA TAT TTA AAA TCC<br>Val Ala Thr Asn Met Ser Asn Leu Ala Leu Lys Glu Tyr Leu Lys Ser<br>285 290 295     | 915  |
| CAA GAT TTG GAA TTG AAG CAT TGC GCG ATT GGG GAT AAG TTT GTG AGC<br>Gln Asp Leu Glu Leu Lys His Cys Ala Ile Gly Asp Lys Phe Val Ser<br>300 305 310     | 963  |
| GAA TGC ATG CAA TTG AAT AAA GCC AAT TTT GGA GGC GAG CAA AGC GGG<br>Glu Cys Met Gln Leu Asn Lys Ala Asn Phe Gly Gly Glu Gln Ser Gly<br>315 320 325 330 | 1011 |
| CAT ATC ATT TTT AGC GAT TAC GCT AAA ACA GGC GAT GGT TTG GTG TGC<br>His Ile Ile Phe Ser Asp Tyr Ala Lys Thr Gly Asp Gly Leu Val Cys<br>335 340 345     | 1059 |
| GCT TTG CAA GTG AGC GCG TTA GTG TTA GAA AGC AAG CAG GTA AGC TCT<br>Ala Leu Gln Val Ser Ala Leu Val Leu Glu Ser Lys Gln Val Ser Ser<br>350 355 360     | 1107 |
| GTT GCG TTA AAC CCC TTT GAA TTA TAC CCC CAA AGC CTA GTG AAT TTG<br>Val Ala Leu Asn Pro Phe Glu Leu Tyr Pro Gln Ser Leu Val Asn Leu<br>365 370 375     | 1155 |
| AAT GTC CAA AAA AAG CCC CCT TTA GAA AGC CTG AAA GGT TAT AGC GCT<br>Asn Val Gln Lys Lys Pro Pro Leu Glu Ser Leu Lys Gly Tyr Ser Ala<br>380 385 390     | 1203 |
| CTT TTA AAA GAA TTA GAC AAG CTA GAA ATC CGC CAT TTG ATC CGT TAT<br>Leu Leu Lys Glu Leu Asp Lys Leu Glu Ile Arg His Leu Ile Arg Tyr<br>395 400 405 410 | 1251 |
| AGC GGC ACT GAA AAC AAA TTG CGA ATC CTT TTA GAA GCT AAA GAT GAA<br>Ser Gly Thr Glu Asn Lys Leu Arg Ile Leu Leu Glu Ala Lys Asp Glu<br>415 420 425     | 1299 |
| AAG CTT TTA GAA TCC AAA ATG CAA GAA TTA AAA GAG TTT TTT GAA GGG<br>Lys Leu Leu Glu Ser Lys Met Gln Glu Leu Lys Glu Phe Phe Glu Gly<br>430 435 440 445 | 1347 |

430

435

440

CAT TTG TGC TAAAAACCAC TAAAAAAGC CTGTTGGTTT TTATGG  
 His Leu Cys  
 445

1392

## (2) INFORMATION FOR SEQ ID NO:452:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

Met Lys Ile Phe Gly Thr Asp Gly Val Arg Gly Lys Ala Gly Val Lys  
 1 5 10 15  
 Leu Thr Pro Met Phe Val Met Arg Leu Gly Ile Ala Ala Gly Leu Tyr  
 20 25 30  
 Phe Lys Lys His Ser Gln Thr Asn Lys Ile Leu Ile Gly Lys Asp Thr  
 35 40 45  
 Arg Lys Ser Gly Tyr Met Val Glu Asn Ala Leu Val Ser Ala Leu Thr  
 50 55 60  
 Ser Ile Gly Tyr Asn Val Ile Gln Ile Gly Pro Met Pro Thr Pro Ala  
 65 70 75 80  
 Ile Ala Phe Leu Thr Glu Asp Met Arg Cys Asp Ala Gly Ile Met Ile  
 85 90 95  
 Ser Ala Ser His Asn Pro Phe Glu Asp Asn Gly Ile Lys Phe Phe Asn  
 100 105 110  
 Ser Tyr Gly Tyr Lys Leu Lys Glu Glu Glu Glu Lys Ala Ile Glu Glu  
 115 120 125  
 Ile Phe His Asp Glu Glu Leu Leu His Ser Ser Tyr Lys Val Gly Glu  
 130 135 140  
 Ser Val Gly Ser Ala Lys Arg Ile Asp Asp Val Ile Gly Arg Tyr Ile  
 145 150 155 160  
 Ala His Leu Lys His Ser Phe Pro Lys His Leu Asn Leu Gln Ser Leu  
 165 170 175  
 Arg Ile Val Leu Asp Thr Ala Asn Gly Ala Ala Tyr Lys Val Ala Pro  
 180 185 190  
 Val Val Phe Ser Glu Leu Gly Ala Asp Val Leu Val Ile Asn Asp Glu  
 195 200 205  
 Pro Asn Gly Cys Asn Ile Asn Asp Gln Cys Gly Ala Leu His Pro Asn  
 210 215 220  
 Gln Leu Ser Gln Glu Val Lys Lys Tyr Arg Ala Asp Leu Gly Phe Ala  
 225 230 235 240  
 Phe Asp Gly Asp Ala Asp Arg Leu Val Val Val Asp Asn Leu Gly Asn  
 245 250 255  
 Ile Val His Gly Asp Lys Leu Leu Gly Val Leu Gly Val Tyr Gln Lys  
 260 265 270  
 Ser Lys Asn Ala Leu Ser Ser Gln Ala Val Val Ala Thr Asn Met Ser  
 275 280 285  
 Asn Leu Ala Leu Lys Glu Tyr Leu Lys Ser Gln Asp Leu Glu Leu Lys  
 290 295 300  
 His Cys Ala Ile Gly Asp Lys Phe Val Ser Glu Cys Met Gln Leu Asn

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Lys | Ala | Asn | Phe | Gly | Gly | Glu | Gln | Ser | Gly | His | Ile | Ile | Phe | Ser | Asp |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Tyr | Ala | Lys | Thr | Gly | Asp | Gly | Leu | Val | Cys | Ala | Leu | Gln | Val | Ser | Ala |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Leu | Val | Leu | Glu | Ser | Lys | Gln | Val | Ser | Ser | Val | Ala | Leu | Asn | Pro | Phe |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Glu | Leu | Tyr | Pro | Gln | Ser | Leu | Val | Asn | Leu | Asn | Val | Gln | Lys | Lys | Pro |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Pro | Leu | Glu | Ser | Leu | Lys | Gly | Tyr | Ser | Ala | Leu | Leu | Lys | Glu | Leu | Asp |
|     | 385 |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Lys | Leu | Glu | Ile | Arg | His | Leu | Ile | Arg | Tyr | Ser | Gly | Thr | Glu | Asn | Lys |
|     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |     |
| Leu | Arg | Ile | Leu | Glu | Ala | Lys | Asp | Glu | Lys | Leu | Leu | Glu | Ser | Lys |     |
|     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |     |
| Met | Gln | Glu | Leu | Lys | Glu | Phe | Phe | Glu | Gly | His | Leu | Cys |     |     |     |
|     | 435 |     |     |     |     | 440 |     |     |     |     |     | 445 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...441
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

|            |          |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| TTTTATCAAA | GGATTCTT | ATG | ACA | AAG | ACC | GCT | AAA | GTC | AAT | GAC | ATC | GTT | 51  |
|            |          | Met | Thr | Lys | Thr | Ala | Lys | Val | Asn | Asp | Ile | Val |     |
|            |          | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |
| CGT        | GAT      | TGG | GTC | GTT | TTA | GAC | GCC | AAA | GAC | AAG | GTT | TTT | 99  |
| Arg        | Asp      | Trp | Val | Val | Leu | Asp | Ala | Lys | Asp | Lys | Val | Phe |     |
|            |          | 15  |     |     |     | 20  |     |     |     |     | 25  |     |     |
| ATC        | ACT      | GAA | ATC | GCT | GTG | CTT | TTA | AGA | GGG | AAA | CAC | CGC | 147 |
| Ile        | Thr      | Glu | Ile | Ala | Val | Leu | Leu | Arg | Gly | Lys | His | Arg |     |
|            |          | 30  |     |     |     | 35  |     |     |     |     | 40  |     |     |
| ACC        | CCT      | AAT | GTG | GAT | TGT | GGG | GAT | TTT | GTG | GTG | GTT | ATC | 195 |
| Thr        | Pro      | Asn | Val | Asp | Cys | Gly | Asp | Phe | Val | Val | Val | Ile |     |
|            | 45       |     |     |     | 50  |     |     |     |     |     | 55  |     |     |
| AAG        | GTT      | AAA | TTT | TCA | GGC | ATG | AAA | TTA | GAG | GAT | AAA | GAG | 243 |
| Lys        | Val      | Lys | Phe | Ser | Gly | Met | Lys | Leu | Glu | Asp | Lys | Glu |     |
|            | 60       |     |     |     | 65  |     |     |     | 70  |     |     | 75  |     |
| CAT        | TCA      | GGC | TAT | TTT | GGC | AGC | ACT | AAG | AGC | AAG | ACT | CTC | 291 |
| His        | Ser      | Gly | Tyr | Phe | Gly | Ser | Thr | Lys | Ser | Lys | Thr | Leu |     |
|            |          |     |     |     |     |     |     |     |     |     |     | Gln |     |
|            |          |     |     |     |     |     |     |     |     |     |     | Glu |     |
|            |          |     |     |     |     |     |     |     |     |     |     | Met |     |



(ii) MOLECULE TYPE: Genomic DNA  
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 19...2058  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

|                                                                 |          |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------------------------------------------------------|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| TAGCTTTTGA                                                      | TTGAAAGC | ATG | GGT | TCT | TAC | TTT | ATG | GAG | TGT | CCA | ATG | AAA | 51  |
|                                                                 |          | Met | Gly | Ser | Tyr | Phe | Met | Glu | Cys | Pro | Met | Lys |     |
|                                                                 |          | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |
| AAG AAA GCT AAC GAA GAA AAA GCC CAA AAA AGA GCT AAA ACA GAA GCC |          |     |     |     |     |     |     |     |     |     |     |     | 99  |
| Lys Lys Ala Asn Glu Glu Lys Ala Gln Lys Arg Ala Lys Thr Glu Ala |          |     |     |     |     |     |     |     |     |     |     |     |     |
|                                                                 | 15       |     |     |     |     | 20  |     |     |     |     | 25  |     |     |
| AAA GCA GAA GCC ACA CAA GAA AAT AAA ACT AAA GAA AAC AAT AAA GCC |          |     |     |     |     |     |     |     |     |     |     |     | 147 |
| Lys Ala Glu Ala Thr Gln Glu Asn Lys Thr Lys Glu Asn Asn Lys Ala |          |     |     |     |     |     |     |     |     |     |     |     |     |
|                                                                 | 30       |     |     |     |     | 35  |     |     |     |     | 40  |     |     |
| AAA GAA AGC AAA ATT AAA GAA AGC AAA ATC AAA GAA GCT AAA GCG AAA |          |     |     |     |     |     |     |     |     |     |     |     | 195 |
| Lys Glu Ser Lys Ile Lys Glu Ser Lys Ile Lys Glu Ala Lys Ala Lys |          |     |     |     |     |     |     |     |     |     |     |     |     |
|                                                                 | 45       |     |     |     |     | 50  |     |     |     |     | 55  |     |     |
| GAA CCT ATT CCT GTT AAA AAG CTT AGT TTT AAT GAA GCG TTA GAA GAA |          |     |     |     |     |     |     |     |     |     |     |     | 243 |
| Glu Pro Ile Pro Val Lys Lys Leu Ser Phe Asn Glu Ala Leu Glu Glu |          |     |     |     |     |     |     |     |     |     |     |     |     |
|                                                                 | 60       |     |     |     |     | 65  |     |     |     |     | 70  |     | 75  |
| TTG TTC GCT AAT TCC TTA AGC GAT TGC GTT TCT TAT GAG TCC ATC ATT |          |     |     |     |     |     |     |     |     |     |     |     | 291 |
| Leu Phe Ala Asn Ser Leu Ser Asp Cys Val Ser Tyr Glu Ser Ile Ile |          |     |     |     |     |     |     |     |     |     |     |     |     |
|                                                                 | 80       |     |     |     |     |     |     |     |     |     |     |     | 90  |
| CAA ATC AGC GCG AAA GTC CCC ACT CTA GCC CAA ATC AAA AAA ATC AAA |          |     |     |     |     |     |     |     |     |     |     |     | 339 |
| Gln Ile Ser Ala Lys Val Pro Thr Leu Ala Gln Ile Lys Lys Ile Lys |          |     |     |     |     |     |     |     |     |     |     |     |     |
|                                                                 | 95       |     |     |     |     |     |     |     |     |     |     |     | 100 |
| GAA TTG TGC CAA AAA TAC CAA AAG AAA TTA GTC AGC TCT TCA GAA TAC |          |     |     |     |     |     |     |     |     |     |     |     | 387 |
| Glu Leu Cys Gln Lys Tyr Gln Lys Lys Leu Val Ser Ser Ser Glu Tyr |          |     |     |     |     |     |     |     |     |     |     |     |     |
|                                                                 | 110      |     |     |     |     |     |     |     |     |     |     |     | 115 |
| GCT AAA AAA CTC AAT GCG ATT GAC AAG ATT AAA AAA ACC GAA GAA AAG |          |     |     |     |     |     |     |     |     |     |     |     | 435 |
| Ala Lys Lys Leu Asn Ala Ile Asp Lys Ile Lys Lys Thr Glu Glu Lys |          |     |     |     |     |     |     |     |     |     |     |     |     |
|                                                                 | 125      |     |     |     |     |     |     |     |     |     |     |     | 130 |
| CAA AAA GTT TTA GAT GAA GAA TTA GAA GAT GGC TAT GAC TTT TTG AAA |          |     |     |     |     |     |     |     |     |     |     |     | 483 |
| Gln Lys Val Leu Asp Glu Glu Leu Glu Asp Gly Tyr Asp Phe Leu Lys |          |     |     |     |     |     |     |     |     |     |     |     |     |
|                                                                 | 140      |     |     |     |     |     |     |     |     |     |     |     | 145 |
| GAA AAG GAT TTT TTA GAG TGG AGC AGA AGC GAT AGC CCA GTG CGC ATG |          |     |     |     |     |     |     |     |     |     |     |     | 531 |
| Glu Lys Asp Phe Leu Glu Trp Ser Arg Ser Asp Ser Pro Val Arg Met |          |     |     |     |     |     |     |     |     |     |     |     |     |
|                                                                 | 160      |     |     |     |     |     |     |     |     |     |     |     | 165 |
| TAT TTG CGC GAA ATG GGG GAT ATA AAA CTT TTA AGC AAA GAT GAA GAG |          |     |     |     |     |     |     |     |     |     |     |     | 579 |
| Tyr Leu Arg Glu Met Gly Asp Ile Lys Leu Leu Ser Lys Asp Glu Glu |          |     |     |     |     |     |     |     |     |     |     |     |     |
|                                                                 | 175      |     |     |     |     |     |     |     |     |     |     |     | 180 |
|                                                                 |          |     |     |     |     |     |     |     |     |     |     |     | 185 |

|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| ATT<br>Ile        | GAA<br>Glu        | TTG<br>Leu<br>190 | AGC<br>Ser        | AAG<br>Lys        | CAA<br>Gln        | ATC<br>Ile        | CGC<br>Arg<br>195 | TTG<br>Leu        | GGT<br>Gly        | GAA<br>Glu        | GAC<br>Asp        | ATT<br>Ile<br>200 | ATT<br>Ile        | TTA<br>Leu        | GAC<br>Asp        | 627  |
| GCG<br>Ala        | ATC<br>Ile<br>205 | TGC<br>Cys        | TCG<br>Ser        | GTG<br>Val        | CCG<br>Pro        | TAT<br>Tyr<br>210 | TTG<br>Leu<br>210 | ATT<br>Ile        | GAT<br>Asp        | TTT<br>Phe<br>215 | ATC<br>Ile<br>215 | TAT<br>Tyr        | GCG<br>Ala        | TAT<br>Tyr        | AAA<br>Lys        | 675  |
| GAC<br>Asp<br>220 | GCT<br>Ala        | TTA<br>Leu        | ATC<br>Ile        | AAT<br>Asn<br>225 | CGT<br>Arg<br>225 | GAA<br>Glu<br>225 | AGA<br>Arg        | AGG<br>Arg        | GTT<br>Val        | AAA<br>Lys<br>230 | GAG<br>Glu        | CTT<br>Leu        | TTC<br>Phe        | AGG<br>Arg        | AGC<br>Ser<br>235 | 723  |
| TTT<br>Phe        | GAT<br>Asp        | GAT<br>Asp        | GAC<br>Asp<br>240 | GAT<br>Asp<br>240 | GAA<br>Glu<br>240 | AAT<br>Asn<br>240 | AGC<br>Ser        | GTG<br>Val        | AGC<br>Ser<br>245 | GAT<br>Asp<br>245 | TCT<br>Ser        | AAA<br>Lys<br>250 | AAA<br>Lys<br>250 | GAT<br>Asp<br>250 | GAA<br>Glu<br>250 | 771  |
| GAC<br>Asp        | AAC<br>Asn        | GAA<br>Glu<br>255 | GAA<br>Glu<br>255 | GAT<br>Asp<br>255 | GAA<br>Glu<br>255 | GAA<br>Glu<br>255 | AAC<br>Asn<br>260 | GAA<br>Glu<br>260 | GAA<br>Glu<br>260 | AGG<br>Arg        | AAA<br>Lys        | AAA<br>Lys<br>265 | GTC<br>Val<br>265 | GTT<br>Val        | TCT<br>Ser        | 819  |
| GAA<br>Glu        | AAA<br>Lys<br>270 | GAC<br>Asp<br>270 | AAG<br>Lys        | AAG<br>Lys        | CGT<br>Arg        | GTA<br>Val<br>275 | GAA<br>Glu<br>275 | AAG<br>Lys<br>275 | GTT<br>Val        | CAA<br>Gln        | GAA<br>Glu<br>280 | AGC<br>Ser<br>280 | TTT<br>Phe        | AAA<br>Lys        | GCC<br>Ala        | 867  |
| CTA<br>Leu<br>285 | GAC<br>Asp        | AAG<br>Lys        | GCT<br>Ala        | AAA<br>Lys        | AAA<br>Lys        | GAA<br>Glu<br>290 | TGG<br>Trp<br>290 | CTT<br>Leu        | AAA<br>Lys        | GCC<br>Ala<br>295 | CTT<br>Leu<br>295 | GAA<br>Glu        | GCC<br>Ala        | CCC<br>Pro        | ATA<br>Ile        | 915  |
| GAT<br>Asp<br>300 | GAA<br>Glu        | AGA<br>Arg        | GAA<br>Glu        | GAC<br>Asp<br>305 | GAA<br>Glu<br>305 | TTG<br>Leu<br>305 | GTG<br>Val        | CGT<br>Arg        | TCA<br>Ser        | TTG<br>Leu<br>310 | ACC<br>Thr        | CTA<br>Leu        | GCT<br>Ala        | TAC<br>Tyr        | AAA<br>Lys<br>315 | 963  |
| CGC<br>Arg        | CAA<br>Gln        | ACA<br>Thr        | CTC<br>Leu<br>320 | AAA<br>Lys<br>320 | GAC<br>Asp<br>320 | AGA<br>Arg        | CTC<br>Leu        | TAT<br>Tyr        | GAT<br>Asp<br>325 | TTA<br>Leu        | GAA<br>Glu        | CCT<br>Pro        | ACC<br>Thr        | AGC<br>Ser<br>330 | AAA<br>Lys        | 1011 |
| CTG<br>Leu        | ATT<br>Ile        | AAT<br>Asn<br>335 | GAA<br>Glu<br>335 | TTA<br>Leu<br>335 | GTC<br>Val        | AAA<br>Lys        | ACG<br>Thr<br>340 | ATG<br>Met<br>340 | GAA<br>Glu        | ACC<br>Thr<br>345 | ACT<br>Thr<br>345 | TTA<br>Leu<br>345 | AAA<br>Lys<br>345 | AGC<br>Ser        | GGC<br>Gly        | 1059 |
| GAT<br>Asp        | GGG<br>Gly<br>350 | TTT<br>Phe<br>350 | GAA<br>Glu<br>350 | AAA<br>Lys<br>350 | GAG<br>Glu        | TTG<br>Leu<br>355 | AAA<br>Lys<br>355 | CGC<br>Arg        | TTG<br>Leu        | GAA<br>Glu        | TAC<br>Tyr<br>360 | AAA<br>Lys<br>360 | CTG<br>Leu        | CCC<br>Pro        | TTA<br>Leu        | 1107 |
| TTC<br>Phe<br>365 | AAT<br>Asn<br>365 | GAC<br>Asp        | ACT<br>Thr        | CTC<br>Leu        | ATC<br>Ile        | GCA<br>Ala<br>370 | AAC<br>Asn<br>370 | CAT<br>His        | AAA<br>Lys        | AAA<br>Lys<br>375 | ATC<br>Ile<br>375 | CTT<br>Leu        | GCC<br>Ala        | AAT<br>Asn        | ATC<br>Ile        | 1155 |
| ACT<br>Thr<br>380 | AAC<br>Asn        | ATG<br>Met        | ACT<br>Thr        | AAA<br>Lys        | GAA<br>Glu<br>385 | GAT<br>Asp<br>385 | ATT<br>Ile        | ATC<br>Ile        | GCT<br>Ala        | CAA<br>Gln<br>390 | GTG<br>Val        | CCA<br>Pro        | GAA<br>Glu        | GCG<br>Ala        | ACT<br>Thr<br>395 | 1203 |
| ATG<br>Met        | GTG<br>Val        | AGC<br>Ser        | GTG<br>Val<br>400 | TAT<br>Tyr<br>400 | ATG<br>Met        | GAT<br>Asp        | CTT<br>Leu        | AAA<br>Lys<br>405 | AAG<br>Lys<br>405 | CTT<br>Leu        | TTT<br>Phe<br>410 | TTG<br>Leu        | ACT<br>Thr<br>410 | AAA<br>Lys        | GAA<br>Glu        | 1251 |
| GCG<br>Ala        | AGC<br>Ser        | GAA<br>Glu        | GAA<br>Glu        | GGC<br>Gly        | TTT<br>Phe        | GAT<br>Asp        | CTA<br>Leu        | GCC<br>Ala        | CCC<br>Pro        | AAC<br>Asn        | AAG<br>Lys        | CTA<br>Leu        | AAA<br>Lys        | GAA<br>Glu        | ATT<br>Ile        | 1299 |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
|            | 415        |            |            |            |            | 420        |            |            |            |            | 425        |            |            |            |            |      |
| TTA<br>Leu | GAG<br>Glu | CAA<br>Gln | ATC<br>Ile | AAA<br>Lys | AGA<br>Arg | GGG<br>Gly | AAG<br>Lys | TTG<br>Leu | ATT<br>Ile | TCC<br>Ser | GAT<br>Asp | CGC<br>Arg | GCT<br>Ala | AAA<br>Lys | AAC<br>Asn | 1347 |
|            | 430        |            |            |            |            | 435        |            |            |            |            | 440        |            |            |            |            |      |
| AAA<br>Lys | ATG<br>Met | GCT<br>Ala | AAA<br>Lys | TCC<br>Ser | AAT<br>Asn | TTA<br>Leu | AGG<br>Arg | TTG<br>Leu | GTG<br>Val | GTG<br>Val | AGC<br>Ser | ATC<br>Ile | GCT<br>Ala | AAA<br>Lys | CGA<br>Arg | 1395 |
|            | 445        |            |            |            |            | 450        |            |            |            |            | 455        |            |            |            |            |      |
| TTC<br>Phe | ACG<br>Thr | AGC<br>Ser | AGA<br>Arg | GGC<br>Gly | TTA<br>Leu | CCA<br>Pro | TTC<br>Phe | TTG<br>Leu | GAT<br>Asp | TTG<br>Leu | ATT<br>Ile | CAA<br>Gln | GAG<br>Glu | GGC<br>Gly | AAT<br>Asn | 1443 |
|            | 460        |            |            |            |            | 465        |            |            |            |            | 470        |            |            |            |            |      |
| ATT<br>Ile | GGC<br>Gly | TTG<br>Leu | ATG<br>Met | AAA<br>Lys | GCG<br>Ala | GTG<br>Val | GAT<br>Asp | AAG<br>Lys | TTT<br>Phe | GAG<br>Glu | CAT<br>His | GAA<br>Glu | AAG<br>Lys | GGC<br>Gly | TTC<br>Phe | 1491 |
|            | 480        |            |            |            |            | 485        |            |            |            |            | 490        |            |            |            |            |      |
| AAG<br>Lys | TTT<br>Phe | TCT<br>Ser | ACC<br>Thr | TAT<br>Tyr | GCG<br>Ala | ACC<br>Thr | TGG<br>Trp | TGG<br>Trp | ATC<br>Ile | AAA<br>Lys | CAA<br>Gln | GCT<br>Ala | ATC<br>Ile | AGC<br>Ser | AGA<br>Arg | 1539 |
|            | 495        |            |            |            |            | 500        |            |            |            |            | 505        |            |            |            |            |      |
| GCC<br>Ala | ATA<br>Ile | GCC<br>Ala | GAT<br>Asp | CAG<br>Gln | GCC<br>Ala | CGC<br>Arg | ACT<br>Thr | ATC<br>Ile | CGC<br>Arg | ATC<br>Ile | CCC<br>Pro | ATT<br>Ile | CAC<br>His | ATG<br>Met | ATT<br>Ile | 1587 |
|            | 510        |            |            |            |            | 515        |            |            |            |            | 520        |            |            |            |            |      |
| GAT<br>Asp | ACG<br>Thr | ATT<br>Ile | AAT<br>Asn | CGC<br>Arg | ATC<br>Ile | AAT<br>Asn | AAA<br>Lys | GTC<br>Val | ATG<br>Met | CGC<br>Arg | AAA<br>Lys | CAC<br>His | ATT<br>Ile | CAA<br>Gln | GAA<br>Glu | 1635 |
|            | 525        |            |            |            |            | 530        |            |            |            |            | 535        |            |            |            |            |      |
| AAC<br>Asn | GGC<br>Gly | AAA<br>Lys | GAG<br>Glu | CCT<br>Pro | GAT<br>Asp | TTA<br>Leu | GAA<br>Glu | GTG<br>Val | GTG<br>Val | GCT<br>Ala | GAA<br>Glu | GAA<br>Glu | GTG<br>Val | GGG<br>Gly | CTT<br>Leu | 1683 |
|            | 540        |            |            |            |            | 545        |            |            |            |            | 550        |            |            |            |            |      |
| TCG<br>Ser | TTA<br>Leu | GAT<br>Asp | AAA<br>Lys | GTG<br>Val | AAG<br>Lys | AAT<br>Asn | GTG<br>Val | ATT<br>Ile | AAG<br>Lys | GTG<br>Val | ACT<br>Thr | AAA<br>Lys | GAG<br>Glu | CCT<br>Pro | ATC<br>Ile | 1731 |
|            | 560        |            |            |            |            | 565        |            |            |            |            | 570        |            |            |            |            |      |
| AGT<br>Ser | TTG<br>Leu | GAA<br>Glu | ACC<br>Thr | CCA<br>Pro | GTC<br>Val | GGC<br>Gly | AAT<br>Asn | GAT<br>Asp | GAT<br>Asp | GAT<br>Asp | GGC<br>Gly | AAG<br>Lys | TTT<br>Phe | GGG<br>Gly | GAT<br>Asp | 1779 |
|            | 575        |            |            |            |            | 580        |            |            |            |            | 585        |            |            |            |            |      |
| TTC<br>Phe | GTG<br>Val | GAA<br>Glu | GAT<br>Asp | AAG<br>Lys | AAT<br>Asn | ATC<br>Ile | GTC<br>Val | AGC<br>Ser | TCC<br>Ser | ATT<br>Ile | GAT<br>Asp | CAC<br>His | ATC<br>Ile | ATG<br>Met | CGA<br>Arg | 1827 |
|            | 590        |            |            |            |            | 595        |            |            |            |            | 600        |            |            |            |            |      |
| GAA<br>Glu | GAT<br>Asp | TTG<br>Leu | AAA<br>Lys | GCA<br>Ala | CAA<br>Gln | ATT<br>Ile | GAA<br>Glu | AGC<br>Ser | GTT<br>Val | TTG<br>Leu | GAT<br>Asp | CAG<br>Gln | TTG<br>Leu | AAT<br>Asn | GAG<br>Glu | 1875 |
|            | 605        |            |            |            |            | 610        |            |            |            |            | 615        |            |            |            |            |      |
| CGA<br>Arg | GAA<br>Glu | AAA<br>Lys | GCG<br>Ala | GTG<br>Val | ATC<br>Ile | CGC<br>Arg | ATG<br>Met | CGT<br>Arg | TTT<br>Phe | GGG<br>Gly | CTT<br>Leu | TTA<br>Leu | GAC<br>Asp | GAT<br>Asp | GAA<br>Glu | 1923 |
|            | 620        |            |            |            |            | 625        |            |            |            |            | 630        |            |            |            |            |      |
| AGC<br>Ser | GAT<br>Asp | CGA<br>Arg | ACT<br>Thr | TTA<br>Leu | GAA<br>Glu | GAA<br>Glu | ATT<br>Ile | GGC<br>Gly | AAG<br>Lys | GAA<br>Glu | TTG<br>Leu | AAT<br>Asn | GTT<br>Val | ACT<br>Thr | AGA<br>Arg | 1971 |
|            | 640        |            |            |            |            | 645        |            |            |            |            | 650        |            |            |            |            |      |





|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Glu | Trp | Leu | Lys | Ala | Leu | Glu | Ala | Pro | Ile | Asp | Glu | Arg | Glu | Asp |
| 290 |     |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Glu | Leu | Val | Arg | Ser | Leu | Thr | Leu | Ala | Tyr | Lys | Arg | Gln | Thr | Leu | Lys |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Asp | Arg | Leu | Tyr | Asp | Leu | Glu | Pro | Thr | Ser | Lys | Leu | Ile | Asn | Glu | Leu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Val | Lys | Thr | Met | Glu | Thr | Thr | Leu | Lys | Ser | Gly | Asp | Gly | Phe | Glu | Lys |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Glu | Leu | Lys | Arg | Leu | Glu | Tyr | Lys | Leu | Pro | Leu | Phe | Asn | Asp | Thr | Leu |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ile | Ala | Asn | His | Lys | Lys | Ile | Leu | Ala | Asn | Ile | Thr | Asn | Met | Thr | Lys |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Glu | Asp | Ile | Ile | Ala | Gln | Val | Pro | Glu | Ala | Thr | Met | Val | Ser | Val | Tyr |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Met | Asp | Leu | Lys | Lys | Leu | Phe | Leu | Thr | Lys | Glu | Ala | Ser | Glu | Glu | Gly |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Phe | Asp | Leu | Ala | Pro | Asn | Lys | Leu | Lys | Glu | Ile | Leu | Glu | Gln | Ile | Lys |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Arg | Gly | Lys | Leu | Ile | Ser | Asp | Arg | Ala | Lys | Asn | Lys | Met | Ala | Lys | Ser |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Asn | Leu | Arg | Leu | Val | Val | Ser | Ile | Ala | Lys | Arg | Phe | Thr | Ser | Arg | Gly |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Leu | Pro | Phe | Leu | Asp | Leu | Ile | Gln | Glu | Gly | Asn | Ile | Gly | Leu | Met | Lys |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Ala | Val | Asp | Lys | Phe | Glu | His | Glu | Lys | Gly | Phe | Lys | Phe | Ser | Thr | Tyr |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Ala | Thr | Trp | Trp | Ile | Lys | Gln | Ala | Ile | Ser | Arg | Ala | Ile | Ala | Asp | Gln |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Ala | Arg | Thr | Ile | Arg | Ile | Pro | Ile | His | Met | Ile | Asp | Thr | Ile | Asn | Arg |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Ile | Asn | Lys | Val | Met | Arg | Lys | His | Ile | Gln | Glu | Asn | Gly | Lys | Glu | Pro |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Asp | Leu | Glu | Val | Val | Ala | Glu | Glu | Val | Gly | Leu | Ser | Leu | Asp | Lys | Val |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |
| Lys | Asn | Val | Ile | Lys | Val | Thr | Lys | Glu | Pro | Ile | Ser | Leu | Glu | Thr | Pro |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |
| Val | Gly | Asn | Asp | Asp | Asp | Gly | Lys | Phe | Gly | Asp | Phe | Val | Glu | Asp | Lys |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     | 590 |     |     |     |
| Asn | Ile | Val | Ser | Ser | Ile | Asp | His | Ile | Met | Arg | Glu | Asp | Leu | Lys | Ala |
|     |     | 595 |     |     |     | 600 |     |     |     |     |     | 605 |     |     |     |
| Gln | Ile | Glu | Ser | Val | Leu | Asp | Gln | Leu | Asn | Glu | Arg | Glu | Lys | Ala | Val |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |
| Ile | Arg | Met | Arg | Phe | Gly | Leu | Leu | Asp | Asp | Glu | Ser | Asp | Arg | Thr | Leu |
| 625 |     |     |     | 630 |     |     |     |     |     | 635 |     |     |     |     | 640 |
| Glu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 25...717  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AAGAATACGT GTGATTGGGA GAAA ATG GTG CAA AAA ATT GGC ATT TTA GGG  | 51  |
| Met Val Gln Lys Ile Gly Ile Leu Gly                             |     |
| 1 5                                                             |     |
| GCG ATG AGA GAA GAA ATA ACC CCT ATA CTA GAA TTG TTT GGC GTG GAT | 99  |
| Ala Met Arg Glu Glu Ile Thr Pro Ile Leu Glu Leu Phe Gly Val Asp |     |
| 10 15 20 25                                                     |     |
| TTT GAA GAG ATC CCT TTA GGG GGG AAT GTC TTC CAT AAA GGC GTT TAT | 147 |
| Phe Glu Glu Ile Pro Leu Gly Gly Asn Val Phe His Lys Gly Val Tyr |     |
| 30 35 40                                                        |     |
| CAC AAC AAG GAA ATC ATT GTC GCT TAT AGC AAG ATT GGC AAG GTG CAT | 195 |
| His Asn Lys Glu Ile Ile Val Ala Tyr Ser Lys Ile Gly Lys Val His |     |
| 45 50 55                                                        |     |
| TCC ACT TTA ACC ACA ACG AGC ATG ATT TTA GCG TTT GGC GTT CAA AAG | 243 |
| Ser Thr Leu Thr Thr Thr Ser Met Ile Leu Ala Phe Gly Val Gln Lys |     |
| 60 65 70                                                        |     |
| GTG CTT TTT AGC GGG GTG GCT GGA AGC TTA GTT AAA GAT TTA AAA ATC | 291 |
| Val Leu Phe Ser Gly Val Ala Gly Ser Leu Val Lys Asp Leu Lys Ile |     |
| 75 80 85                                                        |     |
| AAT GAT TTA CTA GTG GCT ATT CAA TTA GTC CAG CAT GAT GTG GAT TTG | 339 |
| Asn Asp Leu Leu Val Ala Ile Gln Leu Val Gln His Asp Val Asp Leu |     |
| 90 95 100 105                                                   |     |
| AGC GCG TTT GAT CAC CCT TTA GGG TTC ATC CCA GAA AGC GCG ATT TTT | 387 |
| Ser Ala Phe Asp His Pro Leu Gly Phe Ile Pro Glu Ser Ala Ile Phe |     |
| 110 115 120                                                     |     |
| ATT GAA ACG AGC GAA AGT TTG AAC GCT TTG GCT AAA GAA GTC GCT AAT | 435 |
| Ile Glu Thr Ser Glu Ser Leu Asn Ala Leu Ala Lys Glu Val Ala Asn |     |
| 125 130 135                                                     |     |
| GAA CAG CAT ATC GTG CTC AAA GAA GGC GTC ATC GCA TCA GGC GAT CAG | 483 |
| Glu Gln His Ile Val Leu Lys Glu Gly Val Ile Ala Ser Gly Asp Gln |     |
| 140 145 150                                                     |     |
| TTT GTG CAT AGC AAA GAA AGG AAA GAG TTT TTA GTT AGC GAG TTT AAA | 531 |
| Phe Val His Ser Lys Glu Arg Lys Glu Phe Leu Val Ser Glu Phe Lys |     |
| 155 160 165                                                     |     |
| GCG AGC GCG GTG GAA ATG GAG GGG GCG AGC GTG GCG TTT GTG TGC CAA | 579 |
| Ala Ser Ala Val Glu Met Glu Gly Ala Ser Val Ala Phe Val Cys Gln |     |
| 170 175 180 185                                                 |     |



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1986 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:
- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 56...1945  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

|                                                                 |                 |
|-----------------------------------------------------------------|-----------------|
| GGTGTCTTA AACAGCAGGG TGAAAGAGAT TTAAAAAGAA AGCGCTCTGC ATTCT ATG | 58              |
|                                                                 | Met             |
|                                                                 | 1               |
| CAA GAT AGT TTG CAT TTT AAG GTT AAT GAA GTG CAA GGG GTT TTA GAA | 106             |
| Gln Asp Ser Leu His Phe Lys Val Asn Glu Val Gln Gly Val Leu Glu |                 |
|                                                                 | 5 10 15         |
| AAC ACT TAT ACG AGC ATG GGC ATT GTT AAA GAA ATG CTC CCT AAA GAC | 154             |
| Asn Thr Tyr Thr Ser Met Gly Ile Val Lys Glu Met Leu Pro Lys Asp |                 |
|                                                                 | 20 25 30        |
| ACC AAA AGA GAA ATC AAA ATC GGC TTG TTA AAA AAC TTC ATT TTA GCC | 202             |
| Thr Lys Arg Glu Ile Lys Ile Gly Leu Leu Lys Asn Phe Ile Leu Ala |                 |
|                                                                 | 35 40 45        |
| AAT TCG CAT GTC GCT GGG GTG AGC ATG TTT TTT AAA GGC AGA GAA GAT | 250             |
| Asn Ser His Val Ala Gly Val Ser Met Phe Phe Lys Gly Arg Glu Asp |                 |
|                                                                 | 50 55 60 65     |
| TTA AGA TTA ACG CTT TTA AGG GAT AAC AAT ACG ATT AAG CTA GTG GAA | 298             |
| Leu Arg Leu Thr Leu Leu Arg Asp Asn Asn Thr Ile Lys Leu Val Glu |                 |
|                                                                 | 70 75 80        |
| AAT CCG TCA TTA GAG AAT AGC CCT TTA GCG CAA AAA GCG ATG AAA AAT | 346             |
| Asn Pro Ser Leu Glu Asn Ser Pro Leu Ala Gln Lys Ala Met Lys Asn |                 |
|                                                                 | 85 90 95        |
| AAA GAA ATT TCT AAA AGT TTG GGT TAT TAT AGG AAA ATG CCT AAT GGG | 394             |
| Lys Glu Ile Ser Lys Ser Leu Gly Tyr Tyr Arg Lys Met Pro Asn Gly |                 |
|                                                                 | 100 105 110     |
| GCG GAA GTT TAT GGG GTG GAT ATT CTT TTA CCT TTA TTG AAT GAG AAC | 442             |
| Ala Glu Val Tyr Gly Val Asp Ile Leu Leu Pro Leu Leu Asn Glu Asn |                 |
|                                                                 | 115 120 125     |
| GCT CAA GAG GTT GTA GGG GCT TTG ATG ATT TTT ATT TCC ATT GAC AGC | 490             |
| Ala Gln Glu Val Val Gly Ala Leu Met Ile Phe Ile Ser Ile Asp Ser |                 |
|                                                                 | 130 135 140 145 |
| TTC AGC AAT GAA ATC ACT AAA AAC AGG AGC GAT TTA TTT TTA ATT GGC | 538             |
| Phe Ser Asn Glu Ile Thr Lys Asn Arg Ser Asp Leu Phe Leu Ile Gly |                 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |  |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|--|--|--|--|--|
|     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     |     | 160 |      |  |  |  |  |  |  |
| ACT | AAA | GGT | AAA | GTG | CTT | TTG | AGC | GCG | AAT | AAG | AGT | TTG | CAA | GAC | AAA | 586  |  |  |  |  |  |  |
| Thr | Lys | Gly | Lys | Val | Leu | Leu | Ser | Ala | Asn | Lys | Ser | Leu | Gln | Asp | Lys |      |  |  |  |  |  |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     |     | 175 |      |  |  |  |  |  |  |
| CCT | ATC | GCA | GAA | ATT | TAT | AAG | AGC | GTG | CCT | AAA | GCC | ACC | AAC | GAA | GTG | 634  |  |  |  |  |  |  |
| Pro | Ile | Ala | Glu | Ile | Tyr | Lys | Ser | Val | Pro | Lys | Ala | Thr | Asn | Glu | Val |      |  |  |  |  |  |  |
|     |     |     | 180 |     |     |     |     |     | 185 |     |     |     |     |     | 190 |      |  |  |  |  |  |  |
| ATG | GCT | ATT | TTA | GAA | AAC | GGC | TCT | AAA | GCG | ACT | TTA | GAA | TAC | TTA | GAT | 682  |  |  |  |  |  |  |
| Met | Ala | Ile | Leu | Glu | Asn | Gly | Ser | Lys | Ala | Thr | Leu | Glu | Tyr | Leu | Asp |      |  |  |  |  |  |  |
|     |     |     | 195 |     |     |     |     |     | 200 |     |     |     |     |     | 205 |      |  |  |  |  |  |  |
| CCC | TTT | AGC | CAT | AAG | GAA | AAT | TTT | TTA | GCC | GTT | GAA | ACC | TTT | AAA | ATG | 730  |  |  |  |  |  |  |
| Pro | Phe | Ser | His | Lys | Glu | Asn | Phe | Leu | Ala | Val | Glu | Thr | Phe | Lys | Met |      |  |  |  |  |  |  |
| 210 |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |     | 225 |      |  |  |  |  |  |  |
| CTA | GGC | AAA | ACA | GAA | AGT | AAA | GAC | AAT | CTT | AAT | TGG | ATG | ATC | GCT | TTA | 778  |  |  |  |  |  |  |
| Leu | Gly | Lys | Thr | Glu | Ser | Lys | Asp | Asn | Leu | Asn | Trp | Met | Ile | Ala | Leu |      |  |  |  |  |  |  |
|     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     |     | 240 |      |  |  |  |  |  |  |
| ATC | ATT | GAA | AAA | GAC | AAG | GTC | TAT | GAG | CAA | GTA | GGC | TCG | GTG | CGT | TTT | 826  |  |  |  |  |  |  |
| Ile | Ile | Glu | Lys | Asp | Lys | Val | Tyr | Glu | Gln | Val | Gly | Ser | Val | Arg | Phe |      |  |  |  |  |  |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     |     | 255 |      |  |  |  |  |  |  |
| GTG | GTG | ATC | ATA | GCG | AGC | GCA | ATC | ATG | GTG | TTA | GCC | TTG | ATT | ATA | GCG | 874  |  |  |  |  |  |  |
| Val | Val | Ile | Ile | Ala | Ser | Ala | Ile | Met | Val | Leu | Ala | Leu | Ile | Ile | Ala |      |  |  |  |  |  |  |
|     |     |     | 260 |     |     |     |     |     | 265 |     |     |     |     |     | 270 |      |  |  |  |  |  |  |
| ATC | ACT | CTC | TTA | ATG | CGA | GCG | ATC | GTG | AGC | AGT | CGT | TTG | GAA | GCC | GTT | 922  |  |  |  |  |  |  |
| Ile | Thr | Leu | Leu | Met | Arg | Ala | Ile | Val | Ser | Ser | Arg | Leu | Glu | Ala | Val |      |  |  |  |  |  |  |
|     |     |     | 275 |     |     |     |     |     | 280 |     |     |     |     |     | 285 |      |  |  |  |  |  |  |
| TCT | AGC | ACC | TTG | TCT | CAT | TTC | TTT | AAA | TTA | TTG | AAC | AAT | CAA | GCC | AAT | 970  |  |  |  |  |  |  |
| Ser | Ser | Thr | Leu | Ser | His | Phe | Phe | Lys | Leu | Leu | Asn | Asn | Gln | Ala | Asn |      |  |  |  |  |  |  |
| 290 |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |     | 305 |      |  |  |  |  |  |  |
| TCT | AGC | GGT | ATT | AAA | TTG | ATT | GAA | GCG | AAA | TCC | AAT | GAC | GAG | TTA | GGC | 1018 |  |  |  |  |  |  |
| Ser | Ser | Gly | Ile | Lys | Leu | Ile | Glu | Ala | Lys | Ser | Asn | Asp | Glu | Leu | Gly |      |  |  |  |  |  |  |
|     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     |     | 320 |      |  |  |  |  |  |  |
| CGC | ATG | CAA | ACA | GCG | ATC | AAT | AAA | AAT | ATC | TTG | CAA | ACC | CAA | AAA | ATC | 1066 |  |  |  |  |  |  |
| Arg | Met | Gln | Thr | Ala | Ile | Asn | Lys | Asn | Ile | Leu | Gln | Thr | Gln | Lys | Ile |      |  |  |  |  |  |  |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     |     | 335 |      |  |  |  |  |  |  |
| ATG | CAA | GAA | GAC | AGG | CAA | GCC | GTC | CAA | GAC | ACC | ATT | AAA | GTG | GTT | TCA | 1114 |  |  |  |  |  |  |
| Met | Gln | Glu | Asp | Arg | Gln | Ala | Val | Gln | Asp | Thr | Ile | Lys | Val | Val | Ser |      |  |  |  |  |  |  |
|     |     |     | 340 |     |     |     |     |     | 345 |     |     |     |     |     | 350 |      |  |  |  |  |  |  |
| GAT | GTG | AAA | GCA | GGG | AAT | TTT | GCG | GTG | CGC | ATC | ACG | GCT | GAG | CCC | GCA | 1162 |  |  |  |  |  |  |
| Asp | Val | Lys | Ala | Gly | Asn | Phe | Ala | Val | Arg | Ile | Thr | Ala | Glu | Pro | Ala |      |  |  |  |  |  |  |
|     |     |     | 355 |     |     |     |     |     | 360 |     |     |     |     |     | 365 |      |  |  |  |  |  |  |
| AGC | CCT | GAT | TTG | AAA | GAA | TTG | AGG | GAC | GCG | CTA | AAT | GGG | ATC | ATG | GAT | 1210 |  |  |  |  |  |  |
| Ser | Pro | Asp | Leu | Lys | Glu | Leu | Arg | Asp | Ala | Leu | Asn | Gly | Ile | Met | Asp |      |  |  |  |  |  |  |
| 370 |     |     | 375 |     |     |     |     |     | 380 |     |     |     |     |     | 385 |      |  |  |  |  |  |  |

|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| TAT<br>Tyr        | TTG<br>Leu        | CAA<br>Gln        | GAA<br>Glu        | AGC<br>Ser<br>390 | GTA<br>Val        | GGG<br>Gly        | ACT<br>Thr        | CAC<br>His        | ATG<br>Met<br>395 | CCA<br>Pro        | AGC<br>Ser        | ATT<br>Ile        | TTC<br>Phe        | AAA<br>Lys<br>400 | ATC<br>Ile        | 1258 |
| TTT<br>Phe        | GAA<br>Glu        | AGC<br>Ser        | TAT<br>Tyr<br>405 | TCT<br>Ser        | GGT<br>Gly        | TTG<br>Leu        | GAT<br>Asp        | TTT<br>Phe<br>410 | AGA<br>Arg        | GGC<br>Gly        | CGG<br>Arg        | ATC<br>Ile        | CAA<br>Gln<br>415 | AAC<br>Asn        | GCT<br>Ala        | 1306 |
| TCG<br>Ser        | GGT<br>Gly        | AGG<br>Arg<br>420 | GTG<br>Val        | GAA<br>Glu        | CTG<br>Leu        | GTT<br>Val        | ACT<br>Thr<br>425 | AAC<br>Asn        | GCT<br>Ala        | TTA<br>Leu        | GGG<br>Gly        | CAA<br>Gln<br>430 | GAA<br>Glu        | ATC<br>Ile        | CAA<br>Gln        | 1354 |
| AAA<br>Lys        | ATG<br>Met<br>435 | CTA<br>Leu        | GAA<br>Glu        | ACT<br>Thr        | TCG<br>Ser        | TCT<br>Ser<br>440 | AAT<br>Asn        | TTT<br>Phe        | GCC<br>Ala        | AAA<br>Lys        | GAT<br>Asp<br>445 | TTA<br>Leu        | GCG<br>Ala        | AAC<br>Asn        | GAT<br>Asp        | 1402 |
| AGC<br>Ser<br>450 | GCG<br>Ala        | AAT<br>Asn        | TTA<br>Leu        | AAA<br>Lys        | GAG<br>Glu<br>455 | TGC<br>Cys        | GTG<br>Val        | CAA<br>Gln        | AAT<br>Asn        | TTA<br>Leu<br>460 | GAA<br>Glu        | AAA<br>Lys        | GCT<br>Ala        | TCA<br>Ser        | AAC<br>Asn<br>465 | 1450 |
| TCC<br>Ser        | CAA<br>Gln        | CAC<br>His        | AAA<br>Lys        | AGC<br>Ser<br>470 | TTG<br>Leu        | ATG<br>Met        | GAA<br>Glu        | ACT<br>Thr        | TCC<br>Ser<br>475 | AAA<br>Lys        | ACG<br>Thr        | ATA<br>Ile        | GAA<br>Glu        | AAT<br>Asn<br>480 | ATC<br>Ile        | 1498 |
| ACC<br>Thr        | ACT<br>Thr        | TCC<br>Ser        | ATT<br>Ile<br>485 | CAA<br>Gln        | GGC<br>Gly        | GTG<br>Val        | AGC<br>Ser        | TCT<br>Ser<br>490 | CAA<br>Gln        | AGT<br>Ser        | GAA<br>Glu        | GCC<br>Ala        | ATG<br>Met<br>495 | ATT<br>Ile        | GAA<br>Glu        | 1546 |
| CAA<br>Gln        | GGG<br>Gly<br>500 | CAA<br>Gln        | GAC<br>Asp        | ATT<br>Ile        | AAA<br>Lys        | AGC<br>Ser        | ATT<br>Ile<br>505 | GTA<br>Val        | GAA<br>Glu        | ATC<br>Ile        | ATT<br>Ile        | AGA<br>Arg<br>510 | GAT<br>Asp        | ATT<br>Ile        | GCT<br>Ala        | 1594 |
| GAT<br>Asp        | CAA<br>Gln<br>515 | ACC<br>Thr        | AAT<br>Asn        | CTT<br>Leu        | TTA<br>Leu        | GCC<br>Ala<br>520 | TTA<br>Leu        | AAC<br>Asn        | GCC<br>Ala        | GCT<br>Ala        | ATT<br>Ile<br>525 | GAA<br>Glu        | GCC<br>Ala        | GCA<br>Ala        | AGG<br>Arg        | 1642 |
| GCC<br>Ala<br>530 | GGC<br>Gly        | GAG<br>Glu        | CAT<br>His        | GGC<br>Gly        | AGA<br>Arg<br>535 | GGC<br>Gly        | TTT<br>Phe        | GCG<br>Ala        | GTG<br>Val        | GTG<br>Val<br>540 | GCT<br>Ala        | GAT<br>Asp        | GAG<br>Glu        | GTA<br>Val        | AGA<br>Arg<br>545 | 1690 |
| AAG<br>Lys        | CTC<br>Leu        | GCT<br>Ala        | GAA<br>Glu        | AGG<br>Arg<br>550 | ACG<br>Thr        | CAA<br>Gln        | AAA<br>Lys        | TCG<br>Ser        | CTC<br>Leu<br>555 | AGC<br>Ser        | GAG<br>Glu        | ATT<br>Ile        | GAA<br>Glu        | GCC<br>Ala<br>560 | AAT<br>Asn        | 1738 |
| ATC<br>Ile        | AAT<br>Asn        | ATT<br>Ile        | TTA<br>Leu<br>565 | GTG<br>Val        | CAA<br>Gln        | AGC<br>Ser        | ATT<br>Ile        | TCA<br>Ser<br>570 | GAC<br>Asp        | ACG<br>Thr        | AGC<br>Ser        | GAA<br>Glu        | AGC<br>Ser<br>575 | ATT<br>Ile        | AAA<br>Lys        | 1786 |
| AAC<br>Asn        | CAG<br>Gln        | GTT<br>Val<br>580 | AAA<br>Lys        | GAA<br>Glu        | GTG<br>Val        | GAA<br>Glu        | GAA<br>Glu<br>585 | ATC<br>Ile        | AAC<br>Asn        | GCT<br>Ala        | TCT<br>Ser        | ATT<br>Ile<br>590 | GAA<br>Glu        | GCC<br>Ala        | TTA<br>Leu        | 1834 |
| AGA<br>Arg        | TCG<br>Ser<br>595 | GTT<br>Val        | ACT<br>Thr        | GAG<br>Glu        | GGC<br>Gly        | AAT<br>Asn<br>600 | CTA<br>Leu        | AAA<br>Lys        | ATC<br>Ile        | GCT<br>Ala        | AGC<br>Ser<br>605 | GAT<br>Asp        | TCT<br>Ser        | TTA<br>Leu        | GAA<br>Glu        | 1882 |
| ATC<br>Ile        | AGT<br>Ser        | CAA<br>Gln        | GAA<br>Glu        | ATT<br>Ile        | GAC<br>Asp        | AAA<br>Lys        | GTT<br>Val        | TCT<br>Ser        | AAC<br>Asn        | GAT<br>Asp        | ATT<br>Ile        | TTA<br>Leu        | GAA<br>Glu        | GAT<br>Asp        | GTG<br>Val        | 1930 |

610

615

620

625

AAT AAA AAG CAG TTT TAATGCTCAT TCATATTTGC TGCTCAGTGG ATAACCTCTA T 1986  
 Asn Lys Lys Gln Phe  
 630

1986

## (2) INFORMATION FOR SEQ ID NO:460:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 630 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

Met Gln Asp Ser Leu His Phe Lys Val Asn Glu Val Gln Gly Val Leu  
 1 5 10 15  
 Glu Asn Thr Tyr Thr Ser Met Gly Ile Val Lys Glu Met Leu Pro Lys  
 20 25 30  
 Asp Thr Lys Arg Glu Ile Lys Ile Gly Leu Leu Lys Asn Phe Ile Leu  
 35 40 45  
 Ala Asn Ser His Val Ala Gly Val Ser Met Phe Phe Lys Gly Arg Glu  
 50 55 60  
 Asp Leu Arg Leu Thr Leu Leu Arg Asp Asn Asn Thr Ile Lys Leu Val  
 65 70 75 80  
 Glu Asn Pro Ser Leu Glu Asn Ser Pro Leu Ala Gln Lys Ala Met Lys  
 85 90 95  
 Asn Lys Glu Ile Ser Lys Ser Leu Gly Tyr Tyr Arg Lys Met Pro Asn  
 100 105 110  
 Gly Ala Glu Val Tyr Gly Val Asp Ile Leu Leu Pro Leu Leu Asn Glu  
 115 120 125  
 Asn Ala Gln Glu Val Val Gly Ala Leu Met Ile Phe Ile Ser Ile Asp  
 130 135 140  
 Ser Phe Ser Asn Glu Ile Thr Lys Asn Arg Ser Asp Leu Phe Leu Ile  
 145 150 155 160  
 Gly Thr Lys Gly Lys Val Leu Leu Ser Ala Asn Lys Ser Leu Gln Asp  
 165 170 175  
 Lys Pro Ile Ala Glu Ile Tyr Lys Ser Val Pro Lys Ala Thr Asn Glu  
 180 185 190  
 Val Met Ala Ile Leu Glu Asn Gly Ser Lys Ala Thr Leu Glu Tyr Leu  
 195 200 205  
 Asp Pro Phe Ser His Lys Glu Asn Phe Leu Ala Val Glu Thr Phe Lys  
 210 215 220  
 Met Leu Gly Lys Thr Glu Ser Lys Asp Asn Leu Asn Trp Met Ile Ala  
 225 230 235 240  
 Leu Ile Ile Glu Lys Asp Lys Val Tyr Glu Gln Val Gly Ser Val Arg  
 245 250 255  
 Phe Val Val Ile Ile Ala Ser Ala Ile Met Val Leu Ala Leu Ile Ile  
 260 265 270  
 Ala Ile Thr Leu Leu Met Arg Ala Ile Val Ser Ser Arg Leu Glu Ala  
 275 280 285  
 Val Ser Ser Thr Leu Ser His Phe Phe Lys Leu Leu Asn Asn Gln Ala  
 290 295 300



[illegible]

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1758 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 8...1702  
(D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

|         |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GAGATAA | ATG | ATG | TTT | TCT | TCA | ATG | TTT | GCT | TCG | TTG | GGG | ACT | CGT | ATC | 49  |     |
| Met     | Met | Phe | Ser | Ser | Met | Phe | Ala | Ser | Leu | Gly | Thr | Arg | Ile |     |     |     |
| 1       |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     |     |     |
| ATG     | CTG | GTC | GTG | TTA | GCC | GCT | CTT | TTA | GGT | TTA | GGG | GGG | CTT | TTT | ATT | 97  |
| Met     | Leu | Val | Val | Leu | Ala | Ala | Leu | Leu | Gly | Leu | Gly | Gly | Leu | Phe | Ile |     |
| 15      |     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |
| GGT     | TTT | GTA | AAG | GTT | ATG | CAA | AAA | GAT | GTG | TTA | GCG | CAA | CTC | ATG | GAG | 145 |
| Gly     | Phe | Val | Lys | Val | Met | Gln | Lys | Asp | Val | Leu | Ala | Gln | Leu | Met | Glu |     |
|         |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| CAT     | TTA | GAA | ACC | GGG | CAA | TAC | AAA | AAG | CGT | GAA | AAA | ACG | CTC | GCT | TAC | 193 |
| His     | Leu | Glu | Thr | Gly | Gln | Tyr | Lys | Lys | Arg | Glu | Lys | Thr | Leu | Ala | Tyr |     |
|         |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| ATG     | ACA | AAA | ATT | ATT | GAA | CAG | GGC | ATT | CAT | GAG | TAT | TAC | AAA | AAT | TTT | 241 |
| Met     | Thr | Lys | Ile | Ile | Glu | Gln | Gly | Ile | His | Glu | Tyr | Tyr | Lys | Asn | Phe |     |
|         |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |
| GAC     | AAT | GCT | ACT | GCA | AGA | AAA | ATG | GCG | TTA | GAT | TAT | TTC | AAA | CGC | ATC | 289 |
| Asp     | Asn | Ala | Thr | Ala | Arg | Lys | Met | Ala | Leu | Asp | Tyr | Phe | Lys | Arg | Ile |     |
|         | 80  |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |
| AAC     | GAC | GAT | AAG | GGC | ATG | ATT | TAT | ATG | GTG | GTG | GTG | GAT | AAA | AAC | GGG | 337 |
| Asn     | Asp | Asp | Lys | Gly | Met | Ile | Tyr | Met | Val | Val | Val | Asp | Lys | Asn | Gly |     |
| 95      |     |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |
| GTG     | GTA | TTG | TTT | GAT | CCG | GTC | AAT | CCT | AAA | ACC | GTA | GNC | CAA | TCA | GGG | 385 |
| Val     | Val | Leu | Phe | Asp | Pro | Val | Asn | Pro | Lys | Thr | Val | Xaa | Gln | Ser | Gly |     |
|         |     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| CTT     | GAC | GCT | CAG | AGC | GTT | GAT | GGG | GTG | TAT | TAT | GTT | AGG | GGG | TAT | TTG | 433 |
| Leu     | Asp | Ala | Gln | Ser | Val | Asp | Gly | Val | Tyr | Tyr | Val | Arg | Gly | Tyr | Leu |     |
|         |     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| GAG     | GCG | GCC | AAA | AAA | GGG | GGA | GGC | TAC | ACT | TAT | TAT | AAA | ATG | CCT | AAA | 481 |
| Glu     | Ala | Ala | Lys | Lys | Gly | Gly | Gly | Tyr | Thr | Tyr | Tyr | Lys | Met | Pro | Lys |     |
|         |     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |
| TAC     | GAT | GGA | GGC | GTA | CCG | GAG | AAA | AAA | TTC | GCC | TAC | TCG | CAT | TAT | GAT | 529 |
| Tyr     | Asp | Gly | Gly | Val | Pro | Glu | Lys | Lys | Phe | Ala | Tyr | Ser | His | Tyr | Asp |     |
|         | 160 |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |
| GAA     | GTT | TCT | CAA | ATG | GTG | ATC | GCA | ACG | ACT | TCC | TAT | TAC | ACT | GAC | ATT | 577 |
| Glu     | Val | Ser | Gln | Met | Val | Ile | Ala | Thr | Thr | Ser | Tyr | Tyr | Thr | Asp | Ile |     |
| 175     |     |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |
| AAC     | ACA | GAA | AAT | AAA | GCG | ATC | AAA | GAA | GGC | GTG | AAT | AAG | GTT | TTT | GAT | 625 |
| Asn     | Thr | Glu | Asn | Lys | Ala | Ile | Lys | Glu | Gly | Val | Asn | Lys | Val | Phe | Asp |     |
|         |     |     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |
| GAA     | AAC | ACC | ACG | AAA | TTA | TTC | CTT | TGG | ATA | CTG | ACA | GCG | ACG | ATA | GCG | 673 |
| Glu     | Asn | Thr | Thr | Lys | Leu | Phe | Leu | Trp | Ile | Leu | Thr | Ala | Thr | Ile | Ala |     |
|         |     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |

|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| CTA<br>Leu        | GTG<br>Val        | GTT<br>Val<br>225 | TTG<br>Leu        | ACG<br>Thr        | CTC<br>Leu        | ATA<br>Ile        | TAC<br>Tyr<br>230 | GCT<br>Ala        | AAA<br>Lys        | TTA<br>Leu        | AGG<br>Arg        | ATC<br>Ile<br>235 | GTG<br>Val        | AAA<br>Lys        | CGC<br>Arg        | 721  |
| ATT<br>Ile        | GAT<br>Asp<br>240 | GAA<br>Glu        | CTG<br>Leu        | GTC<br>Val        | CTT<br>Leu        | AAA<br>Lys<br>245 | ATC<br>Ile        | AAC<br>Asn        | GCT<br>Ala        | TTT<br>Phe<br>250 | AGC<br>Ser        | CGT<br>Arg        | GGG<br>Gly        | GAT<br>Asp        | AAG<br>Lys        | 769  |
| GAT<br>Asp<br>255 | TTG<br>Leu        | AGA<br>Arg        | GCC<br>Ala        | AAA<br>Lys<br>260 | ATT<br>Ile        | GAT<br>Asp        | GTG<br>Val        | GGT<br>Gly        | GAT<br>Asp<br>265 | CGC<br>Arg        | AAC<br>Asn        | GAT<br>Asp        | GAA<br>Glu        | ATC<br>Ile        | TCG<br>Ser<br>270 | 817  |
| CAA<br>Gln        | GTG<br>Val        | GGC<br>Gly        | CGT<br>Arg        | GGG<br>Gly<br>275 | ATC<br>Ile        | AAT<br>Asn        | TTG<br>Leu        | TTT<br>Phe<br>280 | GTG<br>Val        | GAA<br>Glu        | AAC<br>Asn        | GCC<br>Ala        | CGC<br>Arg        | TTG<br>Leu<br>285 | ATT<br>Ile        | 865  |
| ATG<br>Met        | GAA<br>Glu        | GAG<br>Glu        | ATT<br>Ile<br>290 | AAA<br>Lys        | GGG<br>Gly        | ATT<br>Ile        | TCC<br>Ser        | ACC<br>Thr<br>295 | CTC<br>Leu        | AAT<br>Asn        | AAA<br>Lys        | ACT<br>Thr<br>300 | TCA<br>Ser        | ATG<br>Met        | GAT<br>Asp        | 913  |
| AAA<br>Lys        | TTA<br>Leu        | GTC<br>Val<br>305 | CAA<br>Gln        | ATC<br>Ile        | ACG<br>Thr        | CAA<br>Gln        | GAA<br>Glu<br>310 | ACC<br>Thr        | CAA<br>Gln        | AAG<br>Lys        | AGC<br>Ser        | ATG<br>Met<br>315 | AAA<br>Lys        | GAT<br>Asp        | TCC<br>Ser        | 961  |
| TCA<br>Ser        | ACC<br>Thr<br>320 | ACC<br>Thr        | CTA<br>Leu        | AAT<br>Asn        | TCC<br>Ser        | GTG<br>Val<br>325 | AAA<br>Lys        | AAT<br>Asn        | AAA<br>Lys        | GCC<br>Ala        | ACT<br>Thr<br>330 | GAT<br>Asp        | ATA<br>Ile        | GCG<br>Ala        | AGC<br>Ser        | 1009 |
| ATG<br>Met<br>335 | ATG<br>Met        | AAT<br>Asn        | GCT<br>Ala        | TCC<br>Ser        | ATA<br>Ile<br>340 | GAG<br>Glu        | CAA<br>Gln        | TCT<br>Ser        | CAA<br>Gln        | GGG<br>Gly<br>345 | TTA<br>Leu        | AGG<br>Arg        | AAG<br>Lys        | CGT<br>Arg        | TTG<br>Leu<br>350 | 1057 |
| ATT<br>Ile        | GAA<br>Glu        | ACG<br>Thr        | CAA<br>Gln        | GGG<br>Gly<br>355 | CTG<br>Leu        | GTC<br>Val        | AAA<br>Lys        | GAG<br>Glu        | AGC<br>Ser<br>360 | AAG<br>Lys        | GAT<br>Asp        | GCG<br>Ala        | ATC<br>Ile        | GGG<br>Gly<br>365 | GAT<br>Asp        | 1105 |
| TTA<br>Leu        | TTT<br>Phe        | TCT<br>Ser        | CAA<br>Gln<br>370 | ATC<br>Ile        | ACA<br>Thr        | GAG<br>Glu        | AGC<br>Ser        | GCG<br>Ala<br>375 | CAC<br>His        | ACT<br>Thr        | GAA<br>Glu        | GAG<br>Glu        | GAA<br>Glu<br>380 | CTC<br>Leu        | TCT<br>Ser        | 1153 |
| AGC<br>Ser        | AAA<br>Lys        | GTG<br>Val<br>385 | GAG<br>Glu        | CAG<br>Gln        | CTA<br>Leu        | AGC<br>Ser        | CGT<br>Arg<br>390 | AAC<br>Asn        | GCT<br>Ala        | GAT<br>Asp        | GAT<br>Asp        | GTC<br>Val<br>395 | AAA<br>Lys        | TCC<br>Ser        | ATT<br>Ile        | 1201 |
| CTG<br>Leu        | GAT<br>Asp<br>400 | ATT<br>Ile        | ATC<br>Ile        | AAT<br>Asn        | GAT<br>Asp        | ATT<br>Ile<br>405 | GCC<br>Ala        | GAT<br>Asp        | CAA<br>Gln        | ACG<br>Thr<br>410 | AAT<br>Asn        | TTA<br>Leu        | TTA<br>Leu        | GCC<br>Ala        | CTA<br>Leu        | 1249 |
| AAC<br>Asn<br>415 | GCT<br>Ala        | GCT<br>Ala        | ATT<br>Ile        | GAA<br>Glu        | GCC<br>Ala<br>420 | GCA<br>Ala        | AGG<br>Arg        | GCT<br>Ala        | GGC<br>Gly        | GAG<br>Glu<br>425 | CAT<br>His        | GGC<br>Gly        | AGA<br>Arg        | GGC<br>Gly        | TTT<br>Phe<br>430 | 1297 |
| GCG<br>Ala        | GTG<br>Val        | GTG<br>Val        | GCT<br>Ala<br>435 | GAT<br>Asp        | GAA<br>Glu        | GTT<br>Val        | AGG<br>Arg        | AAT<br>Asn<br>440 | TTA<br>Leu        | GCC<br>Ala        | GGG<br>Gly        | CGC<br>Arg        | ACT<br>Thr        | CAA<br>Gln<br>445 | AAG<br>Lys        | 1345 |
| TCT<br>Ser        | TTA<br>Leu        | GCC<br>Ala        | GAA<br>Glu        | ATC<br>Ile        | AAT<br>Asn        | TCC<br>Ser        | ACT<br>Thr        | ATC<br>Ile        | ATG<br>Met        | GTG<br>Val        | ATT<br>Ile        | GTC<br>Val        | CAA<br>Gln        | GAA<br>Glu        | ATC<br>Ile        | 1393 |

| 450                      |     |     |     |     |     |     |            |            |            | 455  |     |     |     |     | 460  |      |  |  |  |  |
|--------------------------|-----|-----|-----|-----|-----|-----|------------|------------|------------|------|-----|-----|-----|-----|------|------|--|--|--|--|
| AAT                      | GCC | GTG | AGT | TCG | CAA | ATG | AAT        | CTC        | AAT        | TCG  | CAA | AAA | ATG | GAG | CGT  | 1441 |  |  |  |  |
| Asn                      | Ala | Val | Ser | Ser | Gln | Met | Asn        | Leu        | Asn        | Ser  | Gln | Lys | Met | Glu | Arg  |      |  |  |  |  |
| 465                      |     |     |     |     |     | 470 |            |            |            |      |     | 475 |     |     |      |      |  |  |  |  |
| TTG                      | AGC | GAT | ATG | AGT | AAA | AGC | GTG        | CAA        | GAA        | ACT  | TAC | GAA | AAA | ATG | AGT  | 1489 |  |  |  |  |
| Leu                      | Ser | Asp | Met | Ser | Lys | Ser | Val        | Gln        | Glu        | Thr  | Tyr | Glu | Lys | Met | Ser  |      |  |  |  |  |
| 480                      |     |     |     |     |     | 485 |            |            |            |      |     | 490 |     |     |      |      |  |  |  |  |
| TCT                      | AAT | TTA | AGC | TCA | GTC | GTG | TCA        | GAC        | AGC        | AAT  | CAA | AGC | ATG | GAC | GAT  | 1537 |  |  |  |  |
| Ser                      | Asn | Leu | Ser | Ser | Val | Val | Ser        | Asp        | Ser        | Asn  | Gln | Ser | Met | Asp | Asp  |      |  |  |  |  |
| 495                      |     |     |     |     |     | 500 |            |            |            |      |     | 505 |     |     | 510  |      |  |  |  |  |
| TAC                      | GCC | AAA | TCC | GGA | CAC | CAA | ATT        | GAA        | GTT        | ATG  | GTA | AGC | GAT | TTT | GCA  | 1585 |  |  |  |  |
| Tyr                      | Ala | Lys | Ser | Gly | His | Gln | Ile        | Glu        | Val        | Met  | Val | Ser | Asp | Phe | Ala  |      |  |  |  |  |
|                          |     |     | 515 |     |     |     |            |            | 520        |      |     |     |     |     | 525  |      |  |  |  |  |
| GAG                      | GTG | GAA | AAA | GTG | GCT | TCT | AAG        | ACT        | TTA        | GCG  | GAT | TCT | TCA | GAT | ATT  | 1633 |  |  |  |  |
| Glu                      | Val | Glu | Lys | Val | Ala | Ser | Lys        | Thr        | Leu        | Ala  | Asp | Ser | Ser | Asp | Ile  |      |  |  |  |  |
|                          |     |     | 530 |     |     |     |            |            | 535        |      |     |     |     |     | 540  |      |  |  |  |  |
| TTA                      | AAC | ATC | GCT | ACG | CAT | GTG | AGT        | GGA        | ACG        | ACC  | ATG | AAT | TTA | GAC | AAA  | 1681 |  |  |  |  |
| Leu                      | Asn | Ile | Ala | Thr | His | Val | Ser        | Gly        | Thr        | Thr  | Met | Asn | Leu | Asp | Lys  |      |  |  |  |  |
|                          |     |     | 545 |     |     |     |            |            | 550        |      |     |     |     |     | 555  |      |  |  |  |  |
| CAA                      | GTG | AAT | TTG | TTT | AAA | ACT | TAATCAGGGG | GAGTTTATTA | AAAAAGGGTT | GGAT |     |     |     |     |      | 1736 |  |  |  |  |
| Gln                      | Val | Asn | Leu | Phe | Lys | Thr |            |            |            |      |     |     |     |     |      |      |  |  |  |  |
|                          |     |     | 560 |     |     | 565 |            |            |            |      |     |     |     |     |      |      |  |  |  |  |
| TGTTAAAAGT TTCTGTGATC AC |     |     |     |     |     |     |            |            |            |      |     |     |     |     | 1758 |      |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Phe | Ser | Ser | Met | Phe | Ala | Ser | Leu | Gly | Thr | Arg | Ile | Met | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Val | Leu | Ala | Leu | Leu | Gly | Leu | Gly | Gly | Leu | Phe | Ile | Gly | Phe |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Lys | Val | Met | Gln | Lys | Asp | Val | Leu | Ala | Gln | Leu | Met | Glu | His | Leu |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Glu | Thr | Gly | Gln | Tyr | Lys | Lys | Arg | Glu | Lys | Thr | Leu | Ala | Tyr | Met | Thr |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Lys | Ile | Ile | Glu | Gln | Gly | Ile | His | Glu | Tyr | Tyr | Lys | Asn | Phe | Asp | Asn |
|     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Thr | Ala | Arg | Lys | Met | Ala | Leu | Asp | Tyr | Phe | Lys | Arg | Ile | Asn | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Lys | Gly | Met | Ile | Tyr | Met | Val | Val | Val | Asp | Lys | Asn | Gly | Val | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Phe | Asp | Pro | Val | Asn | Pro | Lys | Thr | Val | Xaa | Gln | Ser | Gly | Leu | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Gln | Ser | Val | Asp | Gly | Val | Tyr | Tyr | Val | Arg | Gly | Tyr | Leu | Glu | Ala |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Ala | Lys | Lys | Gly | Gly | Gly | Tyr | Thr | Tyr | Tyr | Lys | Met | Pro | Lys | Tyr | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Gly | Val | Pro | Glu | Lys | Lys | Phe | Ala | Tyr | Ser | His | Tyr | Asp | Glu | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Gln | Met | Val | Ile | Ala | Thr | Thr | Ser | Tyr | Tyr | Thr | Asp | Ile | Asn | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Asn | Lys | Ala | Ile | Lys | Glu | Gly | Val | Asn | Lys | Val | Phe | Asp | Glu | Asn |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | Thr | Lys | Leu | Phe | Leu | Trp | Ile | Leu | Thr | Ala | Thr | Ile | Ala | Leu | Val |
|     |     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Val | Leu | Thr | Leu | Ile | Tyr | Ala | Lys | Leu | Arg | Ile | Val | Lys | Arg | Ile | Asp |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Leu | Val | Leu | Lys | Ile | Asn | Ala | Phe | Ser | Arg | Gly | Asp | Lys | Asp | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Arg | Ala | Lys | Ile | Asp | Val | Gly | Asp | Arg | Asn | Asp | Glu | Ile | Ser | Gln | Val |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Arg | Gly | Ile | Asn | Leu | Phe | Val | Glu | Asn | Ala | Arg | Leu | Ile | Met | Glu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Glu | Ile | Lys | Gly | Ile | Ser | Thr | Leu | Asn | Lys | Thr | Ser | Met | Asp | Lys | Leu |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Val | Gln | Ile | Thr | Gln | Glu | Thr | Gln | Lys | Ser | Met | Lys | Asp | Ser | Ser | Thr |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Thr | Leu | Asn | Ser | Val | Lys | Asn | Lys | Ala | Thr | Asp | Ile | Ala | Ser | Met | Met |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asn | Ala | Ser | Ile | Glu | Gln | Ser | Gln | Gly | Leu | Arg | Lys | Arg | Leu | Ile | Glu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Thr | Gln | Gly | Leu | Val | Lys | Glu | Ser | Lys | Asp | Ala | Ile | Gly | Asp | Leu | Phe |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ser | Gln | Ile | Thr | Glu | Ser | Ala | His | Thr | Glu | Glu | Glu | Leu | Ser | Ser | Lys |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Val | Glu | Gln | Leu | Ser | Arg | Asn | Ala | Asp | Asp | Val | Lys | Ser | Ile | Leu | Asp |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Ile | Ile | Asn | Asp | Ile | Ala | Asp | Gln | Thr | Asn | Leu | Leu | Ala | Leu | Asn | Ala |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Ala | Ile | Glu | Ala | Ala | Arg | Ala | Gly | Glu | His | Gly | Arg | Gly | Phe | Ala | Val |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Val | Ala | Asp | Glu | Val | Arg | Asn | Leu | Ala | Gly | Arg | Thr | Gln | Lys | Ser | Leu |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Ala | Glu | Ile | Asn | Ser | Thr | Ile | Met | Val | Ile | Val | Gln | Glu | Ile | Asn | Ala |
|     |     | 450 |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Val | Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...474
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CCTTGAGATT GCTCT ATG GAA GCA TTC ATC ATG CTC GCT ATA TCA GTG GCT  | 51  |
| Met Glu Ala Phe Ile Met Leu Ala Ile Ser Val Ala                   |     |
| 1 5 10                                                            |     |
| TTA TTT TTC ACG GAA TTT AGG GTG GTT GAG GAA TCT TTC ATG CTC TTT   | 99  |
| Leu Phe Phe Thr Glu Phe Arg Val Val Glu Glu Ser Phe Met Leu Phe   |     |
| 15 20 25                                                          |     |
| TGG GTT TCT TGC GTG ATT TGG ACT AAT TTA TCC ATT GAA GTT TTA TTG   | 147 |
| Trp Val Ser Cys Val Ile Trp Thr Asn Leu Ser Ile Glu Val Leu Leu   |     |
| 30 35 40                                                          |     |
| AGG GTG GAA ATC CCT TTA ATC TCT TCC ATA ATC AAG CGG GCG TTT TCC   | 195 |
| Arg Val Glu Ile Pro Leu Ile Ser Ser Ile Ile Lys Arg Ala Phe Ser   |     |
| 45 50 55 60                                                       |     |
| ACA AAC AAA TTG ATC CCA CGG CCC ACT TGC GAG ATT TCA TCG TTG CGA   | 243 |
| Thr Asn Lys Leu Ile Pro Arg Pro Thr Cys Glu Ile Ser Ser Leu Arg   |     |
| 65 70 75                                                          |     |
| TCA CCC ACA TCA ATT TTG GCT CTC AAA TCC TTA TCC CCA CGG CTA AAA   | 291 |
| Ser Pro Thr Ser Ile Leu Ala Leu Lys Ser Leu Ser Pro Arg Leu Lys   |     |
| 80 85 90                                                          |     |
| GCG TTG ATT TTA AGG ACC AGT TCA TCA ATG CGT TTC ACG ATC CTT AAT   | 339 |
| Ala Leu Ile Leu Arg Thr Ser Ser Ser Met Arg Phe Thr Ile Leu Asn   |     |
| 95 100 105                                                        |     |
| TTA GCG TAT ATG AGC GTC AAA ACC ACT AGC GCT ATC GTC GCT GTC AGT   | 387 |
| Leu Ala Tyr Met Ser Val Lys Thr Thr Ser Ala Ile Val Ala Val Ser   |     |
| 110 115 120                                                       |     |
| ATC CAA AGG AAT AAT TTC GTG GTG TTT TCA TCA AAA ACC TTA TTC ACG   | 435 |
| Ile Gln Arg Asn Asn Phe Val Val Phe Ser Ser Lys Thr Leu Phe Thr   |     |
| 125 130 135 140                                                   |     |
| CCT TCT TTG ATC GCT TTA TTT TCT GTG TTA ATG TCA GTG TAATAGGAAG TC | 486 |
| Pro Ser Leu Ile Ala Leu Phe Ser Val Leu Met Ser Val               |     |
| 145 150                                                           |     |

GTTGCGATCA CCATTGAGA AACTTCATCA TAATGCGAG

525

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

Met Glu Ala Phe Ile Met Leu Ala Ile Ser Val Ala Leu Phe Phe Thr  
1 5 10 15  
Glu Phe Arg Val Val Glu Glu Ser Phe Met Leu Phe Trp Val Ser Cys  
20 25 30  
Val Ile Trp Thr Asn Leu Ser Ile Glu Val Leu Leu Arg Val Glu Ile  
35 40 45  
Pro Leu Ile Ser Ser Ile Ile Lys Arg Ala Phe Ser Thr Asn Lys Leu  
50 55 60  
Ile Pro Arg Pro Thr Cys Glu Ile Ser Ser Leu Arg Ser Pro Thr Ser  
65 70 75 80  
Ile Leu Ala Leu Lys Ser Leu Ser Pro Arg Leu Lys Ala Leu Ile Leu  
85 90 95  
Arg Thr Ser Ser Ser Met Arg Phe Thr Ile Leu Asn Leu Ala Tyr Met  
100 105 110  
Ser Val Lys Thr Thr Ser Ala Ile Val Ala Val Ser Ile Gln Arg Asn  
115 120 125  
Asn Phe Val Val Phe Ser Ser Lys Thr Leu Phe Thr Pro Ser Leu Ile  
130 135 140  
Ala Leu Phe Ser Val Leu Met Ser Val  
145 150

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...1164
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

AAATTCAATA AAAAAGGAAA AACC ATG CGC ATG CAA ACC AAA TTA ATC CAT 51  
Met Arg Met Gln Thr Lys Leu Ile His  
1 5  
GGG GGC ATT AGT GAG GAC GCA ACA ACG GGG GCG GTG AGC GTG CCT ATT 99

|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |            |                   |                   |                   |     |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-----|
| Gly<br>10         | Gly               | Ile               | Ser               | Glu               | Asp<br>15         | Ala               | Thr               | Thr               | Gly               | Ala<br>20         | Val               | Ser        | Val               | Pro               | Ile<br>25         |     |
| TAT<br>Tyr        | CAA<br>Gln        | ACT<br>Thr        | TCC<br>Ser        | ACC<br>Thr<br>30  | TAC<br>Tyr        | CGC<br>Arg        | CAA<br>Gln        | GAC<br>Asp        | GCC<br>Ala<br>35  | ATA<br>Ile        | GGC<br>Gly        | CGC<br>Arg | CAT<br>His        | AAG<br>Lys<br>40  | GGC<br>Gly        | 147 |
| TAT<br>Tyr        | GAA<br>Glu        | TAC<br>Tyr        | TCT<br>Ser<br>45  | CGC<br>Arg        | TCA<br>Ser        | GGC<br>Gly        | AAC<br>Asn        | CCC<br>Pro<br>50  | ACG<br>Thr        | CGC<br>Arg        | TTT<br>Phe        | GCT<br>Ala | TTA<br>Leu<br>55  | GAA<br>Glu        | GAA<br>Glu        | 195 |
| CTC<br>Leu        | ATC<br>Ile        | GCT<br>Ala<br>60  | GAT<br>Asp        | TTA<br>Leu        | GAA<br>Glu        | GGG<br>Gly        | GGG<br>Gly<br>65  | GTT<br>Val        | AAG<br>Lys        | GGG<br>Gly        | TTT<br>Phe<br>70  | GCT<br>Ala | TTT<br>Phe        | GCC<br>Ala        | TCT<br>Ser        | 243 |
| GGA<br>Gly        | TTA<br>Leu<br>75  | GCT<br>Ala        | GGA<br>Gly        | ATC<br>Ile        | CAC<br>His        | GCC<br>Ala<br>80  | GTT<br>Val        | TTT<br>Phe        | TCC<br>Ser        | CTC<br>Leu        | TTG<br>Leu<br>85  | CAA<br>Gln | TCA<br>Ser        | GGC<br>Gly        | GAT<br>Asp        | 291 |
| CAT<br>His<br>90  | GTG<br>Val        | TTA<br>Leu        | TTG<br>Leu        | GGC<br>Gly        | GAT<br>Asp<br>95  | GAT<br>Asp        | GTT<br>Val        | TAT<br>Tyr        | GGG<br>Gly        | GGG<br>Gly<br>100 | ACT<br>Thr        | TTC<br>Phe | CGC<br>Arg        | TTG<br>Leu        | TTT<br>Phe<br>105 | 339 |
| AAT<br>Asn        | CAA<br>Gln        | GTG<br>Val        | CTT<br>Leu        | GTC<br>Val<br>110 | AAA<br>Lys        | AAC<br>Asn        | GGG<br>Gly        | CTT<br>Leu        | TCT<br>Ser<br>115 | TGC<br>Cys        | ACC<br>Thr        | ATT<br>Ile | ATA<br>Ile        | GAC<br>Asp<br>120 | ACT<br>Thr        | 387 |
| AGC<br>Ser        | GAT<br>Asp        | ATA<br>Ile        | TCC<br>Ser<br>125 | CAA<br>Gln        | ATT<br>Ile        | AAA<br>Lys        | AAG<br>Lys        | GCT<br>Ala<br>130 | ATC<br>Ile        | AAG<br>Lys        | CCC<br>Pro        | AAC<br>Asn | ACC<br>Thr<br>135 | AAA<br>Lys        | GCC<br>Ala        | 435 |
| CTT<br>Leu        | TAT<br>Tyr        | TTA<br>Leu<br>140 | GAA<br>Glu        | ACC<br>Thr        | CCT<br>Pro        | AGT<br>Ser        | AAC<br>Asn<br>145 | CCC<br>Pro        | TTG<br>Leu        | CTT<br>Leu        | AAA<br>Lys<br>150 | ATC<br>Ile | ACG<br>Thr        | GAT<br>Asp        | TTA<br>Leu        | 483 |
| GCG<br>Ala<br>155 | CAA<br>Gln        | TGC<br>Cys        | GCT<br>Ala        | AGT<br>Ser        | GTC<br>Val        | GCT<br>Ala<br>160 | AAA<br>Lys        | GAT<br>Asp        | CAT<br>His        | GGT<br>Gly        | TTG<br>Leu<br>165 | CTC<br>Leu | ACT<br>Thr        | ATC<br>Ile        | GTG<br>Val        | 531 |
| GAT<br>Asp<br>170 | AAC<br>Asn        | ACC<br>Thr        | TTT<br>Phe        | GCC<br>Ala<br>175 | ACC<br>Thr        | CCC<br>Pro        | TAT<br>Tyr        | TAT<br>Tyr        | CAA<br>Gln        | AAC<br>Asn<br>180 | CCG<br>Pro        | CTT<br>Leu | CTT<br>Leu        | TTG<br>Leu        | GGA<br>Gly<br>185 | 579 |
| GCG<br>Ala        | GAC<br>Asp        | ATT<br>Ile        | GTG<br>Val<br>190 | GCA<br>Ala        | CAT<br>His        | AGC<br>Ser        | GGC<br>Gly        | ACC<br>Thr        | AAA<br>Lys<br>195 | TAC<br>Tyr        | TTA<br>Leu        | GGC<br>Gly | GGG<br>Gly        | CAT<br>His<br>200 | AGC<br>Ser        | 627 |
| GAT<br>Asp        | GTG<br>Val        | GTC<br>Val<br>205 | GCC<br>Ala        | GGG<br>Gly        | CTT<br>Leu        | GTA<br>Val        | ACC<br>Thr        | ACT<br>Thr<br>210 | AAT<br>Asn        | AAT<br>Asn        | GAA<br>Glu        | GCG<br>Ala | CTA<br>Leu<br>215 | GCC<br>Ala        | CAA<br>Gln        | 675 |
| GAG<br>Glu        | ATC<br>Ile        | GCT<br>Ala<br>220 | TTT<br>Phe        | TTC<br>Phe        | CAA<br>Gln        | AAC<br>Asn        | GCT<br>Ala<br>225 | ATC<br>Ile        | GGT<br>Gly        | GGG<br>Gly        | GTT<br>Val<br>230 | TTA<br>Leu | GGC<br>Gly        | CCT<br>Pro        | CAA<br>Gln        | 723 |
| GAC<br>Asp        | AGC<br>Ser<br>235 | TGG<br>Trp        | CTG<br>Leu        | TTG<br>Leu        | CAA<br>Gln<br>240 | AGA<br>Arg        | GGG<br>Gly<br>245 | ATT<br>Ile        | AAA<br>Lys        | ACG<br>Thr        | CTG<br>Leu<br>245 | GGA<br>Gly | TTG<br>Leu        | CGC<br>Arg        | ATG<br>Met        | 771 |



GAA GCC CAT CAA AAA AAC GCT CTT TGT GTG GCT GAG TTT TTA GAA AAA 819  
 Glu Ala His Gln Lys Asn Ala Leu Cys Val Ala Glu Phe Leu Glu Lys  
 250 255 260 265  
 CAC CCT AAA GTG GAA AGG GTT TAT TAC CCG GGC CTT CCC ACT CAC CCT 867  
 His Pro Lys Val Glu Arg Val Tyr Tyr Pro Gly Leu Pro Thr His Pro  
 270 275 280  
 AAT TAC GAA CTA GCT AAA AAA CAG ATG CGT GGC TTT AGC GGG ATG CTC 915  
 Asn Tyr Glu Leu Ala Lys Lys Gln Met Arg Gly Phe Ser Gly Met Leu  
 285 290 295  
 TCT TTC ACT CTC AAA AAT GAT AGC GAG GCG GTT GCT TTT GTA GAA AGC 963  
 Ser Phe Thr Leu Lys Asn Asp Ser Glu Ala Val Ala Phe Val Glu Ser  
 300 305 310  
 CTT AAA CTA TTC ATT TTA GGC GAG AGT TTG GGC GGG GTG GAA AGT TTG 1011  
 Leu Lys Leu Phe Ile Leu Gly Glu Ser Leu Gly Gly Val Glu Ser Leu  
 315 320 325  
 GTG GGG ATT CCG GCA TTT ATG ACC CAT GCG TGC ATC CCT AAA ACG CAA 1059  
 Val Gly Ile Pro Ala Phe Met Thr His Ala Cys Ile Pro Lys Thr Gln  
 330 335 340 345  
 CGA GAA GCT GCT GGG ATT AGA GAT GGC CTG GTG CGC TTG TCT GTA GGG 1107  
 Arg Glu Ala Ala Gly Ile Arg Asp Gly Leu Val Arg Leu Ser Val Gly  
 350 355 360  
 ATT GAG CAT GAA CAG GAT TTG TTA GAA GAT TTA GAG CAA GCG TTC GCT 1155  
 Ile Glu His Glu Gln Asp Leu Leu Glu Asp Leu Glu Gln Ala Phe Ala  
 365 370 375  
 AAA ATA GGC TAAAGTTTCA TTACAATTTA TGAATAAAGG AGTTAAAAAC ATGAA 1209  
 Lys Ile Gly  
 380

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

Met Arg Met Gln Thr Lys Leu Ile His Gly Gly Ile Ser Glu Asp Ala  
 1 5 10 15  
 Thr Thr Gly Ala Val Ser Val Pro Ile Tyr Gln Thr Ser Thr Tyr Arg  
 20 25 30  
 Gln Asp Ala Ile Gly Arg His Lys Gly Tyr Glu Tyr Ser Arg Ser Gly  
 35 40 45  
 Asn Pro Thr Arg Phe Ala Leu Glu Glu Leu Ile Ala Asp Leu Glu Gly  
 50 55 60  
 Gly Val Lys Gly Phe Ala Phe Ala Ser Gly Leu Ala Gly Ile His Ala

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Phe | Ser | Leu | Leu | Gln | Ser | Gly | Asp | His | Val | Leu | Leu | Gly | Asp | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Tyr | Gly | Gly | Thr | Phe | Arg | Leu | Phe | Asn | Gln | Val | Leu | Val | Lys | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Leu | Ser | Cys | Thr | Ile | Ile | Asp | Thr | Ser | Asp | Ile | Ser | Gln | Ile | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Ala | Ile | Lys | Pro | Asn | Thr | Lys | Ala | Leu | Tyr | Leu | Glu | Thr | Pro | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Pro | Leu | Leu | Lys | Ile | Thr | Asp | Leu | Ala | Gln | Cys | Ala | Ser | Val | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Asp | His | Gly | Leu | Leu | Thr | Ile | Val | Asp | Asn | Thr | Phe | Ala | Thr | Pro |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Tyr | Tyr | Gln | Asn | Pro | Leu | Leu | Leu | Gly | Ala | Asp | Ile | Val | Ala | His | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 |     |     |     |
| Gly | Thr | Lys | Tyr | Leu | Gly | Gly | His | Ser | Asp | Val | Val | Ala | Gly | Leu | Val |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | Thr | Asn | Asn | Glu | Ala | Leu | Ala | Gln | Glu | Ile | Ala | Phe | Phe | Gln | Asn |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Ile | Gly | Gly | Val | Leu | Gly | Pro | Gln | Asp | Ser | Trp | Leu | Leu | Gln | Arg |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly | Ile | Lys | Thr | Leu | Gly | Leu | Arg | Met | Glu | Ala | His | Gln | Lys | Asn | Ala |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Cys | Val | Ala | Glu | Phe | Leu | Glu | Lys | His | Pro | Lys | Val | Glu | Arg | Val |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Tyr | Tyr | Pro | Gly | Leu | Pro | Thr | His | Pro | Asn | Tyr | Glu | Leu | Ala | Lys | Lys |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gln | Met | Arg | Gly | Phe | Ser | Gly | Met | Leu | Ser | Phe | Thr | Leu | Lys | Asn | Asp |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ser | Glu | Ala | Val | Ala | Phe | Val | Glu | Ser | Leu | Lys | Leu | Phe | Ile | Leu | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Glu | Ser | Leu | Gly | Gly | Val | Glu | Ser | Leu | Val | Gly | Ile | Pro | Ala | Phe | Met |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Thr | His | Ala | Cys | Ile | Pro | Lys | Thr | Gln | Arg | Glu | Ala | Ala | Gly | Ile | Arg |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Asp | Gly | Leu | Val | Arg | Leu | Ser | Val | Gly | Ile | Glu | His | Glu | Gln | Asp | Leu |
|     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Leu | Glu | Asp | Leu | Glu | Gln | Ala | Phe | Ala | Lys | Ile | Gly |     |     |     |     |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 912 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 46...873
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

|         |     |        |      |       |       |       |        |       |     |     |     |     |     |     |     |     |
|---------|-----|--------|------|-------|-------|-------|--------|-------|-----|-----|-----|-----|-----|-----|-----|-----|
| ATTATTA | ACT | TTTTAT | GCTA | TAATG | CGAGG | GTTCT | TTTCAT | CAAGA | ATG | GTG | ATT | GAC | 57  |     |     |     |
|         |     |        |      |       |       |       |        |       | Met | Val | Ile | Asp |     |     |     |     |
|         |     |        |      |       |       |       |        |       | 1   |     |     |     |     |     |     |     |
| GAG     | ATT | TTT    | CAA  | ATA   | ATG   | ATG   | TTA    | AGA   | AGA | ATT | AAA | GTA | GGT | TCT | AAT | 105 |
| Glu     | Ile | Phe    | Gln  | Ile   | Met   | Met   | Leu    | Arg   | Arg | Ile | Lys | Val | Gly | Ser | Asn |     |
| 5       |     |        |      |       | 10    |       |        |       |     | 15  |     |     |     |     | 20  |     |
| TTG     | AAT | AAA    | AAA  | GAG   | AGT   | TTG   | TTA    | GAT   | GCG | TTT | GTT | AAA | ACC | TAT | CTG | 153 |
| Leu     | Asn | Lys    | Lys  | Glu   | Ser   | Leu   | Leu    | Asp   | Ala | Phe | Val | Lys | Thr | Tyr | Leu |     |
|         |     |        |      | 25    |       |       |        |       | 30  |     |     |     |     | 35  |     |     |
| CAG     | ATT | TTA    | GAA  | CCC   | ATT   | AGT   | TCT    | AAA   | CGC | TTA | AAA | GAG | TTG | GCG | GAC | 201 |
| Gln     | Ile | Leu    | Glu  | Pro   | Ile   | Ser   | Ser    | Lys   | Arg | Leu | Lys | Glu | Leu | Ala | Asp |     |
|         |     |        |      | 40    |       |       |        | 45    |     |     |     |     | 50  |     |     |     |
| TTG     | AAA | ATA    | TCT  | TGC   | GCG   | ACG   | ATC    | AGG   | AAT | TAT | TTT | CAA | ATC | CTT | TCT | 249 |
| Leu     | Lys | Ile    | Ser  | Cys   | Ala   | Thr   | Ile    | Arg   | Asn | Tyr | Phe | Gln | Ile | Leu | Ser |     |
|         |     |        | 55   |       |       |       | 60     |       |     |     |     | 65  |     |     |     |     |
| AAA     | GAG | GGC    | ATG  | CTT   | TAT   | CAA   | GCC    | CAT   | TCT | AGT | GGC | GCT | AGA | TTG | CCC | 297 |
| Lys     | Glu | Gly    | Met  | Leu   | Tyr   | Gln   | Ala    | His   | Ser | Ser | Gly | Ala | Arg | Leu | Pro |     |
|         | 70  |        |      |       |       | 75    |        |       |     |     | 80  |     |     |     |     |     |
| ACT     | TTT | AAG    | GCG  | TTT   | GAA   | AAC   | TAT    | TGG   | CAA | AAG | TCG | TTG | CGC | TTT | GAA | 345 |
| Thr     | Phe | Lys    | Ala  | Phe   | Glu   | Asn   | Tyr    | Trp   | Gln | Lys | Ser | Leu | Arg | Phe | Glu |     |
|         |     |        |      |       | 90    |       |        |       |     | 95  |     |     |     |     | 100 |     |
| ACT     | TTA | AAG    | GTG  | AAT   | GAA   | AAA   | CGC    | CTA   | AAA | AGC | GCG | AGT | GAA | AAT | TTT | 393 |
| Thr     | Leu | Lys    | Val  | Asn   | Glu   | Lys   | Arg    | Leu   | Lys | Ser | Ala | Ser | Glu | Asn | Phe |     |
|         |     |        |      | 105   |       |       |        |       | 110 |     |     |     |     | 115 |     |     |
| GGG     | CTT | TTC    | ACG  | CTG   | TTA   | AAA   | AAA    | CCC   | AGT | TTG | GAG | CGT | TTA | GAA | AGA | 441 |
| Gly     | Leu | Phe    | Thr  | Leu   | Leu   | Lys   | Lys    | Pro   | Ser | Leu | Glu | Arg | Leu | Glu | Arg |     |
|         |     |        | 120  |       |       |       |        | 125   |     |     |     |     | 130 |     |     |     |
| GTC     | ATT | GAG    | TGC  | GAA   | AAA   | CGC   | TTT    | TTG   | ATT | TTG | GAC | TTT | TTG | GCG | TTT | 489 |
| Val     | Ile | Glu    | Cys  | Glu   | Lys   | Arg   | Phe    | Leu   | Ile | Leu | Asp | Phe | Leu | Ala | Phe |     |
|         |     |        | 135  |       |       |       | 140    |       |     |     |     | 145 |     |     |     |     |
| TCT     | TGC | GCA    | CTG  | GGT   | TAC   | AGC   | GTT    | AAA   | ATG | GAA | AAG | TTT | TTA | TTA | GAG | 537 |
| Ser     | Cys | Ala    | Leu  | Gly   | Tyr   | Ser   | Val    | Lys   | Met | Glu | Lys | Phe | Leu | Leu | Glu |     |
|         | 150 |        |      |       |       | 155   |        |       |     |     | 160 |     |     |     |     |     |
| CTT     | GTG | GGC    | AGA  | AGC   | GTT   | AAA   | GAA    | GTG   | CGC | TCA | ATC | GCT | GCT | TCT | TTC | 585 |
| Leu     | Val | Gly    | Arg  | Ser   | Val   | Lys   | Glu    | Val   | Arg | Ser | Ile | Ala | Ala | Ser | Phe |     |
|         | 165 |        |      |       | 170   |       |        |       |     | 175 |     |     |     |     | 180 |     |
| AAT     | GCG | TTG    | AGT  | TTG   | GCC   | AGG   | CAA    | TTA   | GAG | CGT | TTG | GAG | TAT | TCC | AAC | 633 |
| Asn     | Ala | Leu    | Ser  | Leu   | Ala   | Arg   | Gln    | Leu   | Glu | Arg | Leu | Glu | Tyr | Ser | Asn |     |
|         |     |        |      | 185   |       |       |        |       | 190 |     |     |     |     | 195 |     |     |
| ACA     | CAA | ATC    | ACA  | CGC   | TTT   | AAT   | CTG    | ATG   | GGG | TTA | AAA | ACG | CTT | TTA | AAC | 681 |
| Thr     | Gln | Ile    | Thr  | Arg   | Phe   | Asn   | Leu    | Met   | Gly | Leu | Lys | Thr | Leu | Leu | Asn |     |
|         |     |        | 200  |       |       |       |        | 205   |     |     |     |     | 210 |     |     |     |
| AGC     | CCT | TTA    | TTT  | TTT   | GAC   | ATT   | TTA    | GGG   | GGT | AAG | GTT | TTA | GAG | CGT | TTG | 729 |
| Ser     | Pro | Leu    | Phe  | Phe   | Asp   | Ile   | Leu    | Gly   | Gly | Lys | Val | Leu | Glu | Arg | Leu |     |

|                                                                   |     |     |  |     |     |
|-------------------------------------------------------------------|-----|-----|--|-----|-----|
| 215                                                               |     | 220 |  | 225 |     |
| AGT AAG GGT TTG CAT TTT ATA GAG CCT GAT TGC ATG CTA GTA ACA CGC   | 777 |     |  |     |     |
| Ser Lys Gly Leu His Phe Ile Glu Pro Asp Cys Met Leu Val Thr Arg   |     |     |  |     |     |
| 230                                                               |     | 235 |  | 240 |     |
| CCT GTA GAA TTT CAA AAC AAG CGG ATG CAA CTG CTT TGC GTG GGG AAA   | 825 |     |  |     |     |
| Pro Val Glu Phe Gln Asn Lys Arg Met Gln Leu Leu Cys Val Gly Lys   |     |     |  |     |     |
| 245                                                               |     | 250 |  | 255 | 260 |
| CTA GAA TGC GAT TAT GAA GGG TTT TTT CAA ACG ATT TCT GAG GAG GAA T | 874 |     |  |     |     |
| Leu Glu Cys Asp Tyr Glu Gly Phe Phe Gln Thr Ile Ser Glu Glu Glu   |     |     |  |     |     |
|                                                                   |     | 265 |  | 270 | 275 |
| AATGAAAGAT GAACACAACC AAGAACACGA TCATTTAA                         | 912 |     |  |     |     |

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Val Ile Asp Glu Ile Phe Gln Ile Met Met Leu Arg Arg Ile Lys |  |
| 1 5 10 15                                                       |  |
| Val Gly Ser Asn Leu Asn Lys Lys Glu Ser Leu Leu Asp Ala Phe Val |  |
| 20 25 30                                                        |  |
| Lys Thr Tyr Leu Gln Ile Leu Glu Pro Ile Ser Ser Lys Arg Leu Lys |  |
| 35 40 45                                                        |  |
| Glu Leu Ala Asp Leu Lys Ile Ser Cys Ala Thr Ile Arg Asn Tyr Phe |  |
| 50 55 60                                                        |  |
| Gln Ile Leu Ser Lys Glu Gly Met Leu Tyr Gln Ala His Ser Ser Gly |  |
| 65 70 75 80                                                     |  |
| Ala Arg Leu Pro Thr Phe Lys Ala Phe Glu Asn Tyr Trp Gln Lys Ser |  |
| 85 90 95                                                        |  |
| Leu Arg Phe Glu Thr Leu Lys Val Asn Glu Lys Arg Leu Lys Ser Ala |  |
| 100 105 110                                                     |  |
| Ser Glu Asn Phe Gly Leu Phe Thr Leu Leu Lys Lys Pro Ser Leu Glu |  |
| 115 120 125                                                     |  |
| Arg Leu Glu Arg Val Ile Glu Cys Glu Lys Arg Phe Leu Ile Leu Asp |  |
| 130 135 140                                                     |  |
| Phe Leu Ala Phe Ser Cys Ala Leu Gly Tyr Ser Val Lys Met Glu Lys |  |
| 145 150 155 160                                                 |  |
| Phe Leu Leu Glu Leu Val Gly Arg Ser Val Lys Glu Val Arg Ser Ile |  |
| 165 170 175                                                     |  |
| Ala Ala Ser Phe Asn Ala Leu Ser Leu Ala Arg Gln Leu Glu Arg Leu |  |
| 180 185 190                                                     |  |
| Glu Tyr Ser Asn Thr Gln Ile Thr Arg Phe Asn Leu Met Gly Leu Lys |  |
| 195 200 205                                                     |  |
| Thr Leu Leu Asn Ser Pro Leu Phe Phe Asp Ile Leu Gly Gly Lys Val |  |
| 210 215 220                                                     |  |
| Leu Glu Arg Leu Ser Lys Gly Leu His Phe Ile Glu Pro Asp Cys Met |  |
| 225 230 235 240                                                 |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Val | Thr | Arg | Pro | Val | Glu | Phe | Gln | Asn | Lys | Arg | Met | Gln | Leu | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Cys | Val | Gly | Lys | Leu | Glu | Cys | Asp | Tyr | Glu | Gly | Phe | Phe | Gln | Thr | Ile |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Glu | Glu | Glu |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 275 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 50...685
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AGCTCTTTAC TATTTTATTA TCTATCTTTT ATTAAAAAAA CTTGTTATC ATG ATA AAC | 58  |
| Met Ile Asn                                                       |     |
| 1                                                                 |     |
| ATG AAC ACA CAC ACA AGA GGC ATT GAC AGC AAT CTG ATT CAT TCG CTC   | 106 |
| Met Asn Thr His Thr Arg Gly Ile Asp Ser Asn Leu Ile His Ser Leu   |     |
| 5 10 15                                                           |     |
| CAA AGC ATT TCA TTA TCC ATG TTT AGA AAG GGT TTT TTT GGG CTT TAT   | 154 |
| Gln Ser Ile Ser Leu Ser Met Phe Arg Lys Gly Phe Phe Gly Leu Tyr   |     |
| 20 25 30 35                                                       |     |
| CAA GGC TCT ATT TCA GCA CGC ATT GGC GCA AAT CAA TTT GTG ATC AAC   | 202 |
| Gln Gly Ser Ile Ser Ala Arg Ile Gly Ala Asn Gln Phe Val Ile Asn   |     |
| 40 45 50                                                          |     |
| AAA AGA AAC GCT GTT TTT GAT CAA TTG AAT GAA AAC ACC TTA CTG GTT   | 250 |
| Lys Arg Asn Ala Val Phe Asp Gln Leu Asn Glu Asn Thr Leu Leu Val   |     |
| 55 60 65                                                          |     |
| TTG CAT GAC AAA ATA GAT TAC CGC TGG AAA GAA GCG AGC TTG GAT TCG   | 298 |
| Leu His Asp Lys Ile Asp Tyr Arg Trp Lys Glu Ala Ser Leu Asp Ser   |     |
| 70 75 80                                                          |     |
| CCC ATT CAT GCG AGC GTG TAT AGG GAG TTT TTG GAC GCT AAA TTC ATC   | 346 |
| Pro Ile His Ala Ser Val Tyr Arg Glu Phe Leu Asp Ala Lys Phe Ile   |     |
| 85 90 95                                                          |     |
| GCT TAC GCG CGC CCT CCT TAT AGT TTG GCG TAT TCC TTG CGC CAC AAC   | 394 |
| Ala Tyr Ala Arg Pro Pro Tyr Ser Leu Ala Tyr Ser Leu Arg His Asn   |     |
| 100 105 110 115                                                   |     |
| CGA TTG CTC CCT AGA GAT TAT TTA GGG TAT CGT TCT TTG GGC GAA GAA   | 442 |

|     |            |            |            |       |     |     |     |     |     |     |     |     |     |     |     |  |     |
|-----|------------|------------|------------|-------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| Arg | Leu        | Leu        | Pro        | Arg   | Asp | Tyr | Leu | Gly | Tyr | Arg | Ser | Leu | Gly | Glu | Glu |  |     |
|     |            |            |            | 120   |     |     |     |     | 125 |     |     |     |     | 130 |     |  |     |
| ATT | TCC        | ATT        | TTT        | AAC   | CCC | AAA | GAC | TAT | GAC | AGC | TGG | CAA | GAA | AGA | GCG |  | 490 |
| Ile | Ser        | Ile        | Phe        | Asn   | Pro | Lys | Asp | Tyr | Asp | Ser | Trp | Gln | Glu | Arg | Ala |  |     |
|     |            |            | 135        |       |     |     |     | 140 |     |     |     |     | 145 |     |     |  |     |
| GAT | ACA        | GAA        | ATT        | TTA   | CGC | CAA | CTG | CAA | GAG | AGC | AAA | AAA | TAT | TTT | GTT |  | 538 |
| Asp | Thr        | Glu        | Ile        | Leu   | Arg | Gln | Leu | Gln | Glu | Ser | Lys | Lys | Tyr | Phe | Val |  |     |
|     |            | 150        |            |       |     |     | 155 |     |     |     |     | 160 |     |     |     |  |     |
| TTC | ATT        | AAG        | GGG        | TGT   | GGG | ATT | TTT | GCC | TAC | CAC | AGA | GAG | CTT | TCT | AAA |  | 586 |
| Phe | Ile        | Lys        | Gly        | Cys   | Gly | Ile | Phe | Ala | Tyr | His |     | Glu | Leu | Ser | Lys |  |     |
|     | 165        |            |            |       |     | 170 |     |     |     | 175 |     |     |     |     |     |  |     |
| CTC | ATG        | GAA        | GTT        | TTT   | GAT | TTG | ATT | GAA | AAC | TCA | TGC | AAG | GTT | TTA | CGA |  | 634 |
| Leu | Met        | Glu        | Val        | Phe   | Asp | Leu | Ile | Glu | Asn | Ser | Cys | Lys | Val | Leu | Arg |  |     |
|     | 180        |            |            |       | 185 |     |     |     |     | 190 |     |     |     |     | 195 |  |     |
| TTG | GGC        | GAT        | TTA        | ATG   | GAT | TAT | TGC | TAT | AAT | GAT | GAT | CCA | CGA | TTG | AGC |  | 682 |
| Leu | Gly        | Asp        | Leu        | Met   | Asp | Tyr | Cys | Tyr | Asn | Asp | Asp | Pro | Arg | Leu | Ser |  |     |
|     |            |            |            | 200   |     |     |     |     | 205 |     |     |     |     | 210 |     |  |     |
| GTG | TAAAAAGCTA | AAAAGGATAA | AACATGACCA | TCAAC |     |     |     |     |     |     |     |     |     |     |     |  | 720 |
| Val |            |            |            |       |     |     |     |     |     |     |     |     |     |     |     |  |     |

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Ile | Asn | Met | Asn | Thr | His | Thr | Arg | Gly | Ile | Asp | Ser | Asn | Leu | Ile |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| His | Ser | Leu | Gln | Ser | Ile | Ser | Leu | Ser | Met | Phe | Arg | Lys | Gly | Phe | Phe |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Gly | Leu | Tyr | Gln | Gly | Ser | Ile | Ser | Ala | Arg | Ile | Gly | Ala | Asn | Gln | Phe |  |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |
| Val | Ile | Asn | Lys | Arg | Asn | Ala | Val | Phe | Asp | Gln | Leu | Asn | Glu | Asn | Thr |  |  |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |  |  |
| Leu | Leu | Val | Leu | His | Asp | Lys | Ile | Asp | Tyr | Arg | Trp | Lys | Glu | Ala | Ser |  |  |
|     | 65  |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |  |  |
| Leu | Asp | Ser | Pro | Ile | His | Ala | Ser | Val | Tyr | Arg | Glu | Phe | Leu | Asp | Ala |  |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |  |
| Lys | Phe | Ile | Ala | Tyr | Ala | Arg | Pro | Pro | Tyr | Ser | Leu | Ala | Tyr | Ser | Leu |  |  |
|     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |     |  |  |
| Arg | His | Asn | Arg | Leu | Leu | Pro | Arg | Asp | Tyr | Leu | Gly | Tyr | Arg | Ser | Leu |  |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |  |
| Gly | Glu | Glu | Ile | Ser | Ile | Phe | Asn | Pro | Lys | Asp | Tyr | Asp | Ser | Trp | Gln |  |  |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |  |  |

Glu Arg Ala Asp Thr Glu Ile Leu Arg Gln Leu Gln Glu Ser Lys Lys  
 145 150 155 160  
 Tyr Phe Val Phe Ile Lys Gly Cys Gly Ile Phe Ala Tyr His Arg Glu  
 165 170 175  
 Leu Ser Lys Leu Met Glu Val Phe Asp Leu Ile Glu Asn Ser Cys Lys  
 180 185 190  
 Val Leu Arg Leu Gly Asp Leu Met Asp Tyr Cys Tyr Asn Asp Asp Pro  
 195 200 205  
 Arg Leu Ser Val  
 210

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 91...2445
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

|                 |                         |                       |                 |     |
|-----------------|-------------------------|-----------------------|-----------------|-----|
| GGGAGTTTTG TGC  | GATATAT CAAGTTTTTC      | AAAGAGTTGA ACAATAAAAA | TGTGAATCTG      | 60  |
| GTTGGGGGCA AGA  | ACGCTAG TATTGGTGAA      | ATG TTT CAA GAA TTA   | GTG CCT ATT     | 114 |
|                 | Met Phe Gln Glu Leu Val | Pro Ile               |                 |     |
|                 | 1                       | 5                     |                 |     |
| GGT ATT AAA GTG | CCT GAT GGC TTT         | GCG ATC ACC AGC       | GAA GCG TAT TGG | 162 |
| Gly Ile Lys Val | Pro Asp Gly Phe         | Ala Ile Thr Ser       | Glu Ala Tyr Trp |     |
| 10              | 15                      | 20                    |                 |     |
| TAT CTT TTA GAG | CAA GGA GGG GCT         | AAA CAA AAA ATC       | ATA GAG CTT TTA | 210 |
| Tyr Leu Leu Glu | Gln Gly Gly Ala         | Lys Gln Lys Ile       | Ile Glu Leu Leu |     |
| 25              | 30                      | 35                    | 40              |     |
| GAA AAT GTT GAT | GCC ACC GAA ATT         | GAT GTG TTA AAA       | ATC CGC TCC AAA | 258 |
| Glu Asn Val Asp | Ala Thr Glu Ile         | Asp Val Leu Lys       | Ile Arg Ser Lys |     |
|                 | 45                      | 50                    | 55              |     |
| CAA ATC AGA GAG | CTT ATT TTT GGC         | ACG CCT TTT CCT       | AGC GAT TTG AGA | 306 |
| Gln Ile Arg Glu | Leu Ile Phe Gly         | Thr Pro Phe Pro       | Ser Asp Leu Arg |     |
|                 | 60                      | 65                    | 70              |     |
| GAT GAG ATT TTT | CAA GCT TAT GAG         | ATT TTA AGC CAG       | CAA TAC CAC ATG | 354 |
| Asp Glu Ile Phe | Gln Ala Tyr Glu         | Ile Leu Ser Gln       | Gln Tyr His Met |     |
| 75              | 80                      | 85                    |                 |     |
| AAA GAA GCC GAT | GTG GCT GTA AGG         | AGT TCC GCT ACT       | GCA GAA GAT TTG | 402 |
| Lys Glu Ala Asp | Val Ala Val Arg         | Ser Ser Ala Thr       | Ala Glu Asp Leu |     |
| 90              | 95                      | 100                   |                 |     |

|                                                                 |      |
|-----------------------------------------------------------------|------|
| CCG GAC GCT TCT TTT GCC GGG CAG CAA GAC ACT TAT TTA AAC ATT AAG | 450  |
| Pro Asp Ala Ser Phe Ala Gly Gln Gln Asp Thr Tyr Leu Asn Ile Lys |      |
| 105 110 115 120                                                 |      |
| GGT AAA ACC GAA TTG ATC CAC TAT ATC AAA TCC TGT TTA GCG TCG CTT | 498  |
| Gly Lys Thr Glu Leu Ile His Tyr Ile Lys Ser Cys Leu Ala Ser Leu |      |
| 125 130 135                                                     |      |
| TTT ACC GAT AGA GCG ATT AGC TAT AGG GCG AGT CGT GGG TTT GAT CAT | 546  |
| Phe Thr Asp Arg Ala Ile Ser Tyr Arg Ala Ser Arg Gly Phe Asp His |      |
| 140 145 150                                                     |      |
| TTA AAA GTC GCG CTC AGC GTG GGG GTG CAA AAA ATG GTG CGA GCG GAT | 594  |
| Leu Lys Val Ala Leu Ser Val Gly Val Gln Lys Met Val Arg Ala Asp |      |
| 155 160 165                                                     |      |
| AAA GGC AGC GCG GGC GTG ATG TTT TCT ATT GAC ACC GAA ACC GGT TTT | 642  |
| Lys Gly Ser Ala Gly Val Met Phe Ser Ile Asp Thr Glu Thr Gly Phe |      |
| 170 175 180                                                     |      |
| AAA GAC GCG GTG TTT ATC ACT TCA GCG TGG GGG TTA GGC GAA AAT GTG | 690  |
| Lys Asp Ala Val Phe Ile Thr Ser Ala Trp Gly Leu Gly Glu Asn Val |      |
| 185 190 195 200                                                 |      |
| GTG GGT GGC ACG ATA AAC CCT GAT GAA TTT TAT GTG TTT AAG CCC ACT | 738  |
| Val Gly Gly Thr Ile Asn Pro Asp Glu Phe Tyr Val Phe Lys Pro Thr |      |
| 205 210 215                                                     |      |
| TTA GAG CAA AAC AAA CGC CCC ATT ATC AAA CGC CAA CTC GGC AAT AAA | 786  |
| Leu Glu Gln Asn Lys Arg Pro Ile Ile Lys Arg Gln Leu Gly Asn Lys |      |
| 220 225 230                                                     |      |
| ACG CAA AAA ATG GTC TAT GCC CCA AGG GGT AGC GAA CAC CCC ACC AGA | 834  |
| Thr Gln Lys Met Val Tyr Ala Pro Arg Gly Ser Glu His Pro Thr Arg |      |
| 235 240 245                                                     |      |
| AAC ATT AAA ACC ACC AAA AAA GAA TGG CAA TCC TTT TCA TTG AGC GAT | 882  |
| Asn Ile Lys Thr Thr Lys Lys Glu Trp Gln Ser Phe Ser Leu Ser Asp |      |
| 250 255 260                                                     |      |
| GAA GAC GTG CTG ATT TTA GCC AAA TAC GCC ATT GAA ATT GAA AAA CAC | 930  |
| Glu Asp Val Leu Ile Leu Ala Lys Tyr Ala Ile Glu Ile Glu Lys His |      |
| 265 270 275 280                                                 |      |
| TAC TCT AAA GAA GCC AAA CAA TAC CGC CCT ATG GAT ATA GAA TGG GCT | 978  |
| Tyr Ser Lys Glu Ala Lys Gln Tyr Arg Pro Met Asp Ile Glu Trp Ala |      |
| 285 290 295                                                     |      |
| AAA GAT GGC GAG AGC GGG GAA ATC TTT ATC GTT CAA GCG CGC CCA GAA | 1026 |
| Lys Asp Gly Glu Ser Gly Glu Ile Phe Ile Val Gln Ala Arg Pro Glu |      |
| 300 305 310                                                     |      |
| ACC GTT CAA AGC CAA AAA AGT AAA GAA GAA AGT CAA GTC TTT GAA AAA | 1074 |
| Thr Val Gln Ser Gln Lys Ser Lys Glu Glu Ser Gln Val Phe Glu Lys |      |
| 315 320 325                                                     |      |
| TTC AAA TTC AAA AAC CCT AAC GAA AAG AAA GAG ATT ATC TTA CAA GGC | 1122 |
| Phe Lys Phe Lys Asn Pro Asn Glu Lys Lys Glu Ile Ile Leu Gln Gly |      |



| 330                                                                                                                                                   | 335 | 340 |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----|------|
| AGA GCG ATT GGG AGT AAA AAT GGC TCA GGA AAA GTG CGC ATC ATC AAT<br>Arg Ala Ile Gly Ser Lys Ile Gly Ser Gly Lys Val Arg Ile Ile Asn<br>345 350 355 360 |     |     | 1170 |
| GAT TTG GAG CAC ATG AAT TCT TTT AAA GAG GGC GAA ATT TTA GTT ACG<br>Asp Leu Glu His Met Asn Ser Phe Lys Glu Gly Glu Ile Leu Val Thr<br>365 370 375     |     |     | 1218 |
| GAT AAC ACC GAT CCG GAC TGG GAG CCT TGC ATG AAA AAA GCG AGC GCG<br>Asp Asn Thr Asp Pro Asp Trp Glu Pro Cys Met Lys Lys Ala Ser Ala<br>380 385 390     |     |     | 1266 |
| GTT ATC ACT AAT CGT GGA GGG CGC ACT TGC CAT GCC GCT ATT GTG GCG<br>Val Ile Thr Asn Arg Gly Gly Arg Thr Cys His Ala Ala Ile Val Ala<br>395 400 405     |     |     | 1314 |
| AGA GAA ATT GGC GTG CCA GCT ATC GTT GGG GTG AGC GGG GCG ACT GAT<br>Arg Glu Ile Gly Val Pro Ala Ile Val Gly Val Ser Gly Ala Thr Asp<br>410 415 420     |     |     | 1362 |
| AGC CTT TAT ACC GGC ATG GAA ATC ACG GTT TCT TGC GCT GAG GGC GAA<br>Ser Leu Tyr Thr Gly Met Glu Ile Thr Val Ser Cys Ala Glu Gly Glu<br>425 430 435 440 |     |     | 1410 |
| GAG GGC TAT GTG TAT GCG GGC ATT TAT GAG CAT GAA ATT GAA AGG GTG<br>Glu Gly Tyr Val Tyr Ala Gly Ile Tyr Glu His Glu Ile Glu Arg Val<br>445 450 455     |     |     | 1458 |
| GAG CTT TCT AAC ATG CAA GAA ACT CAA ACA AAA ATT TAC ATC AAT ATT<br>Glu Leu Ser Asn Met Gln Glu Thr Gln Thr Lys Ile Tyr Ile Asn Ile<br>460 465 470     |     |     | 1506 |
| GGA AAC CCT GAA AAA GCC TTT GGC TTT TCT CAA CTC CCT AAT CAC GGC<br>Gly Asn Pro Glu Lys Ala Phe Gly Phe Ser Gln Leu Pro Asn His Gly<br>475 480 485     |     |     | 1554 |
| GTA GGG CTA GCC AGG ATG GAA ATG ATT ATT TTA AAT CAA ATC AAA GCC<br>Val Gly Leu Ala Arg Met Glu Met Ile Ile Leu Asn Gln Ile Lys Ala<br>490 495 500     |     |     | 1602 |
| CAC CCT TTA GCT TTA GTG GAT TTG CAC CAC AAA AAA AGC GTG AAA GAA<br>His Pro Leu Ala Leu Val Asp Leu His His Lys Lys Ser Val Lys Glu<br>505 510 515 520 |     |     | 1650 |
| AAA AAT GAA ATT GAA AAC CTC ATG GCA GGC TAT GCT AAC CCT AAA GAT<br>Lys Asn Glu Ile Glu Asn Leu Met Ala Gly Tyr Ala Asn Pro Lys Asp<br>525 530 535     |     |     | 1698 |
| TTT TTT GTG AAA AAA ATC GCT GAA GGC ATT GGC ATG ATC AGT GCA GCG<br>Phe Phe Val Lys Lys Ile Ala Glu Gly Ile Gly Met Ile Ser Ala Ala<br>540 545 550     |     |     | 1746 |
| TTT TAC CCT AAA CCT GTC ATT GTG AGA ACG AGC GAT TTC AAA TCC AAT<br>Phe Tyr Pro Lys Pro Val Ile Val Arg Thr Ser Asp Phe Lys Ser Asn<br>555 560 565     |     |     | 1794 |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| GAA TAC ATG CGC ATG CTT GGC GGC TCT AGC TAT GAG CCT AAT GAA GAA<br>Glu Tyr Met Arg Met Leu Gly Gly Ser Ser Tyr Glu Pro Asn Glu Glu<br>570 575 580     | 1842 |
| AAC CCC ATG CTT GGC TAT AGG GGG GCT AGT CGG TAT TAT TCA GAG AGC<br>Asn Pro Met Leu Gly Tyr Arg Gly Ala Ser Arg Tyr Tyr Ser Glu Ser<br>585 590 595 600 | 1890 |
| TAT AAT GAA GCG TTT TCG TGG GAG TGT GAA GCC TTA GCG TTA GTG AGG<br>Tyr Asn Glu Ala Phe Ser Trp Glu Cys Glu Ala Leu Ala Leu Val Arg<br>605 610 615     | 1938 |
| GAA GAA ATG GGA TTA ACC AAC ATG AAA GTG ATG ATC CCT TTT TTG CGA<br>Glu Glu Met Gly Leu Thr Asn Met Lys Val Met Ile Pro Phe Leu Arg<br>620 625 630     | 1986 |
| ACC ATT GAA GAG GGT AAA AAA GTC CTA GAA ATC TTA AGA AAA AAC AAT<br>Thr Ile Glu Glu Gly Lys Lys Val Leu Glu Ile Leu Arg Lys Asn Asn<br>635 640 645     | 2034 |
| TTA GAA TCC GGT AAA AAC GGG CTT GAA ATT TAT ATC ATG TGC GAA TTG<br>Leu Glu Ser Gly Lys Asn Gly Leu Glu Ile Tyr Ile Met Cys Glu Leu<br>650 655 660     | 2082 |
| CCG GTG AAT GTC ATT TTG GCT GAT GAT TTC TTG AGC TTG TTT GAT GGC<br>Pro Val Asn Val Ile Leu Ala Asp Asp Phe Leu Ser Leu Phe Asp Gly<br>665 670 675 680 | 2130 |
| TTT TCT ATT GGA TCA AAC GAT TTA ACC CAG CTC ACT TTA GGC GTG GAT<br>Phe Ser Ile Gly Ser Asn Asp Leu Thr Gln Leu Thr Leu Gly Val Asp<br>685 690 695     | 2178 |
| AGA GAC AGC GAA TTG GTC AGC CAT GTC TTT GAT GAA AGG AAT GAA GCG<br>Arg Asp Ser Glu Leu Val Ser His Val Phe Asp Glu Arg Asn Glu Ala<br>700 705 710     | 2226 |
| ATG CTA AAG ATG TTT AAA AAA GCG ATT GAA GCT TGC AAA AGG CAC AAC<br>Met Leu Lys Met Phe Lys Lys Ala Ile Glu Ala Cys Lys Arg His Asn<br>715 720 725     | 2274 |
| AAA TAT TGC GGG ATT TGC GGG CAA GCC CCA AGC GAT TAC CCT GAA GTA<br>Lys Tyr Cys Gly Ile Cys Gly Gln Ala Pro Ser Asp Tyr Pro Glu Val<br>730 735 740     | 2322 |
| ACA GAG TTT TTA GTC AAA GAG GGC ATC ACT TCC ATT TCT TTA AAC CCT<br>Thr Glu Phe Leu Val Lys Glu Gly Ile Thr Ser Ile Ser Leu Asn Pro<br>745 750 755 760 | 2370 |
| GAT AGC GTG ATC CCC ACT TGG AAC GCT GTA GCC AAG TTA GAA AAA GAA<br>Asp Ser Val Ile Pro Thr Trp Asn Ala Val Ala Lys Leu Glu Lys Glu<br>765 770 775     | 2418 |
| CTA AAA GAA CAT GGC TTA ACT GAA CAT TGATAATAAA TAAATCAATC TAACTTG<br>Leu Lys Glu His Gly Leu Thr Glu His<br>780 785                                   | 2472 |
| AGTGGATTTT TCGTATTAGT TTCCAT                                                                                                                          | 2498 |

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 785 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Gln | Glu | Leu | Val | Pro | Ile | Gly | Ile | Lys | Val | Pro | Asp | Gly | Phe | 1   | 5   | 10  | 15  |
| Ala | Ile | Thr | Ser | Glu | Ala | Tyr | Trp | Tyr | Leu | Leu | Glu | Gln | Gly | Gly | Ala | 20  | 25  | 30  |     |
| Lys | Gln | Lys | Ile | Ile | Glu | Leu | Leu | Glu | Asn | Val | Asp | Ala | Thr | Glu | Ile | 35  | 40  | 45  |     |
| Asp | Val | Leu | Lys | Ile | Arg | Ser | Lys | Gln | Ile | Arg | Glu | Leu | Ile | Phe | Gly | 50  | 55  | 60  |     |
| Thr | Pro | Phe | Pro | Ser | Asp | Leu | Arg | Asp | Glu | Ile | Phe | Gln | Ala | Tyr | Glu | 65  | 70  | 75  | 80  |
| Ile | Leu | Ser | Gln | Gln | Tyr | His | Met | Lys | Glu | Ala | Asp | Val | Ala | Val | Arg | 85  | 90  | 95  |     |
| Ser | Ser | Ala | Thr | Ala | Glu | Asp | Leu | Pro | Asp | Ala | Ser | Phe | Ala | Gly | Gln | 100 | 105 | 110 |     |
| Gln | Asp | Thr | Tyr | Leu | Asn | Ile | Lys | Gly | Lys | Thr | Glu | Leu | Ile | His | Tyr | 115 | 120 | 125 |     |
| Ile | Lys | Ser | Cys | Leu | Ala | Ser | Leu | Phe | Thr | Asp | Arg | Ala | Ile | Ser | Tyr | 130 | 135 | 140 |     |
| Arg | Ala | Ser | Arg | Gly | Phe | Asp | His | Leu | Lys | Val | Ala | Leu | Ser | Val | Gly | 145 | 150 | 155 | 160 |
| Val | Gln | Lys | Met | Val | Arg | Ala | Asp | Lys | Gly | Ser | Ala | Gly | Val | Met | Phe | 165 | 170 | 175 |     |
| Ser | Ile | Asp | Thr | Glu | Thr | Gly | Phe | Lys | Asp | Ala | Val | Phe | Ile | Thr | Ser | 180 | 185 | 190 |     |
| Ala | Trp | Gly | Leu | Gly | Glu | Asn | Val | Val | Gly | Gly | Thr | Ile | Asn | Pro | Asp | 195 | 200 | 205 |     |
| Glu | Phe | Tyr | Val | Phe | Lys | Pro | Thr | Leu | Glu | Gln | Asn | Lys | Arg | Pro | Ile | 210 | 215 | 220 |     |
| Ile | Lys | Arg | Gln | Leu | Gly | Asn | Lys | Thr | Gln | Lys | Met | Val | Tyr | Ala | Pro | 225 | 230 | 235 | 240 |
| Arg | Gly | Ser | Glu | His | Pro | Thr | Arg | Asn | Ile | Lys | Thr | Thr | Lys | Lys | Glu | 245 | 250 | 255 |     |
| Trp | Gln | Ser | Phe | Ser | Leu | Ser | Asp | Glu | Asp | Val | Leu | Ile | Leu | Ala | Lys | 260 | 265 | 270 |     |
| Tyr | Ala | Ile | Glu | Ile | Glu | Lys | His | Tyr | Ser | Lys | Glu | Ala | Lys | Gln | Tyr | 275 | 280 | 285 |     |
| Arg | Pro | Met | Asp | Ile | Glu | Trp | Ala | Lys | Asp | Gly | Glu | Ser | Gly | Glu | Ile | 290 | 295 | 300 |     |
| Phe | Ile | Val | Gln | Ala | Arg | Pro | Glu | Thr | Val | Gln | Ser | Gln | Lys | Ser | Lys | 305 | 310 | 315 | 320 |
| Glu | Glu | Ser | Gln | Val | Phe | Glu | Lys | Phe | Lys | Phe | Lys | Asn | Pro | Asn | Glu | 325 | 330 | 335 |     |
| Lys | Lys | Glu | Ile | Ile | Leu | Gln | Gly | Arg | Ala | Ile | Gly | Ser | Lys | Ile | Gly | 340 | 345 | 350 |     |
| Ser | Gly | Lys | Val | Arg | Ile | Ile | Asn | Asp | Leu | Glu | His | Met | Asn | Ser | Phe | 355 | 360 | 365 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Glu | Gly | Glu | Ile | Leu | Val | Thr | Asp | Asn | Thr | Asp | Pro | Asp | Trp | Glu | 370 | 375 | 380 |
| Pro | Cys | Met | Lys | Lys | Ala | Ser | Ala | Val | Ile | Thr | Asn | Arg | Gly | Gly | Arg | 385 | 390 | 395 |
| Thr | Cys | His | Ala | Ala | Ile | Val | Ala | Arg | Glu | Ile | Gly | Val | Pro | Ala | Ile | 405 | 410 | 415 |
| Val | Gly | Val | Ser | Gly | Ala | Thr | Asp | Ser | Leu | Tyr | Thr | Gly | Met | Glu | Ile | 420 | 425 | 430 |
| Thr | Val | Ser | Cys | Ala | Glu | Gly | Glu | Glu | Gly | Tyr | Val | Tyr | Ala | Gly | Ile | 435 | 440 | 445 |
| Tyr | Glu | His | Glu | Ile | Glu | Arg | Val | Glu | Leu | Ser | Asn | Met | Gln | Glu | Thr | 450 | 455 | 460 |
| Gln | Thr | Lys | Ile | Tyr | Ile | Asn | Ile | Gly | Asn | Pro | Glu | Lys | Ala | Phe | Gly | 465 | 470 | 475 |
| Phe | Ser | Gln | Leu | Pro | Asn | His | Gly | Val | Gly | Leu | Ala | Arg | Met | Glu | Met | 485 | 490 | 495 |
| Ile | Ile | Leu | Asn | Gln | Ile | Lys | Ala | His | Pro | Leu | Ala | Leu | Val | Asp | Leu | 500 | 505 | 510 |
| His | His | Lys | Lys | Ser | Val | Lys | Glu | Lys | Asn | Glu | Ile | Glu | Asn | Leu | Met | 515 | 520 | 525 |
| Ala | Gly | Tyr | Ala | Asn | Pro | Lys | Asp | Phe | Phe | Val | Lys | Lys | Ile | Ala | Glu | 530 | 535 | 540 |
| Gly | Ile | Gly | Met | Ile | Ser | Ala | Ala | Phe | Tyr | Pro | Lys | Pro | Val | Ile | Val | 545 | 550 | 555 |
| Arg | Thr | Ser | Asp | Phe | Lys | Ser | Asn | Glu | Tyr | Met | Arg | Met | Leu | Gly | Gly | 565 | 570 | 575 |
| Ser | Ser | Tyr | Glu | Pro | Asn | Glu | Glu | Asn | Pro | Met | Leu | Gly | Tyr | Arg | Gly | 580 | 585 | 590 |
| Ala | Ser | Arg | Tyr | Tyr | Ser | Glu | Ser | Tyr | Asn | Glu | Ala | Phe | Ser | Trp | Glu | 595 | 600 | 605 |
| Cys | Glu | Ala | Leu | Ala | Leu | Val | Arg | Glu | Glu | Met | Gly | Leu | Thr | Asn | Met | 610 | 615 | 620 |
| Lys | Val | Met | Ile | Pro | Phe | Leu | Arg | Thr | Ile | Glu | Glu | Gly | Lys | Lys | Val | 625 | 630 | 635 |
| Leu | Glu | Ile | Leu | Arg | Lys | Asn | Asn | Leu | Glu | Ser | Gly | Lys | Asn | Gly | Leu | 645 | 650 | 655 |
| Glu | Ile | Tyr | Ile | Met | Cys | Glu | Leu | Pro | Val | Asn | Val | Ile | Leu | Ala | Asp | 660 | 665 | 670 |
| Asp | Phe | Leu | Ser | Leu | Phe | Asp | Gly | Phe | Ser | Ile | Gly | Ser | Asn | Asp | Leu | 675 | 680 | 685 |
| Thr | Gln | Leu | Thr | Leu | Gly | Val | Asp | Arg | Asp | Ser | Glu | Leu | Val | Ser | His | 690 | 695 | 700 |
| Val | Phe | Asp | Glu | Arg | Asn | Glu | Ala | Met | Leu | Lys | Met | Phe | Lys | Lys | Ala | 705 | 710 | 715 |
| Ile | Glu | Ala | Cys | Lys | Arg | His | Asn | Lys | Tyr | Cys | Gly | Ile | Cys | Gly | Gln | 725 | 730 | 735 |
| Ala | Pro | Ser | Asp | Tyr | Pro | Glu | Val | Thr | Glu | Phe | Leu | Val | Lys | Glu | Gly | 740 | 745 | 750 |
| Ile | Thr | Ser | Ile | Ser | Leu | Asn | Pro | Asp | Ser | Val | Ile | Pro | Thr | Trp | Asn | 755 | 760 | 765 |
| Ala | Val | Ala | Lys | Leu | Glu | Lys | Glu | Leu | Lys | Glu | His | Gly | Leu | Thr | Glu | 770 | 775 | 780 |
| His |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 785 |     |     |

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 565 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 61...483  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GTTATCTTTA ATCAATCAGA TGATAGAATT TATCTTTTAT TTTTGAATTG GGAGCATTTG | 60  |
| ATG AAA AAA TTA GCG GTT TCT TTA TTA TTT ACA GGG ACT TTT TTG GGG   | 108 |
| Met Lys Lys Leu Ala Val Ser Leu Leu Phe Thr Gly Thr Phe Leu Gly   |     |
| 1 5 10 15                                                         |     |
| CTT TTT TTG AAT GCG AGC GAT TTT AAG AGC ATG GAT GAC AAG CAA CTA   | 156 |
| Leu Phe Leu Asn Ala Ser Asp Phe Lys Ser Met Asp Asp Lys Gln Leu   |     |
| 20 25 30                                                          |     |
| TTA GAG CAA GCA GGG AAA GTT GCT CCT AGC GAA GTC CCT GAG TTT CGC   | 204 |
| Leu Glu Gln Ala Gly Lys Val Ala Pro Ser Glu Val Pro Glu Phe Arg   |     |
| 35 40 45                                                          |     |
| GCG GAA GTC AAT AAG CGA TTA GCA GTG ATG AAA GAA GAA GAT CGT AAA   | 252 |
| Ala Glu Val Asn Lys Arg Leu Ala Val Met Lys Glu Glu Asp Arg Lys   |     |
| 50 55 60                                                          |     |
| AAT TAT AAA GCG GAT TTT AAG AAA GCG ATG GAT AAG AAT TTA GCT TCT   | 300 |
| Asn Tyr Lys Ala Asp Phe Lys Lys Ala Met Asp Lys Asn Leu Ala Ser   |     |
| 65 70 75 80                                                       |     |
| TTA AGC CAA GAA GAT CGC AAC AAG CGT AAA AAA GAA ATT CTT GAA GCG   | 348 |
| Leu Ser Gln Glu Asp Arg Asn Lys Arg Lys Lys Glu Ile Leu Glu Ala   |     |
| 85 90 95                                                          |     |
| ATT GCT AAC AAA AAG AAA ACA ATG ACC ATG AAA GAA TAT CGT GAA GAA   | 396 |
| Ile Ala Asn Lys Lys Lys Thr Met Thr Met Lys Glu Tyr Arg Glu Glu   |     |
| 100 105 110                                                       |     |
| GGG TTG GAT TTG CAT GAT TGC GCA TGC GAA GGC CCT TTT CAT GAT CAT   | 444 |
| Gly Leu Asp Leu His Asp Cys Ala Cys Glu Gly Pro Phe His Asp His   |     |
| 115 120 125                                                       |     |
| GAG AGA AAA AAA GGG AAA AAA CCA AGC CAT CAT AAG CAT TAGCGCTTAG GG | 495 |
| Glu Arg Lys Lys Gly Lys Lys Pro Ser His His Lys His               |     |
| 130 135 140                                                       |     |
| TGTGCTAACT TTTTGTGATT TTTGTGAAAC CACGCCGTAA GTCCCTAGCT TTTGGCTGTG | 555 |
| GGGATTAAGG                                                        | 565 |

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Lys | Leu | Ala | Val | Ser | Leu | Leu | Phe | Thr | Gly | Thr | Phe | Leu | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Phe | Leu | Asn | Ala | Ser | Asp | Phe | Lys | Ser | Met | Asp | Asp | Lys | Gln | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Glu | Gln | Ala | Gly | Lys | Val | Ala | Pro | Ser | Glu | Val | Pro | Glu | Phe | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Glu | Val | Asn | Lys | Arg | Leu | Ala | Val | Met | Lys | Glu | Glu | Asp | Arg | Lys |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Tyr | Lys | Ala | Asp | Phe | Lys | Lys | Ala | Met | Asp | Lys | Asn | Leu | Ala | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Ser | Gln | Glu | Asp | Arg | Asn | Lys | Arg | Lys | Lys | Glu | Ile | Leu | Glu | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Ala | Asn | Lys | Lys | Lys | Thr | Met | Thr | Met | Lys | Glu | Tyr | Arg | Glu | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Leu | Asp | Leu | His | Asp | Cys | Ala | Cys | Glu | Gly | Pro | Phe | His | Asp | His |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Arg | Lys | Lys | Gly | Lys | Lys | Pro | Ser | His | His | Lys | His |     |     |     |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 558 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 51...506  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

|                                                                 |            |            |            |            |         |     |
|-----------------------------------------------------------------|------------|------------|------------|------------|---------|-----|
| GGGTGCATGG                                                      | GCCTCAAAAA | GTCGCTATCA | TTCTCTACTA | AAGGATAAGA | ATG GAA | 56  |
|                                                                 |            |            |            |            | Met Glu |     |
|                                                                 |            |            |            |            | 1       |     |
| AAA TTA GAA GTA GGG CAA TTA GCC CCT GAT TTT AGA TTG AAA AAC AGC |            |            |            |            |         | 104 |
| Lys Leu Glu Val Gly Gln Leu Ala Pro Asp Phe Arg Leu Lys Asn Ser |            |            |            |            |         |     |
|                                                                 | 5          |            |            | 10         |         | 15  |
| GAT GGC GTG GAA ATT TCT TTA AAA GAT TTG CTC CAT AAA AAA GTG GTG |            |            |            |            |         | 152 |
| Asp Gly Val Glu Ile Ser Leu Lys Asp Leu Leu His Lys Lys Val Val |            |            |            |            |         |     |
|                                                                 | 20         |            |            | 25         |         | 30  |

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| CTG TAT TTC TAC CCT AAA GAC AAC ACC CCC GGA TGC ACT CTA GAA GCC   | 200 |
| Leu Tyr Phe Tyr Pro Lys Asp Asn Thr Pro Gly Cys Thr Leu Glu Ala   |     |
| 35 40 45 50                                                       |     |
| AAA GAC TTT AGC GCT CTA TTT AGT GAA TTT GAA AAG AAA AAC GCT GTT   | 248 |
| Lys Asp Phe Ser Ala Leu Phe Ser Glu Phe Glu Lys Lys Asn Ala Val   |     |
| 55 60 65                                                          |     |
| GTC GTA GGC ATA AGC CCT GAT AAC GCG CAA TCG CAT CAA AAA TTT ATC   | 296 |
| Val Val Gly Ile Ser Pro Asp Asn Ala Gln Ser His Gln Lys Phe Ile   |     |
| 70 75 80                                                          |     |
| AGC CAA TGC TCT TTG AAT GTG ATT TTG CTC TGC GAT GAA GAT AAA AAA   | 344 |
| Ser Gln Cys Ser Leu Asn Val Ile Leu Leu Cys Asp Glu Asp Lys Lys   |     |
| 85 90 95                                                          |     |
| GCC GCC AAT CTT TAC AAA GCT TAT GGC AAA CGC ATG CTT TAT GGG AAG   | 392 |
| Ala Ala Asn Leu Tyr Lys Ala Tyr Gly Lys Arg Met Leu Tyr Gly Lys   |     |
| 100 105 110                                                       |     |
| GAG CAT TTG GGG ATT ATC CGC TCC ACC TTC ATT ATC AAC ACG CAA GGC   | 440 |
| Glu His Leu Gly Ile Ile Arg Ser Thr Phe Ile Ile Asn Thr Gln Gly   |     |
| 115 120 125 130                                                   |     |
| GTT TTA GAA AAA TGT TTC TAC AAT GTC AAA GCG AAA GGC CAT GCT CAA   | 488 |
| Val Leu Glu Lys Cys Phe Tyr Asn Val Lys Ala Lys Gly His Ala Gln   |     |
| 135 140 145                                                       |     |
| AAG GTT TTA GAG AGT TTG TAGTTTAACT TTCTAACTTT CGCCCATTTT AATTTGAG | 544 |
| Lys Val Leu Glu Ser Leu                                           |     |
| 150                                                               |     |
| ATTTTTTTAGC CATT                                                  | 558 |

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Glu Lys Leu Glu Val Gly Gln Leu Ala Pro Asp Phe Arg Leu Lys |  |
| 1 5 10 15                                                       |  |
| Asn Ser Asp Gly Val Glu Ile Ser Leu Lys Asp Leu Leu His Lys Lys |  |
| 20 25 30                                                        |  |
| Val Val Leu Tyr Phe Tyr Pro Lys Asp Asn Thr Pro Gly Cys Thr Leu |  |
| 35 40 45                                                        |  |
| Glu Ala Lys Asp Phe Ser Ala Leu Phe Ser Glu Phe Glu Lys Lys Asn |  |
| 50 55 60                                                        |  |
| Ala Val Val Val Gly Ile Ser Pro Asp Asn Ala Gln Ser His Gln Lys |  |
| 65 70 75 80                                                     |  |
| Phe Ile Ser Gln Cys Ser Leu Asn Val Ile Leu Leu Cys Asp Glu Asp |  |
| 85 90 95                                                        |  |

Lys Lys Ala Ala Asn Leu Tyr Lys Ala Tyr Gly Lys Arg Met Leu Tyr  
                   100                  105                  110  
 Gly Lys Glu His Leu Gly Ile Ile Arg Ser Thr Phe Ile Ile Asn Thr  
                   115                  120                  125  
 Gln Gly Val Leu Glu Lys Cys Phe Tyr Asn Val Lys Ala Lys Gly His  
                   130                  135                  140  
 Ala Gln Lys Val Leu Glu Ser Leu  
 145                  150

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...651
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ACTTAGAAGG GGTGATTT ATG AGT AAA GAG CTT ATT TTA AAG CGC ATT AAA | 51  |
| Met Ser Lys Glu Leu Ile Leu Lys Arg Ile Lys                     |     |
| 1                  5                  10                        |     |
| GAA GCC AGA GCC AAG CAT GCC ATT CAG GGA GCG AAC CCT ATT TAT AGG | 99  |
| Glu Ala Arg Ala Lys His Ala Ile Gln Gly Ala Asn Pro Ile Tyr Arg |     |
| 15                  20                  25                      |     |
| AAT ATC ATT AAA GTG GAG TTT GAG GAC TTG GTG GAA GAA TAC AAG CAT | 147 |
| Asn Ile Ile Lys Val Glu Phe Glu Asp Leu Val Glu Glu Tyr Lys His |     |
| 30                  35                  40                      |     |
| TTC CAA GTG TTG AAT AAA GCT GAA GTC ATT GAA AGC GCT AAA GAA AAT | 195 |
| Phe Gln Val Leu Asn Lys Ala Glu Val Ile Glu Ser Ala Lys Glu Asn |     |
| 45                  50                  55                      |     |
| TTA GAG CAA GCC ATT TTA AAG GCT TTA GAA AAT TTT AAA AGC AAA AAA | 243 |
| Leu Glu Gln Ala Ile Leu Lys Ala Leu Glu Asn Phe Lys Ser Lys Lys |     |
| 60                  65                  70                  75  |     |
| ATC TTA CAC TCC ACA GAT TTG AAT TTG AAT TTT GAA GCG TTT AAG GAT | 291 |
| Ile Leu His Ser Thr Asp Leu Asn Leu Asn Phe Glu Ala Phe Lys Asp |     |
| 80                  85                  90                      |     |
| TTT ACT TTA CAG CCT TAT GAT AAA GAA ATT GAA GCG ATG CGT GAA GAG | 339 |
| Phe Thr Leu Gln Pro Tyr Asp Lys Glu Ile Glu Ala Met Arg Glu Glu |     |
| 95                  100                  105                    |     |
| TTG TTT GAG ATT GAT ACG GCT TTA TTG CAT GGG GTT TGT GGG ATT TCA | 387 |
| Leu Phe Glu Ile Asp Thr Ala Leu Leu His Gly Val Cys Gly Ile Ser |     |
| 110                  115                  120                   |     |



```

AGC TTG GGC ATG ATT GGG GCG GTC TCT TCG CAT GCA AGC CCG CGA TTG 435
Ser Leu Gly Met Ile Gly Ala Val Ser Ser His Ala Ser Pro Arg Leu
 125 130 135

CTT TCG CTC ATC ACC CTT AAT TGC ATC ATC TTA TTG AAA AAA GAA TCC 483
Leu Ser Leu Ile Thr Leu Asn Cys Ile Ile Leu Leu Lys Lys Glu Ser
 140 145 150 155

ATT GTG CGC AAT TTG AGT GAA GGC ATG CAA GCT TTA AAA AAC CAA AGC 531
Ile Val Arg Asn Leu Ser Glu Gly Met Gln Ala Leu Lys Asn Gln Ser
 160 165 170

CAA AAC GGT GCA TTA CCC ACA AAC ATG CTC CTT ATT GGC GGG CCT AGC 579
Gln Asn Gly Ala Leu Pro Thr Asn Met Leu Leu Ile Gly Gly Pro Ser
 175 180 185

CGG ACA GCT GAC ATT GAA TTA AAA ACC GTT TTT GGG GTG CAT GGG CCT 627
Arg Thr Ala Asp Ile Glu Leu Lys Thr Val Phe Gly Val His Gly Pro
 190 195 200

CAA AAA GTC GCT ATC ATT CTC TAC TAAAGGATAA GAATGGAAAA ATTAGAAGTA 681
Gln Lys Val Ala Ile Ile Leu Tyr
 205 210

GGGCAATTAG CCCCTGATT 700

```

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

```

Met Ser Lys Glu Leu Ile Leu Lys Arg Ile Lys Glu Ala Arg Ala Lys
 1 5 10 15
His Ala Ile Gln Gly Ala Asn Pro Ile Tyr Arg Asn Ile Ile Lys Val
 20 25 30
Glu Phe Glu Asp Leu Val Glu Glu Tyr Lys His Phe Gln Val Leu Asn
 35 40 45
Lys Ala Glu Val Ile Glu Ser Ala Lys Glu Asn Leu Glu Gln Ala Ile
 50 55 60
Leu Lys Ala Leu Glu Asn Phe Lys Ser Lys Lys Ile Leu His Ser Thr
 65 70 75 80
Asp Leu Asn Leu Asn Phe Glu Ala Phe Lys Asp Phe Thr Leu Gln Pro
 85 90 95
Tyr Asp Lys Glu Ile Glu Ala Met Arg Glu Glu Leu Phe Glu Ile Asp
 100 105 110
Thr Ala Leu Leu His Gly Val Cys Gly Ile Ser Ser Leu Gly Met Ile
 115 120 125
Gly Ala Val Ser Ser His Ala Ser Pro Arg Leu Leu Ser Leu Ile Thr
 130 135 140
Leu Asn Cys Ile Ile Leu Leu Lys Lys Glu Ser Ile Val Arg Asn Leu
 145 150 155 160

```

Ser Glu Gly Met Gln Ala Leu Lys Asn Gln Ser Gln Asn Gly Ala Leu  
165 170 175  
Pro Thr Asn Met Leu Leu Ile Gly Gly Pro Ser Arg Thr Ala Asp Ile  
180 185 190  
Glu Leu Lys Thr Val Phe Gly Val His Gly Pro Gln Lys Val Ala Ile  
195 200 205  
Ile Leu Tyr  
210

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...531
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| TATTCCAATA ACGACTACCC TATTATTTTG CCTAGCGGTT CATGCACAGG G ATG ATG | 57  |
| Met Met                                                          |     |
| 1                                                                |     |
| CGG CAT GAT TAT TTG GAA TTG TTT GAA GGG CAT GCG GAA TTC AAC ATG  | 105 |
| Arg His Asp Tyr Leu Glu Leu Phe Glu Gly His Ala Glu Phe Asn Met  |     |
| 5 10 15                                                          |     |
| GTT AAA GAT TTT TGC TCT AGG GTG TAT GAA TTG AGC GAA TTT TTG GAT  | 153 |
| Val Lys Asp Phe Cys Ser Arg Val Tyr Glu Leu Ser Glu Phe Leu Asp  |     |
| 20 25 30                                                         |     |
| AAA AAA TTG CAA GTC AAA TAT GAA GAT AAG GGC GAA CCC CTT AAA ATC  | 201 |
| Lys Lys Leu Gln Val Lys Tyr Glu Asp Lys Gly Glu Pro Leu Lys Ile  |     |
| 35 40 45 50                                                      |     |
| ACA TGG CAT TCT AAT TGC CAT GCC TTA AGG GTG GCT AAA GTG ATT GAC  | 249 |
| Thr Trp His Ser Asn Cys His Ala Leu Arg Val Ala Lys Val Ile Asp  |     |
| 55 60 65                                                         |     |
| TCG GCG AAA AAC CTC ATC AGA CAG CTT AAA AAT GTG GAA CTC ATT GAA  | 297 |
| Ser Ala Lys Asn Leu Ile Arg Gln Leu Lys Asn Val Glu Leu Ile Glu  |     |
| 70 75 80                                                         |     |
| TTG GAA AAA GAA GAA GAA TGC TGC GGG TTT GGG GGG ACT TTT TCG GTT  | 345 |
| Leu Glu Lys Glu Glu Glu Cys Cys Gly Phe Gly Gly Thr Phe Ser Val  |     |
| 85 90 95                                                         |     |
| AAA GAG CCT GAA ATT TCA GCG GTT ATG GTT AAA GAA AAG ATT AAA AAC  | 393 |
| Lys Glu Pro Glu Ile Ser Ala Val Met Val Lys Glu Lys Ile Lys Asn  |     |
| 100 105 110                                                      |     |

ATA GAA AGC CGT CAA GTG GAT GTG ATT GTT TCA GCG GAT GCT GGG TGT 441  
 Ile Glu Ser Arg Gln Val Asp Val Ile Val Ser Ala Asp Ala Gly Cys  
 115 120 125 130

TTG ATG AAT ATC AGC ACC GCT ATG CAA AAA ATG GGC TCT TTG ACA AAA 489  
 Leu Met Asn Ile Ser Thr Ala Met Gln Lys Met Gly Ser Leu Thr Lys  
 135 140 145

CCC ATG CAT TTT TAT GAC TTT TTA GCC TCA AGA CTT GGG CTT TAACATTAA 540  
 Pro Met His Phe Tyr Asp Phe Leu Ala Ser Arg Leu Gly Leu  
 150 155 160

AGAATTATTT TAAGGAATGA TCATGGAAAA A 571

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

Met Met Arg His Asp Tyr Leu Glu Leu Phe Glu Gly His Ala Glu Phe  
 1 5 10 15  
 Asn Met Val Lys Asp Phe Cys Ser Arg Val Tyr Glu Leu Ser Glu Phe  
 20 25 30  
 Leu Asp Lys Lys Leu Gln Val Lys Tyr Glu Asp Lys Gly Glu Pro Leu  
 35 40 45  
 Lys Ile Thr Trp His Ser Asn Cys His Ala Leu Arg Val Ala Lys Val  
 50 55 60  
 Ile Asp Ser Ala Lys Asn Leu Ile Arg Gln Leu Lys Asn Val Glu Leu  
 65 70 75 80  
 Ile Glu Leu Glu Lys Glu Glu Glu Cys Cys Gly Phe Gly Gly Thr Phe  
 85 90 95  
 Ser Val Lys Glu Pro Glu Ile Ser Ala Val Met Val Lys Glu Lys Ile  
 100 105 110  
 Lys Asn Ile Glu Ser Arg Gln Val Asp Val Ile Val Ser Ala Asp Ala  
 115 120 125  
 Gly Cys Leu Met Asn Ile Ser Thr Ala Met Gln Lys Met Gly Ser Leu  
 130 135 140  
 Thr Lys Pro Met His Phe Tyr Asp Phe Leu Ala Ser Arg Leu Gly Leu  
 145 150 155 160

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 759 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 70...714  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AACCTGCAAA CCCACCTTAA AAGGCTCAAA AGAAGTGAGT TTGTGGGCCA AAAAAAGGAA | 60  |
| TTAGAGGGC ATG GGG AGG TTT TCT TTA AAA GAA ATT TTA ATG CTC AGC CTT | 111 |
| Met Gly Arg Phe Ser Leu Lys Glu Ile Leu Met Leu Ser Leu           |     |
| 1 5 10                                                            |     |
| ACC TTA TTG GCT TTA CTG GGT TGG ATT TTT GGC AAA CCT TTA GGC TTG   | 159 |
| Thr Leu Leu Ala Leu Leu Gly Trp Ile Phe Gly Lys Pro Leu Gly Leu   |     |
| 15 20 25 30                                                       |     |
| CAT GCG AGT GCG ACG GCT TTG ATT GTC ATG GTT TTA ATG GCG TTT TGT   | 207 |
| His Ala Ser Ala Thr Ala Leu Ile Val Met Val Leu Met Ala Phe Cys   |     |
| 35 40 45                                                          |     |
| AAG ATT GTA AGC TAT GAA GAC ATC ATT AAA AAC AAG AGC GCG TTC AAT   | 255 |
| Lys Ile Val Ser Tyr Glu Asp Ile Ile Lys Asn Lys Ser Ala Phe Asn   |     |
| 50 55 60                                                          |     |
| ATT TTT TTA TTG CTT GGA TCG CTG CTC ACG ATG GCT GGC GGG CTT AAA   | 303 |
| Ile Phe Leu Leu Leu Gly Ser Leu Leu Thr Met Ala Gly Gly Leu Lys   |     |
| 65 70 75                                                          |     |
| AAT GTA GGG TTT TTA AAT TTT ATC GGC AAT GCG GCT CAA AAT TTT TTA   | 351 |
| Asn Val Gly Phe Leu Asn Phe Ile Gly Asn Ala Ala Gln Asn Phe Leu   |     |
| 80 85 90                                                          |     |
| GAG CAT GCT CAC TTG GAT CCG TTA ATA GCG GTC TTG TTT ATT GTA GCC   | 399 |
| Glu His Ala His Leu Asp Pro Leu Ile Ala Val Leu Phe Ile Val Ala   |     |
| 95 100 105 110                                                    |     |
| CTC TTT TAT CTG TCG CAT TAT TTT TTC GCA AGC ATC ACC GCT CAT GTG   | 447 |
| Leu Phe Tyr Leu Ser His Tyr Phe Phe Ala Ser Ile Thr Ala His Val   |     |
| 115 120 125                                                       |     |
| AGC GCG TTA TTC GCG CTT TTT GTA GGG ATT GGT TCG CAC ATT CAA GGG   | 495 |
| Ser Ala Leu Phe Ala Leu Phe Val Gly Ile Gly Ser His Ile Gln Gly   |     |
| 130 135 140                                                       |     |
| GTC AAT TTG CAA GAA TTG AGC TTG TTT TTA ATG TTT TCT TTA GGG ATT   | 543 |
| Val Asn Leu Gln Glu Leu Ser Leu Phe Leu Met Phe Ser Leu Gly Ile   |     |
| 145 150 155                                                       |     |
| ATG GGG ATT TTA ACG CCC TAT GGC ACA GGC CCA TCC ACC ATT TAT TAC   | 591 |
| Met Gly Ile Leu Thr Pro Tyr Gly Thr Gly Pro Ser Thr Ile Tyr Tyr   |     |
| 160 165 170                                                       |     |
| GGG AGC GGG TAT ATT CAA AGC AAG GAT TTT TGG AAA TGG GGG TTT ATT   | 639 |
| Gly Ser Gly Tyr Ile Gln Ser Lys Asp Phe Trp Lys Trp Gly Phe Ile   |     |
| 175 180 185 190                                                   |     |
| TTT GGC TTT TTG TAT TTA ATC GTG TTT TTA AGC GTG TGC ACA CCT TGG   | 687 |
| Phe Gly Phe Leu Tyr Leu Ile Val Phe Leu Ser Val Cys Thr Pro Trp   |     |



(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 37...309
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

|                                                                   |                         |     |
|-------------------------------------------------------------------|-------------------------|-----|
| AAGGGGGGAT TTATATCGGT AAAGAGTTGT TTAAGC                           | ATG GCT AGT GGC CTT TTT | 54  |
|                                                                   | Met Ala Ser Gly Leu Phe |     |
|                                                                   | 1 5                     |     |
| GAA AAC GAT GGA ATC AAA GAC AAC AAA GCG CGA GAT TTT TTC TAT AGC   |                         | 102 |
| Glu Asn Asp Gly Ile Lys Asp Asn Lys Ala Arg Asp Phe Phe Tyr Ser   |                         |     |
|                                                                   | 10 15 20                |     |
| CAT AGC TCC CTA ATT GTC TTT TTC CTT TTA CTG CTT GGG TTT GGG TAT   |                         | 150 |
| His Ser Ser Leu Ile Val Phe Phe Leu Leu Leu Leu Gly Phe Gly Tyr   |                         |     |
|                                                                   | 25 30 35                |     |
| TAT TTA GGG AAG TTG CTT TTT GGG GGC TCT TCT TTA GAA GTT TAT TTG   |                         | 198 |
| Tyr Leu Gly Lys Leu Leu Phe Gly Gly Ser Ser Leu Glu Val Tyr Leu   |                         |     |
|                                                                   | 40 45 50                |     |
| GAT TTA AGA GAC AAG CAT GAA CGA TTG CAG CAA GAA ATC ACC GAA TTG   |                         | 246 |
| Asp Leu Arg Asp Lys His Glu Arg Leu Gln Gln Glu Ile Thr Glu Leu   |                         |     |
|                                                                   | 55 60 65 70             |     |
| CAA AGC AAG AAT GTG CGC TTG CAA AAG CGT TTG TTT GAG TTG AAG GAA   |                         | 294 |
| Gln Ser Lys Asn Val Arg Leu Gln Lys Arg Leu Phe Glu Leu Lys Glu   |                         |     |
|                                                                   | 75 80 85                |     |
| TTA CGG CCT AGA GAT TAGATTTAAG GAAAATGGTA GTGTTAAAAA AGATGATAGG T |                         | 350 |
| Leu Arg Pro Arg Asp                                               |                         |     |
|                                                                   | 90                      |     |
| TTGGTGG                                                           |                         | 357 |

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

|                                                                 |          |
|-----------------------------------------------------------------|----------|
| Met Ala Ser Gly Leu Phe Glu Asn Asp Gly Ile Lys Asp Asn Lys Ala |          |
| 1 5 10 15                                                       |          |
| Arg Asp Phe Phe Tyr Ser His Ser Ser Leu Ile Val Phe Phe Leu Leu |          |
|                                                                 | 20 25 30 |
| Leu Leu Gly Phe Gly Tyr Tyr Leu Gly Lys Leu Leu Phe Gly Gly Ser |          |
|                                                                 | 35 40 45 |
| Ser Leu Glu Val Tyr Leu Asp Leu Arg Asp Lys His Glu Arg Leu Gln |          |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| 50  |     |     |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |  |  |
| Gln | Glu | Ile | Thr | Glu | Leu | Gln | Ser | Lys | Asn | Val | Arg | Leu | Gln | Lys | Arg |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |
| Leu | Phe | Glu | Leu | Lys | Glu | Leu | Arg | Pro | Arg | Asp |     |     |     |     |     |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...675
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| ATG | ATA | GAA | GTT | TTA | ATG | ATA | GAA | GAT | GAT | ATA | GAA | TTA | GCC | GAG | TTT |  | 48  |
| Met | Ile | Glu | Val | Leu | Met | Ile | Glu | Asp | Asp | Ile | Glu | Leu | Ala | Glu | Phe |  |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |     |
| TTG | AGC | GAG | TTT | TTG | CTC | CAA | CAT | GGC | ATT | CAT | GTA | ACC | AAT | TAC | GAT |  | 96  |
| Leu | Ser | Glu | Phe | Leu | Leu | Gln | His | Gly | Ile | His | Val | Thr | Asn | Tyr | Asp |  |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |     |
| GAG | CCA | TAT | ACC | GGC | ATT | AGT | GCG | GCT | AAC | ACA | CAA | AAT | TAT | GAT | TTG |  | 144 |
| Glu | Pro | Tyr | Thr | Gly | Ile | Ser | Ala | Ala | Asn | Thr | Gln | Asn | Tyr | Asp | Leu |  |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |     |
| TTG | TTG | TTG | GAT | TTG | ACT | TTG | CCT | AAT | TTA | GAC | GGG | CTT | GAA | GTG | TGT |  | 192 |
| Leu | Leu | Leu | Asp | Leu | Thr | Leu | Pro | Asn | Leu | Asp | Gly | Leu | Glu | Val | Cys |  |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |     |
| AGG | CGC | ATC | TCC | AAA | CAA | AAA | CAT | ATC | CCT | ATT | ATT | ATT | TCT | TCA | GCG |  | 240 |
| Arg | Arg | Ile | Ser | Lys | Gln | Lys | His | Ile | Pro | Ile | Ile | Ile | Ser | Ser | Ala |  |     |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |  |     |
| AGA | AGT | GAT | GTG | GAA | GAT | AAG | ATT | AAA | GCA | CTA | GAT | TAT | GGG | GCT | GAT |  | 288 |
| Arg | Ser | Asp | Val | Glu | Asp | Lys | Ile | Lys | Ala | Leu | Asp | Tyr | Gly | Ala | Asp |  |     |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |  |     |
| GAT | TAC | CTC | CCT | AAA | CCC | TAT | GAT | CCT | AAA | GAA | TTA | TTA | GCT | CGC | ATC |  | 336 |
| Asp | Tyr | Leu | Pro | Lys | Pro | Tyr | Asp | Pro | Lys | Glu | Leu | Leu | Ala | Arg | Ile |  |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |     |
| CAA | TCG | CTA | CTC | AGG | CGT | TCT | CAT | AAA | AAA | GAA | GAA | GTG | AGT | GAG | CCA |  | 384 |
| Gln | Ser | Leu | Leu | Arg | Arg | Ser | His | Lys | Lys | Glu | Glu | Val | Ser | Glu | Pro |  |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |     |
| GGC | GAT | GCG | AAT | ATC | TTT | AGG | GTG | GAT | AAG | GAT | AGC | CGA | GAA | GTG | TAT |  | 432 |
| Gly | Asp | Ala | Asn | Ile | Phe | Arg | Val | Asp | Lys | Asp | Ser | Arg | Glu | Val | Tyr |  |     |

| 130                                                             | 135 | 140 |     |
|-----------------------------------------------------------------|-----|-----|-----|
| ATG CAT GAA AAA AAG CTG GAC TTA ACT AGG GCT GAA TAT GAA ATC CTT |     |     | 480 |
| Met His Glu Lys Lys Leu Asp Leu Thr Arg Ala Glu Tyr Glu Ile Leu |     |     |     |
| 145                                                             | 150 | 155 | 160 |
| TCG CTT CTC ATT AGC AAA AAA GGT TAT GTG TTT AGC CGT GAA AGC ATT |     |     | 528 |
| Ser Leu Leu Ile Ser Lys Lys Gly Tyr Val Phe Ser Arg Glu Ser Ile |     |     |     |
|                                                                 | 165 | 170 | 175 |
| GCG ATT GAG AGC GAG AGC ATC AAC CCT GAA AGC TCT AAT AAA AGC ATT |     |     | 576 |
| Ala Ile Glu Ser Glu Ser Ile Asn Pro Glu Ser Ser Asn Lys Ser Ile |     |     |     |
|                                                                 | 180 | 185 | 190 |
| GAT GTG ATC ATT GGC CGT TTG CGA TCT AAG ATT GAA AAA AAT CCT AAA |     |     | 624 |
| Asp Val Ile Ile Gly Arg Leu Arg Ser Lys Ile Glu Lys Asn Pro Lys |     |     |     |
|                                                                 | 195 | 200 | 205 |
| CAA CCG CAA TAC ATC ATC TCT GTT AGA GGG ATT GGT TAT AAA TTA GAA |     |     | 672 |
| Gln Pro Gln Tyr Ile Ile Ser Val Arg Gly Ile Gly Tyr Lys Leu Glu |     |     |     |
|                                                                 | 210 | 215 | 220 |
| TAC TGA                                                         |     |     | 678 |
| Tyr                                                             |     |     |     |
| 225                                                             |     |     |     |

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Glu | Val | Leu | Met | Ile | Glu | Asp | Asp | Ile | Glu | Leu | Ala | Glu | Phe |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Leu | Ser | Glu | Phe | Leu | Leu | Gln | His | Gly | Ile | His | Val | Thr | Asn | Tyr | Asp |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Pro | Tyr | Thr | Gly | Ile | Ser | Ala | Ala | Asn | Thr | Gln | Asn | Tyr | Asp | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Leu | Leu | Asp | Leu | Thr | Leu | Pro | Asn | Leu | Asp | Gly | Leu | Glu | Val | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Arg | Ile | Ser | Lys | Gln | Lys | His | Ile | Pro | Ile | Ile | Ile | Ser | Ser | Ala |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Arg | Ser | Asp | Val | Glu | Asp | Lys | Ile | Lys | Ala | Leu | Asp | Tyr | Gly | Ala | Asp |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asp | Tyr | Leu | Pro | Lys | Pro | Tyr | Asp | Pro | Lys | Glu | Leu | Leu | Ala | Arg | Ile |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Gln | Ser | Leu | Leu | Arg | Arg | Ser | His | Lys | Lys | Glu | Glu | Val | Ser | Glu | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Asp | Ala | Asn | Ile | Phe | Arg | Val | Asp | Lys | Asp | Ser | Arg | Glu | Val | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Met | His | Glu | Lys | Lys | Leu | Asp | Leu | Thr | Arg | Ala | Glu | Tyr | Glu | Ile | Leu |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 145 |     | 150 |     | 155 |     | 160 |     |     |     |     |     |     |     |     |     |
| Ser | Leu | Leu | Ile | Ser | Lys | Lys | Gly | Tyr | Val | Phe | Ser | Arg | Glu | Ser | Ile |
|     |     | 165 |     |     |     | 170 |     |     |     |     |     |     |     | 175 |     |
| Ala | Ile | Glu | Ser | Glu | Ser | Ile | Asn | Pro | Glu | Ser | Ser | Asn | Lys | Ser | Ile |
|     |     | 180 |     |     |     | 185 |     |     |     |     |     |     | 190 |     |     |
| Asp | Val | Ile | Ile | Gly | Arg | Leu | Arg | Ser | Lys | Ile | Glu | Lys | Asn | Pro | Lys |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Gln | Pro | Gln | Tyr | Ile | Ile | Ser | Val | Arg | Gly | Ile | Gly | Tyr | Lys | Leu | Glu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Tyr |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 225 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 72...1082
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

|                                                                 |                                                       |            |            |             |            |    |
|-----------------------------------------------------------------|-------------------------------------------------------|------------|------------|-------------|------------|----|
| AAGTCTATGC                                                      | CACGATCAAT                                            | GGTTTCCCTT | TCAATTCACA | GCTCAAACCTT | TTAGAAGAAC | 60 |
| ATATTGATAA                                                      | A ATG GCA GAA TTA GAG CCG GAC GCT TTT ATT ATC GCT GCG | 110        |            |             |            |    |
|                                                                 | Met Ala Glu Leu Glu Pro Asp Ala Phe Ile Ile Ala Ala   |            |            |             |            |    |
|                                                                 | 1 5 10                                                |            |            |             |            |    |
| CCT GGT GTG GTG AAA CTC GCT TTA AAA ATC GCC CCG CAT ATC CCT ATC | 158                                                   |            |            |             |            |    |
| Pro Gly Val Val Lys Leu Ala Leu Lys Ile Ala Pro His Ile Pro Ile |                                                       |            |            |             |            |    |
| 15 20 25                                                        |                                                       |            |            |             |            |    |
| CAT TTA TCC ACG CAA GCG AAT GTC TTA AAT TTG CTA GAT GCA CAA GTG | 206                                                   |            |            |             |            |    |
| His Leu Ser Thr Gln Ala Asn Val Leu Asn Leu Leu Asp Ala Gln Val |                                                       |            |            |             |            |    |
| 30 35 40 45                                                     |                                                       |            |            |             |            |    |
| TTT TAT GAT TTA GGG GTT AAA CGC ATC GTG TGC GCG AGG GAA TTG AGC | 254                                                   |            |            |             |            |    |
| Phe Tyr Asp Leu Gly Val Lys Arg Ile Val Cys Ala Arg Glu Leu Ser |                                                       |            |            |             |            |    |
| 50 55 60                                                        |                                                       |            |            |             |            |    |
| CTG AAT GAT GCG ATT GAG ATT AAA AAA GCC TTA CCT AAT TTA GAA TTA | 302                                                   |            |            |             |            |    |
| Leu Asn Asp Ala Ile Glu Ile Lys Lys Ala Leu Pro Asn Leu Glu Leu |                                                       |            |            |             |            |    |
| 65 70 75                                                        |                                                       |            |            |             |            |    |
| GAA ATC TTT GTG CAT GGG AGC ATG TGC TTT GCC TTT TCA GGG CGC TGC | 350                                                   |            |            |             |            |    |
| Glu Ile Phe Val His Gly Ser Met Cys Phe Ala Phe Ser Gly Arg Cys |                                                       |            |            |             |            |    |
| 80 85 90                                                        |                                                       |            |            |             |            |    |
| TTG ATT TCG GCC TTA CAA AAG GGG CGC GTG CCT AAT AGA GGG AGT TGC | 398                                                   |            |            |             |            |    |
| Leu Ile Ser Ala Leu Gln Lys Gly Arg Val Pro Asn Arg Gly Ser Cys |                                                       |            |            |             |            |    |
| 95 100 105                                                      |                                                       |            |            |             |            |    |

|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |       |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------|------|
| GCG<br>Ala<br>110 | AAT<br>Asn        | GAT<br>Asp        | TGC<br>Cys        | CGG<br>Arg        | TTT<br>Phe<br>115 | GAT<br>Asp        | TAT<br>Tyr        | GAA<br>Glu        | TAT<br>Tyr        | TAC<br>Tyr<br>120 | GTG<br>Val        | AAA<br>Lys        | AAC<br>Asn        | CCT<br>Pro        | GAT<br>Asp<br>125 | 446   |      |
| AAT<br>Asn        | GGC<br>Gly        | GTG<br>Val        | ATG<br>Met        | ATG<br>Met<br>130 | AGA<br>Arg        | CTG<br>Leu        | GTT<br>Val        | GAA<br>Glu        | GAA<br>Glu<br>135 | GAG<br>Glu        | GGC<br>Gly        | GTA<br>Val        | GGC<br>Gly        | ACG<br>Thr<br>140 | CAT<br>His        | 494   |      |
| ATT<br>Ile        | TTT<br>Phe        | AAC<br>Asn        | GCT<br>Ala<br>145 | AAG<br>Lys        | GAT<br>Asp        | TTG<br>Leu        | AAC<br>Asn        | CTC<br>Leu<br>150 | TCT<br>Ser        | GGC<br>Gly        | CAT<br>His        | ATC<br>Ile        | GCT<br>Ala<br>155 | GAA<br>Glu        | ATT<br>Ile        | 542   |      |
| TTA<br>Leu        | AGT<br>Ser        | TCC<br>Ser<br>160 | AAC<br>Asn        | GCC<br>Ala        | ATT<br>Ile        | AGC<br>Ser        | GCG<br>Ala<br>165 | CTT<br>Leu        | AAG<br>Lys        | ATT<br>Ile        | GAA<br>Glu        | GGG<br>Gly<br>170 | CGC<br>Arg        | ACC<br>Thr        | AAG<br>Lys        | 590   |      |
| TCC<br>Ser        | AGT<br>Ser<br>175 | TAC<br>Tyr        | TAC<br>Tyr        | GCC<br>Ala        | GCG<br>Ala        | CAA<br>Gln<br>180 | ACC<br>Thr        | ACG<br>Thr        | CGC<br>Arg        | ATC<br>Ile        | TAT<br>Tyr<br>185 | CGT<br>Arg        | TTA<br>Leu        | GCG<br>Ala        | GTT<br>Val        | 638   |      |
| GAT<br>Asp<br>190 | GAT<br>Asp        | TTT<br>Phe        | TAC<br>Tyr        | CAT<br>His        | AAC<br>Asn<br>195 | ACC<br>Thr        | TTA<br>Leu        | AAG<br>Lys        | CCG<br>Pro        | AGT<br>Ser<br>200 | TTT<br>Phe        | TAT<br>Tyr        | GCC<br>Ala        | AGC<br>Ser        | GAA<br>Glu<br>205 | 686   |      |
| TTG<br>Leu        | AAC<br>Asn        | ACG<br>Thr        | CTT<br>Leu        | AAA<br>Lys<br>210 | AAC<br>Asn        | AGG<br>Arg        | GGT<br>Gly        | TTT<br>Phe        | ACG<br>Thr<br>215 | GAC<br>Asp        | GGC<br>Gly        | TAT<br>Tyr        | TTG<br>Leu        | ATG<br>Met<br>220 | CGA<br>Arg        | 734   |      |
| AGG<br>Arg        | CCT<br>Pro        | TTT<br>Phe        | GAA<br>Glu<br>225 | AGG<br>Arg        | TTG<br>Leu        | GAT<br>Asp        | ACT<br>Thr        | CAA<br>Gln<br>230 | AAC<br>Asn        | CAC<br>His        | CAA<br>Gln        | ACA<br>Thr        | GCC<br>Ala<br>235 | ATT<br>Ile        | AGC<br>Ser        | 782   |      |
| GAA<br>Glu        | GGG<br>Gly        | GAT<br>Asp<br>240 | TTT<br>Phe        | CAA<br>Gln        | GTC<br>Val        | AAT<br>Asn        | GGC<br>Gly<br>245 | GAA<br>Glu        | ATA<br>Ile        | ACC<br>Thr        | GAA<br>Glu        | GAC<br>Asp<br>250 | GGG<br>Gly        | CGT<br>Arg        | TTT<br>Phe        | 830   |      |
| TTT<br>Phe<br>255 | GCA<br>Ala        | TGC<br>Cys        | AAA<br>Lys        | TTC<br>Phe        | ACC<br>Thr        | ACT<br>Thr<br>260 | ACC<br>Thr        | ACT<br>Thr        | AAC<br>Asn        | ACC<br>Thr        | GCT<br>Ala<br>265 | TAT<br>Tyr        | GAA<br>Glu        | ATC<br>Ile        | ATC<br>Ile        | 878   |      |
| GCT<br>Ala<br>270 | CCC<br>Pro        | AAA<br>Lys        | AAT<br>Asn        | GCG<br>Ala        | GCT<br>Ala<br>275 | ATC<br>Ile        | ACG<br>Thr        | CCC<br>Pro        | ATA<br>Ile        | GTC<br>Val<br>280 | AAT<br>Asn        | GAA<br>Glu        | ATT<br>Ile        | GGC<br>Gly        | AAG<br>Lys<br>285 | 926   |      |
| ATT<br>Ile        | TAC<br>Tyr        | ACC<br>Thr        | TTT<br>Phe        | GAA<br>Glu<br>290 | AAA<br>Lys        | CGC<br>Arg        | TCT<br>Ser        | TAT<br>Tyr        | TTA<br>Leu<br>295 | GTG<br>Val        | CTG<br>Leu        | TAT<br>Tyr        | AAA<br>Lys        | ATC<br>Ile<br>300 | CTT<br>Leu        | 974   |      |
| TTA<br>Leu        | GAA<br>Glu        | AAT<br>Asn        | AAC<br>Asn<br>305 | ACC<br>Thr        | GAG<br>Glu        | CTA<br>Leu        | GAA<br>Glu        | ACT<br>Thr<br>310 | ATC<br>Ile        | CAT<br>His        | AGC<br>Ser        | GGG<br>Gly        | AAC<br>Asn<br>315 | GTG<br>Val        | AAT<br>Asn        | 1022  |      |
| TTA<br>Leu        | GTG<br>Val        | CGA<br>Arg<br>320 | CTG<br>Leu        | CCC<br>Pro        | GCA<br>Ala        | CCC<br>Pro        | TTA<br>Leu<br>325 | CCG<br>Pro        | GCT<br>Ala        | TTT<br>Phe        | AGT<br>Ser        | TTT<br>Phe<br>330 | TTA<br>Leu        | CGC<br>Arg        | ACC<br>Thr        | 1070  |      |
| CAA<br>Gln        | GTC<br>Val        | AGA<br>Arg        | GTC<br>Val        | TAAAAATGGC        |                   |                   | GTTTAGAGAT        |                   |                   | TAGGTATTGA        |                   |                   | AAATGATTAA        |                   |                   | GAGAA | 1127 |

## (2) INFORMATION FOR SEQ ID NO:488:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

```

Met Ala Glu Leu Glu Pro Asp Ala Phe Ile Ile Ala Ala Pro Gly Val
 1 5 10 15
Val Lys Leu Ala Leu Lys Ile Ala Pro His Ile Pro Ile His Leu Ser
 20 25 30
Thr Gln Ala Asn Val Leu Asn Leu Asp Ala Gln Val Phe Tyr Asp
 35 40 45
Leu Gly Val Lys Arg Ile Val Cys Ala Arg Glu Leu Ser Leu Asn Asp
 50 55 60
Ala Ile Glu Ile Lys Lys Ala Leu Pro Asn Leu Glu Leu Glu Ile Phe
 65 70 75 80
Val His Gly Ser Met Cys Phe Ala Phe Ser Gly Arg Cys Leu Ile Ser
 85 90 95
Ala Leu Gln Lys Gly Arg Val Pro Asn Arg Gly Ser Cys Ala Asn Asp
100 105 110
Cys Arg Phe Asp Tyr Glu Tyr Tyr Val Lys Asn Pro Asp Asn Gly Val
115 120 125
Met Met Arg Leu Val Glu Glu Glu Gly Val Gly Thr His Ile Phe Asn
130 135 140
Ala Lys Asp Leu Asn Leu Ser Gly His Ile Ala Glu Ile Leu Ser Ser
145 150 155 160
Asn Ala Ile Ser Ala Leu Lys Ile Glu Gly Arg Thr Lys Ser Ser Tyr
165 170 175
Tyr Ala Ala Gln Thr Thr Arg Ile Tyr Arg Leu Ala Val Asp Asp Phe
180 185 190
Tyr His Asn Thr Leu Lys Pro Ser Phe Tyr Ala Ser Glu Leu Asn Thr
195 200 205
Leu Lys Asn Arg Gly Phe Thr Asp Gly Tyr Leu Met Arg Arg Pro Phe
210 215 220
Glu Arg Leu Asp Thr Gln Asn His Gln Thr Ala Ile Ser Glu Gly Asp
225 230 235 240
Phe Gln Val Asn Gly Glu Ile Thr Glu Asp Gly Arg Phe Phe Ala Cys
245 250 255
Lys Phe Thr Thr Thr Thr Asn Thr Ala Tyr Glu Ile Ile Ala Pro Lys
260 265 270
Asn Ala Ala Ile Thr Pro Ile Val Asn Glu Ile Gly Lys Ile Tyr Thr
275 280 285
Phe Glu Lys Arg Ser Tyr Leu Val Leu Tyr Lys Ile Leu Leu Glu Asn
290 295 300
Asn Thr Glu Leu Glu Thr Ile His Ser Gly Asn Val Asn Leu Val Arg
305 310 315 320
Leu Pro Ala Pro Leu Pro Ala Phe Ser Phe Leu Arg Thr Gln Val Arg
325 330 335

```

Val

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...1038
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATTAAGGAGA AATAAGAA ATG TTA CAA CCC CCT AAA ATT GTC GCT GAA TTG | 51  |
| Met Leu Gln Pro Pro Lys Ile Val Ala Glu Leu                     |     |
| 1 5 10                                                          |     |
| AGC GCT AAT CAT AAC CAG GAT TTA AAC CTA GCC AAA GAA AGC CTT CAT | 99  |
| Ser Ala Asn His Asn Gln Asp Leu Asn Leu Ala Lys Glu Ser Leu His |     |
| 15 20 25                                                        |     |
| GCC ATT AAG GAA AGC GGT GCG GAT TTT GTC AAG CTC CAA ACC TAC ACG | 147 |
| Ala Ile Lys Glu Ser Gly Ala Asp Phe Val Lys Leu Gln Thr Tyr Thr |     |
| 30 35 40                                                        |     |
| CCA AGC TGC ATG ACT TTA AAC TCT AAA GAA GAT CCT TTC ATC ATT CAA | 195 |
| Pro Ser Cys Met Thr Leu Asn Ser Lys Glu Asp Pro Phe Ile Ile Gln |     |
| 45 50 55                                                        |     |
| GGC ACT TTA TGG GAT AAA GAA AAT TTG TAT GAA TTG TAT CAA AAG GCT | 243 |
| Gly Thr Leu Trp Asp Lys Glu Asn Leu Tyr Glu Leu Tyr Gln Lys Ala |     |
| 60 65 70 75                                                     |     |
| TCT ACC CCC CTA GAA TGG CAT GCT GAA TTG TTT GAG TTG GCT AGA AAG | 291 |
| Ser Thr Pro Leu Glu Trp His Ala Glu Leu Phe Glu Leu Ala Arg Lys |     |
| 80 85 90                                                        |     |
| CTT GAT TTA GGC ATT TTT AGC TCG CCT TTT AGT TCA CAA GCT TTA GAG | 339 |
| Leu Asp Leu Gly Ile Phe Ser Ser Pro Phe Ser Ser Gln Ala Leu Glu |     |
| 95 100 105                                                      |     |
| CTT TTA GAG AGC CTA AAT TGC CCC ATG TAT AAA ATC GCT AGT TTT GAA | 387 |
| Leu Leu Glu Ser Leu Asn Cys Pro Met Tyr Lys Ile Ala Ser Phe Glu |     |
| 110 115 120                                                     |     |
| ATC GTT GAT TTG GAC TTG ATT GAA AAG GCC GCT CGC ACA CAA AAG CCC | 435 |
| Ile Val Asp Leu Asp Leu Ile Glu Lys Ala Ala Arg Thr Gln Lys Pro |     |
| 125 130 135                                                     |     |
| ATT ATC CTT TCT AGC GGT ATC GCT ACA CAC ACC GAA TTG CAA GAC GCT | 483 |

|            |            |     |         |            |            |          |     |     |        |      |       |       |         |     |     |  |      |  |
|------------|------------|-----|---------|------------|------------|----------|-----|-----|--------|------|-------|-------|---------|-----|-----|--|------|--|
| Ile        | Ile        | Leu | Ser     | Ser        | Gly        | Ile      | Ala | Thr | His    | Thr  | Glu   | Leu   | Gln     | Asp | Ala |  |      |  |
| 140        |            |     |         |            | 145        |          |     |     |        | 150  |       |       |         |     | 155 |  |      |  |
| ATC        | TCA        | TTG | TGC     | AGA        | AGA        | GTG      | AAT | AAT | TTT    | GAC  | ATC   | ACC   | CTT     | TTA | AAA |  | 531  |  |
| Ile        | Ser        | Leu | Cys     | Arg        | Arg        | Val      | Asn | Asn | Phe    | Asp  | Ile   | Thr   | Leu     | Leu | Lys |  |      |  |
|            |            |     |         | 160        |            |          |     |     | 165    |      |       |       |         | 170 |     |  |      |  |
| TGC        | GTG        | AGC | GCT     | TAT        | CCC        | AGT      | AAA | ATA | GAA    | GAC  | GCT   | AAC   | TTG     | TTG | AGC |  | 579  |  |
| Cys        | Val        | Ser | Ala     | Tyr        | Pro        | Ser      | Lys | Ile | Glu    | Asp  | Ala   | Asn   | Leu     | Leu | Ser |  |      |  |
|            |            |     | 175     |            |            |          |     | 180 |        |      |       |       | 185     |     |     |  |      |  |
| ATG        | GTT        | AAA | TTA     | GGC        | GAA        | ATC      | TTT | GGC | GTT    | AAA  | TTT   | GGC   | TTG     | AGC | GAT |  | 627  |  |
| Met        | Val        | Lys | Leu     | Gly        | Glu        | Ile      | Phe | Gly | Val    | Lys  | Phe   | Gly   | Leu     | Ser | Asp |  |      |  |
|            |            | 190 |         |            |            |          | 195 |     |        |      |       | 200   |         |     |     |  |      |  |
| CAC        | ACG        | ATT | GGC     | TCT        | CTT        | TGC      | CCC | ATT | TTA    | GCC  | ACC   | ACT   | TTA     | GGA | GCG |  | 675  |  |
| His        | Thr        | Ile | Gly     | Ser        | Leu        | Cys      | Pro | Ile | Leu    | Ala  | Thr   | Thr   | Leu     | Gly | Ala |  |      |  |
|            | 205        |     |         |            |            | 210      |     |     |        |      | 215   |       |         |     |     |  |      |  |
| AGC        | ATG        | ATA | GAA     | AAG        | CAT        | TTC      | ATT | TTA | AAC    | AAA  | TCC   | TTA   | CAA     | ACC | CCA |  | 723  |  |
| Ser        | Met        | Ile | Glu     | Lys        | His        | Phe      | Ile | Leu | Asn    | Lys  | Ser   | Leu   | Gln     | Thr | Pro |  |      |  |
| 220        |            |     |         |            | 225        |          |     |     |        | 230  |       |       |         |     | 235 |  |      |  |
| GAC        | AGC        | GCT | TTT     | AGC        | ATG        | GAT      | TTT | AAC | GGA    | TTT  | AAA   | AGC   | ATG     | GTT | GAA |  | 771  |  |
| Asp        | Ser        | Ala | Phe     | Ser        | Met        | Asp      | Phe | Asn | Gly    | Phe  | Lys   | Ser   | Met     | Val | Glu |  |      |  |
|            |            |     |         | 240        |            |          |     |     | 245    |      |       |       |         | 250 |     |  |      |  |
| GCC        | ATC        | AAG | CAA     | AGC        | GTT        | TTA      | GCC | TTA | GGC    | GAA  | GAA   | GAG   | CCA     | AGA | ATC |  | 819  |  |
| Ala        | Ile        | Lys | Gln     | Ser        | Val        | Leu      | Ala | Leu | Gly    | Glu  | Glu   | Glu   | Pro     | Arg | Ile |  |      |  |
|            |            |     | 255     |            |            |          |     | 260 |        |      |       |       | 265     |     |     |  |      |  |
| AAT        | CCA        | AAG | ACT     | TTA        | GAA        | AAG      | CGA | AGA | TTT    | TTT  | GCA   | CGC   | TCT     | TTA | TTT |  | 867  |  |
| Asn        | Pro        | Lys | Thr     | Leu        | Glu        | Lys      | Arg | Arg | Phe    | Phe  | Ala   | Arg   | Ser     | Leu | Phe |  |      |  |
|            |            | 270 |         |            |            |          | 275 |     |        |      |       | 280   |         |     |     |  |      |  |
| GTT        | ATT        | AAG | GAT     | ATT        | CAA        | AAA      | GGC | GAA | GCA    | TTG  | ACT   | GAA   | AAC     | AAT | ATC |  | 915  |  |
| Val        | Ile        | Lys | Asp     | Ile        | Gln        | Lys      | Gly | Glu | Ala    | Leu  | Thr   | Glu   | Asn     | Asn | Ile |  |      |  |
|            | 285        |     |         |            |            | 290      |     |     |        |      | 295   |       |         |     |     |  |      |  |
| AAA        | GCC        | TTA | CGC     | CCC        | AAC        | CTT      | GGC | TTA | CAC    | CCT  | AAA   | TTT   | TAT     | AAA | GAA |  | 963  |  |
| Lys        | Ala        | Leu | Arg     | Pro        | Asn        | Leu      | Gly | Leu | His    | Pro  | Lys   | Phe   | Tyr     | Lys | Glu |  |      |  |
| 300        |            |     |         |            | 305        |          |     |     |        | 310  |       |       |         |     | 315 |  |      |  |
| ATT        | TTA        | GGC | CAA     | AAA        | GCA        | TCA      | AAA | TTC | TTA    | AAA  | GCC   | AAC   | ACC     | CCC | TTA |  | 1011 |  |
| Ile        | Leu        | Gly | Gln     | Lys        | Ala        | Ser      | Lys | Phe | Leu    | Lys  | Ala   | Asn   | Thr     | Pro | Leu |  |      |  |
|            |            |     |         | 320        |            |          |     |     | 325    |      |       |       |         | 330 |     |  |      |  |
| AGC        | GCT        | GAT | GAT     | ATA        | GAA        | CGC      | TCA | TTG | TAGGTT | CGTT | TTGAT | CAAAA | AATGGGG |     |     |  | 1065 |  |
| Ser        | Ala        | Asp | Asp     | Ile        | Glu        | Arg      | Ser | Leu |        |      |       |       |         |     |     |  |      |  |
|            |            |     | 335     |            |            |          |     | 340 |        |      |       |       |         |     |     |  |      |  |
| TTTTTAATTT | TGTTTTATGG | TTT | TAGATTT | GATTTTAAAC | TCATTTTCTT | TATTTTAA |     |     |        |      |       |       |         |     |     |  | 1123 |  |

(2) INFORMATION FOR SEQ ID NO:490:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 340 amino acids
  - (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gln | Pro | Pro | Lys | Ile | Val | Ala | Glu | Leu | Ser | Ala | Asn | His | Asn | 1   | 5   | 10  | 15  |
| Gln | Asp | Leu | Asn | Leu | Ala | Lys | Glu | Ser | Leu | His | Ala | Ile | Lys | Glu | Ser | 20  | 25  | 30  |     |
| Gly | Ala | Asp | Phe | Val | Lys | Leu | Gln | Thr | Tyr | Thr | Pro | Ser | Cys | Met | Thr | 35  | 40  | 45  |     |
| Leu | Asn | Ser | Lys | Glu | Asp | Pro | Phe | Ile | Ile | Gln | Gly | Thr | Leu | Trp | Asp | 50  | 55  | 60  |     |
| Lys | Glu | Asn | Leu | Tyr | Glu | Leu | Tyr | Gln | Lys | Ala | Ser | Thr | Pro | Leu | Glu | 65  | 70  | 75  | 80  |
| Trp | His | Ala | Glu | Leu | Phe | Glu | Leu | Ala | Arg | Lys | Leu | Asp | Leu | Gly | Ile | 85  | 90  | 95  |     |
| Phe | Ser | Ser | Pro | Phe | Ser | Ser | Gln | Ala | Leu | Glu | Leu | Leu | Glu | Ser | Leu | 100 | 105 | 110 |     |
| Asn | Cys | Pro | Met | Tyr | Lys | Ile | Ala | Ser | Phe | Glu | Ile | Val | Asp | Leu | Asp | 115 | 120 | 125 |     |
| Leu | Ile | Glu | Lys | Ala | Ala | Arg | Thr | Gln | Lys | Pro | Ile | Ile | Leu | Ser | Ser | 130 | 135 | 140 |     |
| Gly | Ile | Ala | Thr | His | Thr | Glu | Leu | Gln | Asp | Ala | Ile | Ser | Leu | Cys | Arg | 145 | 150 | 155 | 160 |
| Arg | Val | Asn | Asn | Phe | Asp | Ile | Thr | Leu | Leu | Lys | Cys | Val | Ser | Ala | Tyr | 165 | 170 | 175 |     |
| Pro | Ser | Lys | Ile | Glu | Asp | Ala | Asn | Leu | Leu | Ser | Met | Val | Lys | Leu | Gly | 180 | 185 | 190 |     |
| Glu | Ile | Phe | Gly | Val | Lys | Phe | Gly | Leu | Ser | Asp | His | Thr | Ile | Gly | Ser | 195 | 200 | 205 |     |
| Leu | Cys | Pro | Ile | Leu | Ala | Thr | Thr | Leu | Gly | Ala | Ser | Met | Ile | Glu | Lys | 210 | 215 | 220 |     |
| His | Phe | Ile | Leu | Asn | Lys | Ser | Leu | Gln | Thr | Pro | Asp | Ser | Ala | Phe | Ser | 225 | 230 | 235 | 240 |
| Met | Asp | Phe | Asn | Gly | Phe | Lys | Ser | Met | Val | Glu | Ala | Ile | Lys | Gln | Ser | 245 | 250 | 255 |     |
| Val | Leu | Ala | Leu | Gly | Glu | Glu | Glu | Pro | Arg | Ile | Asn | Pro | Lys | Thr | Leu | 260 | 265 | 270 |     |
| Glu | Lys | Arg | Arg | Phe | Phe | Ala | Arg | Ser | Leu | Phe | Val | Ile | Lys | Asp | Ile | 275 | 280 | 285 |     |
| Gln | Lys | Gly | Glu | Ala | Leu | Thr | Glu | Asn | Asn | Ile | Lys | Ala | Leu | Arg | Pro | 290 | 295 | 300 |     |
| Asn | Leu | Gly | Leu | His | Pro | Lys | Phe | Tyr | Lys | Glu | Ile | Leu | Gly | Gln | Lys | 305 | 310 | 315 | 320 |
| Ala | Ser | Lys | Phe | Leu | Lys | Ala | Asn | Thr | Pro | Leu | Ser | Ala | Asp | Asp | Ile | 325 | 330 | 335 |     |
| Glu | Arg | Ser | Leu |     |     |     |     |     |     |     |     |     |     |     |     | 340 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1234 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 31...1197

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

|            |            |            |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GTGAATGAGC | GTTTGGAGGT | GCTGTTGGAA | ATG | GTT | TTG | ATG | CGG | TTT | GAA | GAG |     | 54  |     |     |     |     |
|            |            |            | Met | Val | Leu | Met | Arg | Phe | Glu | Glu |     |     |     |     |     |     |
|            |            |            | 1   |     |     |     | 5   |     |     |     |     |     |     |     |     |     |
| CCC        | GAT        | CCT        | GGA | AGA | GCT | ATC | AGA | ACC | TTT | CAG | AGC | GTG | AAT | GAC | AGA | 102 |
| Pro        | Asp        | Pro        | Gly | Arg | Ala | Ile | Arg | Thr | Phe | Gln | Ser | Val | Asn | Asp | Arg |     |
|            | 10         |            |     |     |     | 15  |     |     |     |     | 20  |     |     |     |     |     |
| GGC        | GTG        | CCT        | CTC | CTC | TTG | CTA | GAC | AAA | CTA | AAA | TCC | CTT | CTC | ATC | TAT | 150 |
| Gly        | Val        | Pro        | Leu | Leu | Leu | Leu | Asp | Lys | Leu | Lys | Ser | Leu | Leu | Ile | Tyr |     |
|            | 25         |            |     |     | 30  |     |     |     | 35  |     |     |     |     |     | 40  |     |
| TAC        | TCC        | AAC        | ATT | TTT | TGC | GAT | GGG | AAA | AGG | GGG | CTA | GAC | CAA | TTT | ATC | 198 |
| Tyr        | Ser        | Asn        | Ile | Phe | Cys | Asp | Gly | Lys | Arg | Gly | Leu | Asp | Gln | Phe | Ile |     |
|            |            |            | 45  |     |     |     | 50  |     |     |     |     |     | 55  |     |     |     |
| ATC        | GAT        | CAT        | TTT | GGG | GAG | ATC | TTT | AAG | ATC | TTT | GCC | AAG | ATT | AAA | AAG | 246 |
| Ile        | Asp        | His        | Phe | Gly | Glu | Ile | Phe | Lys | Ile | Phe | Ala | Lys | Ile | Lys | Lys |     |
|            |            |            | 60  |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     |
| AGC        | GAC        | CAC        | ATC | TCC | AGC | GTT | GGA | GGC | TTT | GAT | GAA | GGC | GAT | ATC | TTC | 294 |
| Ser        | Asp        | His        | Ile | Ser | Ser | Val | Gly | Gly | Phe | Asp | Glu | Gly | Asp | Ile | Phe |     |
|            |            | 75         |     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     |
| CGC        | TAC        | CAC        | GCA | GGG | AGC | CAA | AAA | TTT | GAT | GGA | ATC | GAG | TTT | TTA | GGG | 342 |
| Arg        | Tyr        | His        | Ala | Gly | Ser | Gln | Lys | Phe | Asp | Gly | Ile | Glu | Phe | Leu | Gly |     |
|            | 90         |            |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     |     |
| CAC        | TAC        | GAA        | GCA | AGC | ACG | GAC | AAA | ACC | TAC | GAG | AAA | CTC | AAA | GAT | GAA | 390 |
| His        | Tyr        | Glu        | Ala | Ser | Thr | Asp | Lys | Thr | Tyr | Glu | Lys | Leu | Lys | Asp | Glu |     |
|            | 105        |            |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |     |
| CTA        | AAA        | AAA        | ATC | AAA | AAA | AGC | AAA | TTG | AAA | AGT | TTC | ATC | CAA | TCC | TAT | 438 |
| Leu        | Lys        | Lys        | Ile | Lys | Lys | Ser | Lys | Leu | Lys | Ser | Phe | Ile | Gln | Ser | Tyr |     |
|            |            |            | 125 |     |     |     |     | 130 |     |     |     |     | 135 |     |     |     |
| GTC        | AGC        | GAT        | TTG | AAA | AAT | TTC | TAT | CAG | GCT | TTT | CTT | GAT | CTA | TTG | AGC | 486 |
| Val        | Ser        | Asp        | Leu | Lys | Asn | Phe | Tyr | Gln | Ala | Phe | Leu | Asp | Leu | Leu | Ser |     |
|            |            |            | 140 |     |     |     |     | 145 |     |     |     |     | 150 |     |     |     |
| GAG        | ATT        | GAC        | ACC | AAC | CCA | ACC | ACC | TTT | AAG | GTC | ATG | CTC | ATC | AAC | AAG | 534 |
| Glu        | Ile        | Asp        | Thr | Asn | Pro | Thr | Thr | Phe | Lys | Val | Met | Leu | Ile | Asn | Lys |     |
|            |            | 155        |     |     |     |     | 160 |     |     |     |     | 165 |     |     |     |     |
| ATC        | GAC        | TCG        | TCT | TTT | TTC | AAT | TCG | CTC | ATC | CGC | CTG | AAA | ATC | AAC | AAC | 582 |
| Ile        | Asp        | Ser        | Ser | Phe | Phe | Asn | Ser | Leu | Ile | Arg | Leu | Lys | Ile | Asn | Asn |     |

|                             |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |
|-----------------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| 170                         |                   |                   |                   | 175               |                   |                   |                   | 180               |                   |                   |                   |                   |                   |                   |                   |      |
| GAA<br>Glu<br>185           | CTA<br>Leu        | GAC<br>Asp        | GAT<br>Asp        | GAA<br>Glu        | ACG<br>Thr<br>190 | CTG<br>Leu        | AAA<br>Lys        | CTC<br>Leu        | TTT<br>Phe        | GCC<br>Ala<br>195 | AAA<br>Lys        | ACC<br>Thr        | GAT<br>Asp        | ATT<br>Ile        | GTG<br>Val<br>200 | 630  |
| CTT<br>Leu                  | TTC<br>Phe        | AAA<br>Lys        | GCT<br>Ala        | ACT<br>Thr<br>205 | AGA<br>Arg        | GAT<br>Asp        | AGG<br>Arg        | CCA<br>Pro        | GGA<br>Gly<br>210 | ACG<br>Thr        | GAC<br>Asp        | AAC<br>Asn        | CTG<br>Leu        | ATT<br>Ile<br>215 | AAT<br>Asn        | 678  |
| GCG<br>Ala                  | TAT<br>Tyr        | CTT<br>Leu        | AAA<br>Lys<br>220 | AAG<br>Lys        | GGC<br>Gly        | AAA<br>Lys        | GAG<br>Glu        | GGA<br>Gly<br>225 | TTG<br>Leu        | AAG<br>Lys        | AGC<br>Ser        | GAG<br>Glu        | ATG<br>Met<br>230 | ATT<br>Ile        | GCT<br>Ala        | 726  |
| CAA<br>Gln                  | TGC<br>Cys        | AGA<br>Arg<br>235 | AAT<br>Asn        | GAT<br>Asp        | ATA<br>Ile        | GGG<br>Gly        | CTG<br>Leu<br>240 | GCT<br>Ala        | TTT<br>Phe        | TGG<br>Trp        | CAG<br>Gln        | TCT<br>Ser<br>245 | GTA<br>Val        | AAC<br>Asn        | AAC<br>Asn        | 774  |
| GCA<br>Ala<br>250           | TCC<br>Ser        | AAC<br>Asn        | TCA<br>Ser        | TCA<br>Ser        | TGC<br>Cys        | TTC<br>Phe<br>255 | CAC<br>His        | TAT<br>Tyr        | ATC<br>Ile        | TTC<br>Phe        | TTT<br>Phe<br>260 | GAA<br>Glu        | AAG<br>Lys        | AAC<br>Asn        | TGC<br>Cys        | 822  |
| CAG<br>Gln<br>265           | GAG<br>Glu        | ATG<br>Met        | GGT<br>Gly        | CTT<br>Leu        | GCC<br>Ala<br>270 | GAT<br>Asp        | CTC<br>Leu        | AAA<br>Lys        | AAA<br>Lys        | TTG<br>Leu<br>275 | ATC<br>Ile        | CCT<br>Pro        | AGG<br>Arg        | AAG<br>Lys        | CAA<br>Gln<br>280 | 870  |
| TTC<br>Phe                  | TCC<br>Ser        | CAA<br>Gln        | GAA<br>Glu        | AAA<br>Lys<br>285 | GAA<br>Glu        | CAC<br>His        | ATC<br>Ile        | ATC<br>Ile        | CCC<br>Pro<br>290 | ATC<br>Ile        | AAT<br>Asn        | TTA<br>Leu        | TTA<br>Leu        | AAA<br>Lys<br>295 | CAG<br>Gln        | 918  |
| GAA<br>Glu                  | TCC<br>Ser        | AAC<br>Asn        | AAT<br>Asn<br>300 | AAG<br>Lys        | ATC<br>Ile        | AGA<br>Arg        | GAT<br>Asp        | CTT<br>Leu<br>305 | GGT<br>Gly        | TTT<br>Phe        | GAA<br>Glu        | GAC<br>Asp        | AAA<br>Lys<br>310 | AAA<br>Lys        | GAT<br>Asp        | 966  |
| CTT<br>Leu                  | GAA<br>Glu<br>315 | GAC<br>Asp        | TAC<br>Tyr        | ATT<br>Ile        | GAC<br>Asp        | ACA<br>Thr        | TAC<br>Tyr<br>320 | GGC<br>Gly        | AAC<br>Asn        | CTC<br>Leu        | ATC<br>Ile        | TCC<br>Ser<br>325 | CTG<br>Leu        | GAA<br>Glu        | AAA<br>Lys        | 1014 |
| TCG<br>Ser<br>330           | CTC<br>Leu        | AAT<br>Asn        | CGT<br>Arg        | AAG<br>Lys        | GCA<br>Ala        | AGC<br>Ser<br>335 | GAT<br>Asp        | AAG<br>Lys        | GAT<br>Asp        | CTG<br>Leu        | TAT<br>Tyr<br>340 | GGA<br>Gly        | AAA<br>Lys        | GAT<br>Asp        | GAA<br>Glu        | 1062 |
| ATC<br>Ile<br>345           | TAT<br>Tyr        | AAA<br>Lys        | AGT<br>Ser        | AGT<br>Ser        | GAG<br>Glu<br>350 | ATC<br>Ile        | CCT<br>Pro        | TTC<br>Phe        | AAC<br>Asn        | AGG<br>Arg<br>355 | CGC<br>Arg        | TTT<br>Phe        | GAT<br>Asp        | ACA<br>Thr        | AAA<br>Lys<br>360 | 1110 |
| AAC<br>Asn                  | TTC<br>Phe        | AAT<br>Asn        | AAG<br>Lys        | AAG<br>Lys<br>365 | GCA<br>Ala        | TTG<br>Leu        | GTA<br>Val        | AAA<br>Lys        | AGA<br>Arg<br>370 | AAT<br>Asn        | GAA<br>Glu        | GAA<br>Glu        | ATG<br>Met        | CGA<br>Arg<br>375 | GAA<br>Glu        | 1158 |
| TGG<br>Trp                  | CTG<br>Leu        | ATC<br>Ile        | GAC<br>Asp<br>380 | ACC<br>Thr        | TTT<br>Phe        | TTT<br>Phe        | AAG<br>Lys        | GAT<br>Asp<br>385 | TTC<br>Phe        | GCC<br>Ala        | GCC<br>Ala        | CAC<br>His        | TAAAGAGAGT        | GA                |                   | 1209 |
| GATTAAAAGA GAGTGATCGC ACTCA |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   | 1234              |      |

(2) INFORMATION FOR SEQ ID NO:492:



(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 389 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Leu | Met | Arg | Phe | Glu | Glu | Pro | Asp | Pro | Gly | Arg | Ala | Ile | Arg |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Thr | Phe | Gln | Ser | Val | Asn | Asp | Arg | Gly | Val | Pro | Leu | Leu | Leu | Leu | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Leu | Lys | Ser | Leu | Leu | Ile | Tyr | Tyr | Ser | Asn | Ile | Phe | Cys | Asp | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Arg | Gly | Leu | Asp | Gln | Phe | Ile | Ile | Asp | His | Phe | Gly | Glu | Ile | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Ile | Phe | Ala | Lys | Ile | Lys | Lys | Ser | Asp | His | Ile | Ser | Ser | Val | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Phe | Asp | Glu | Gly | Asp | Ile | Phe | Arg | Tyr | His | Ala | Gly | Ser | Gln | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Phe | Asp | Gly | Ile | Glu | Phe | Leu | Gly | His | Tyr | Glu | Ala | Ser | Thr | Asp | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Thr | Tyr | Glu | Lys | Leu | Lys | Asp | Glu | Leu | Lys | Lys | Ile | Lys | Lys | Ser | Lys |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Leu | Lys | Ser | Phe | Ile | Gln | Ser | Tyr | Val | Ser | Asp | Leu | Lys | Asn | Phe | Tyr |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Ala | Phe | Leu | Asp | Leu | Leu | Ser | Glu | Ile | Asp | Thr | Asn | Pro | Thr | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Phe | Lys | Val | Met | Leu | Ile | Asn | Lys | Ile | Asp | Ser | Ser | Phe | Phe | Asn | Ser |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Ile | Arg | Leu | Lys | Ile | Asn | Asn | Glu | Leu | Asp | Asp | Glu | Thr | Leu | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Phe | Ala | Lys | Thr | Asp | Ile | Val | Leu | Phe | Lys | Ala | Thr | Arg | Asp | Arg |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Gly | Thr | Asp | Asn | Leu | Ile | Asn | Ala | Tyr | Leu | Lys | Lys | Gly | Lys | Glu |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Leu | Lys | Ser | Glu | Met | Ile | Ala | Gln | Cys | Arg | Asn | Asp | Ile | Gly | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ala | Phe | Trp | Gln | Ser | Val | Asn | Asn | Ala | Ser | Asn | Ser | Ser | Cys | Phe | His |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Tyr | Ile | Phe | Phe | Glu | Lys | Asn | Cys | Gln | Glu | Met | Gly | Leu | Ala | Asp | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Lys | Lys | Leu | Ile | Pro | Arg | Lys | Gln | Phe | Ser | Gln | Glu | Lys | Glu | His | Ile |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Pro | Ile | Asn | Leu | Leu | Lys | Gln | Glu | Ser | Asn | Asn | Lys | Ile | Arg | Asp |
|     |     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |
| Leu | Gly | Phe | Glu | Asp | Lys | Lys | Asp | Leu | Glu | Asp | Tyr | Ile | Asp | Thr | Tyr |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Gly | Asn | Leu | Ile | Ser | Leu | Glu | Lys | Ser | Leu | Asn | Arg | Lys | Ala | Ser | Asp |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Lys | Asp | Leu | Tyr | Gly | Lys | Asp | Glu | Ile | Tyr | Lys | Ser | Ser | Glu | Ile | Pro |
|     |     |     | 340 |     |     |     | 345 |     |     |     |     |     | 350 |     |     |
| Phe | Asn | Arg | Arg | Phe | Asp | Thr | Lys | Asn | Phe | Asn | Lys | Lys | Ala | Leu | Val |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |
| Lys | Arg | Asn | Glu | Glu | Met | Arg | Glu | Trp | Leu | Ile | Asp | Thr | Phe | Phe | Lys |
|     |     | 370 |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |

Asp Phe Ala Ala His  
385

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 889 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...840
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| TTATAAAGGA AAATC ATG GGA TTT TTA AAA GGT AAA AAA GGG CTT ATT GTA | 51  |
| Met Gly Phe Leu Lys Gly Lys Lys Gly Leu Ile Val                  |     |
| 1 5 10                                                           |     |
| GGG GTG GCG AAC AAT AAA TCC ATC GCT TAT GGG ATC GCT CAA TCT TGT  | 99  |
| Gly Val Ala Asn Asn Lys Ser Ile Ala Tyr Gly Ile Ala Gln Ser Cys  |     |
| 15 20 25                                                         |     |
| TTC AAT CAA GGG GCT ACT TTG GCT TTC ACT TAT TTG AAT GAG AGT TTA  | 147 |
| Phe Asn Gln Gly Ala Thr Leu Ala Phe Thr Tyr Leu Asn Glu Ser Leu  |     |
| 30 35 40                                                         |     |
| GAA AAG CGC GTA AGG CCT ATC GCG CAG GAA TTG AAT AGC CCC TAT GTG  | 195 |
| Glu Lys Arg Val Arg Pro Ile Ala Gln Glu Leu Asn Ser Pro Tyr Val  |     |
| 45 50 55 60                                                      |     |
| TAT GAA TTG GAT GTG AGC AAA GAA GAG CAT TTC AAG TCG CTA TAC AAT  | 243 |
| Tyr Glu Leu Asp Val Ser Lys Glu Glu His Phe Lys Ser Leu Tyr Asn  |     |
| 65 70 75                                                         |     |
| AGC GTT AAA AAG GAT TTA GGC TCA TTG GAT TTT ATT GTT CAT AGC GTG  | 291 |
| Ser Val Lys Lys Asp Leu Gly Ser Leu Asp Phe Ile Val His Ser Val  |     |
| 80 85 90                                                         |     |
| GCC TTT GCC CCT AAA GAG GCT TTA GAG GGG AGC TTG TTG GAA ACT TCT  | 339 |
| Ala Phe Ala Pro Lys Glu Ala Leu Glu Gly Ser Leu Leu Glu Thr Ser  |     |
| 95 100 105                                                       |     |
| AAA AGC GCG TTT AAC ACC GCT ATG GAA ATT TCT GTT TAT TCT TTA ATA  | 387 |
| Lys Ser Ala Phe Asn Thr Ala Met Glu Ile Ser Val Tyr Ser Leu Ile  |     |
| 110 115 120                                                      |     |
| GAG CTG ACA AAC ACC CTA AAA CCT TTA TTG AAT AAC GGA GCG TCT GTT  | 435 |
| Glu Leu Thr Asn Thr Leu Lys Pro Leu Leu Asn Asn Gly Ala Ser Val  |     |
| 125 130 135 140                                                  |     |
| TTG ACT CTA AGC TAT TTG GGT AGC ACC AAA TAC ATG GCG CAT TAC AAT  | 483 |

| Leu               | Thr | Leu | Ser | Tyr | Leu | Gly | Ser        | Thr        | Lys        | Tyr  | Met | Ala | His | Tyr | Asn |     |     |
|-------------------|-----|-----|-----|-----|-----|-----|------------|------------|------------|------|-----|-----|-----|-----|-----|-----|-----|
|                   |     |     |     | 145 |     |     |            |            | 150        |      |     |     |     | 155 |     |     |     |
| GTG               | ATG | GGG | TTG | GCT | AAA | GCG | GCC        | CTA        | GAG        | AGT  | GCG | GTG | CGT | TAT | TTA | 531 |     |
| Val               | Met | Gly | Leu | Ala | Lys | Ala | Ala        | Leu        | Glu        | Ser  | Ala | Val | Arg | Tyr | Leu |     |     |
|                   |     |     |     | 160 |     |     |            |            | 165        |      |     |     |     | 170 |     |     |     |
| GCG               | GTG | GAT | TTA | GGC | AAA | CAC | CAT        | ATA        | AGA        | GTG  | AAT | GCC | CTA | TCG | GCC | 579 |     |
| Ala               | Val | Asp | Leu | Gly | Lys | His | His        | Ile        | Arg        | Val  | Asn | Ala | Leu | Ser | Ala |     |     |
|                   |     |     |     | 175 |     |     |            |            | 180        |      |     |     |     | 185 |     |     |     |
| GGG               | CCT | ATT | AGG | ACG | CTC | GCT | TCT        | AGC        | GGG        | ATC  | GCT | GAT | TTT | AGA | ATG | 627 |     |
| Gly               | Pro | Ile | Arg | Thr | Leu | Ala | Ser        | Ser        | Gly        | Ile  | Ala | Asp | Phe | Arg | Met |     |     |
|                   |     |     |     | 190 |     |     |            |            | 195        |      |     |     |     | 200 |     |     |     |
| ATT               | TTA | AAA | TGG | AAT | GAA | ATC | AAC        | GCC        | CCT        | TTA  | AGA | AAA | AAT | GTG | AGT | 675 |     |
| Ile               | Leu | Lys | Trp | Asn | Glu | Ile | Asn        | Ala        | Pro        | Leu  | Arg | Lys | Asn | Val | Ser |     |     |
|                   |     |     |     | 205 |     |     |            |            | 210        |      |     |     |     | 215 |     |     | 220 |
| TTA               | GAA | GAA | GTG | GGC | AAT | GCC | GGG        | ATG        | TAT        | TTG  | CTC | TCT | AGT | TTG | TCT | 723 |     |
| Leu               | Glu | Glu | Val | Gly | Asn | Ala | Gly        | Met        | Tyr        | Leu  | Leu | Ser | Ser | Leu | Ser |     |     |
|                   |     |     |     | 225 |     |     |            |            | 230        |      |     |     |     | 235 |     |     |     |
| AGC               | GGG | GTG | AGT | GGG | GAA | GTG | CAT        | TTT        | GTG        | GAT  | GCT | GGC | TAT | CAT | GTT | 771 |     |
| Ser               | Gly | Val | Ser | Gly | Glu | Val | His        | Phe        | Val        | Asp  | Ala | Gly | Tyr | His | Val |     |     |
|                   |     |     |     | 240 |     |     |            |            | 245        |      |     |     |     | 250 |     |     |     |
| ATG               | GGC | ATG | GGG | GCT | GTG | GAA | GAA        | AAA        | GAT        | AAT  | AAA | GCT | ACG | CTA | CTG | 819 |     |
| Met               | Gly | Met | Gly | Ala | Val | Glu | Glu        | Lys        | Asp        | Asn  | Lys | Ala | Thr | Leu | Leu |     |     |
|                   |     |     |     | 255 |     |     |            |            | 260        |      |     |     |     | 265 |     |     |     |
| TGG               | GAT | TTG | CAT | AAA | GAA | CAA | TAAGGGGTAT | TGATGAAATT | AAGCGAATTG | TTAA |     |     |     |     |     | 874 |     |
| Trp               | Asp | Leu | His | Lys | Glu | Gln |            |            |            |      |     |     |     |     |     |     |     |
|                   |     |     |     | 270 |     |     |            |            | 275        |      |     |     |     |     |     |     |     |
| ACGCCCTATTC TATTG |     |     |     |     |     |     |            |            |            |      |     |     |     |     |     | 889 |     |

(2) INFORMATION FOR SEQ ID NO:494:

## (ii) MOLECULE TYPE: protein

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Phe | Leu | Lys | Gly | Lys | Lys | Gly | Leu | Ile | Val | Gly | Val | Ala | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Lys | Ser | Ile | Ala | Tyr | Gly | Ile | Ala | Gln | Ser | Cys | Phe | Asn | Gln | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Thr | Leu | Ala | Phe | Thr | Tyr | Leu | Asn | Glu | Ser | Leu | Glu | Lys | Arg | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Pro | Ile | Ala | Gln | Glu | Leu | Asn | Ser | Pro | Tyr | Val | Tyr | Glu | Leu | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Ser | Lys | Glu | Glu | His | Phe | Lys | Ser | Leu | Tyr | Asn | Ser | Val | Lys | Lys |





|                   |            |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |
|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| 265               |            |                   |                   | 270               |                   |                   |                   | 275               |                   |                   |                   |                   |                   |                   |                   |      |
| GAA<br>Glu<br>280 | ATT<br>Ile | GAT<br>Asp        | TTC<br>Phe        | GCT<br>Ala        | CAG<br>Gln<br>285 | TGG<br>Trp        | ATG<br>Met        | GTG<br>Val        | TTT<br>Phe        | GGG<br>Gly<br>290 | ACG<br>Thr        | CCG<br>Pro        | TTA<br>Leu        | GCC<br>Ala        | TTT<br>Phe<br>295 | 917  |
| ATC<br>Ile        | ATG<br>Met | CTC<br>Leu        | ATT<br>Ile        | TTA<br>Leu<br>300 | GCG<br>Ala        | TGG<br>Trp        | CTC<br>Leu        | TTG<br>Leu        | CTC<br>Leu<br>305 | ACT<br>Thr        | TAT<br>Tyr        | GTG<br>Val        | ATT<br>Ile        | TTC<br>Phe<br>310 | CCT<br>Pro        | 965  |
| TTA<br>Leu        | AAG<br>Lys | ATT<br>Ile        | AAA<br>Lys<br>315 | GAA<br>Glu        | ATC<br>Ile        | CCA<br>Pro        | GGG<br>Gly        | GGT<br>Gly<br>320 | AAG<br>Lys        | GAA<br>Glu        | GTC<br>Val        | ATT<br>Ile        | AGG<br>Arg<br>325 | GTA<br>Val        | GAG<br>Glu        | 1013 |
| TTA<br>Leu        | AAA<br>Lys | AAA<br>Lys<br>330 | TTA<br>Leu        | GGC<br>Gly        | CGT<br>Arg        | TTG<br>Leu        | AGT<br>Ser<br>335 | CAG<br>Gln        | GCG<br>Ala        | GAA<br>Glu        | ATC<br>Ile        | TCT<br>Ser<br>340 | GTG<br>Val        | GGG<br>Gly        | ATT<br>Ile        | 1061 |
| ATT<br>Ile<br>345 | TTT<br>Phe | ATT<br>Ile        | TTA<br>Leu        | GCG<br>Ala        | TCT<br>Ser<br>350 | TTA<br>Leu        | GGG<br>Gly        | TGG<br>Trp        | ATT<br>Ile        | TTT<br>Phe<br>355 | TTA<br>Leu        | GGC<br>Gly        | GTA<br>Val        | ATG<br>Met        | TTA<br>Leu        | 1109 |
| AAA<br>Lys<br>360 | TCT<br>Ser | TGG<br>Trp        | GGC<br>Gly        | GTT<br>Val        | AAG<br>Lys<br>365 | ATA<br>Ile        | GAT<br>Asp        | AAA<br>Lys        | ATT<br>Ile        | GAT<br>Asp<br>370 | TCA<br>Ser        | GTG<br>Val        | ATC<br>Ile        | GCT<br>Ala        | ATG<br>Met<br>375 | 1157 |
| GGG<br>Gly        | GTT<br>Val | TCT<br>Ser        | GCG<br>Ala        | CTT<br>Leu<br>380 | TTA<br>Leu        | TTC<br>Phe        | ATT<br>Ile        | TTG<br>Leu        | CCC<br>Pro<br>385 | GCT<br>Ala        | AAC<br>Asn        | CAT<br>His        | CAG<br>Gln        | GGC<br>Gly<br>390 | GAT<br>Asp        | 1205 |
| AGG<br>Arg        | CTC<br>Leu | ATT<br>Ile        | GAT<br>Asp<br>395 | TGG<br>Trp        | GGT<br>Gly        | GTT<br>Val        | GCT<br>Ala        | AAA<br>Lys<br>400 | AAA<br>Lys        | CTC<br>Leu        | CCT<br>Pro        | TGG<br>Trp        | GAT<br>Asp<br>405 | GTG<br>Val        | TTG<br>Leu        | 1253 |
| CTT<br>Leu        | TTA<br>Leu | TTT<br>Phe<br>410 | GGC<br>Gly        | GGC<br>Gly        | GGG<br>Gly        | TTA<br>Leu        | GCC<br>Ala<br>415 | TTG<br>Leu        | AGC<br>Ser        | GCG<br>Ala        | CAA<br>Gln        | TTT<br>Phe<br>420 | TCT<br>Ser        | AAA<br>Lys        | ACC<br>Thr        | 1301 |
| GGG<br>Gly<br>425 | TTG<br>Leu | AGT<br>Ser        | TTG<br>Leu        | TGG<br>Trp        | ATC<br>Ile        | GGG<br>Gly<br>430 | CAT<br>His        | TTA<br>Leu        | GTC<br>Val        | TCT<br>Ser        | GGC<br>Gly<br>435 | TTT<br>Phe        | TCG<br>Ser        | CAT<br>His        | TTA<br>Leu        | 1349 |
| CCG<br>Pro<br>440 | ATT<br>Ile | TTA<br>Leu        | TTC<br>Phe        | ATC<br>Ile        | ATT<br>Ile<br>445 | GTC<br>Val        | ATG<br>Met        | GTT<br>Val        | ACT<br>Thr        | TTA<br>Leu<br>450 | ATG<br>Met        | GTC<br>Val        | ATT<br>Ile        | TTC<br>Phe        | TTA<br>Leu<br>455 | 1397 |
| ACC<br>Thr        | GAA<br>Glu | ATC<br>Ile        | ACT<br>Thr        | TCT<br>Ser<br>460 | AAC<br>Asn        | ACC<br>Thr        | GCC<br>Ala        | ACC<br>Thr        | GCT<br>Ala<br>465 | GCC<br>Ala        | GCA<br>Ala        | TTT<br>Phe        | TTA<br>Leu        | CCG<br>Pro<br>470 | GTG<br>Val        | 1445 |
| ATT<br>Ile        | GGA<br>Gly | GGG<br>Gly        | GTT<br>Val<br>475 | GCG<br>Ala        | ATG<br>Met        | GGC<br>Gly        | ATG<br>Met        | GGT<br>Gly<br>480 | TAT<br>Tyr        | GAA<br>Glu        | AAC<br>Asn        | CAT<br>His        | CAG<br>Gln<br>485 | AGC<br>Ser        | TTG<br>Leu        | 1493 |
| TTA<br>Leu        | TTG<br>Leu | ACC<br>Thr<br>490 | ATT<br>Ile        | CCT<br>Pro        | GTA<br>Val        | GCC<br>Ala        | TTG<br>Leu<br>495 | AGT<br>Ser        | GCG<br>Ala        | ACT<br>Thr        | TGC<br>Cys<br>500 | GCG<br>Ala        | TTC<br>Phe        | ATG<br>Met        | CTC<br>Leu        | 1541 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| CCT | GTG | GTC | ACC | CCA | CCG | AAT | GCA | ATA | GCT | TAT | GGC | TCT | GGG | TAT | GTT | 1589 |
| Pro | Val | Val | Thr | Pro | Pro | Asn | Ala | Ile | Ala | Tyr | Gly | Ser | Gly | Tyr | Val |      |
| 505 |     |     |     |     |     | 510 |     |     |     |     | 515 |     |     |     |     |      |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| AAA | ATA | ACG | GAC | ATG | ATT | AAA | GCC | GGT | TTG | TGG | CTT | AAT | CTG | GTA | GGA | 1637 |
| Lys | Ile | Thr | Asp | Met | Ile | Lys | Ala | Gly | Leu | Trp | Leu | Asn | Leu | Val | Gly |      |
| 520 |     |     |     |     | 525 |     |     |     |     | 530 |     |     |     |     | 535 |      |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| GTT | GTT | TTG | ATT | AGC | ACG | TTT | AGC | TAT | TTT | TTG | GTT | TCG | TTA | ATA | TTT | 1685 |
| Val | Val | Leu | Ile | Ser | Thr | Phe | Ser | Tyr | Phe | Leu | Val | Ser | Leu | Ile | Phe |      |
|     |     |     |     | 540 |     |     |     |     | 545 |     |     |     |     | 550 |     |      |

|     |            |            |            |            |            |        |      |
|-----|------------|------------|------------|------------|------------|--------|------|
| AAT | TGATTAAGGA | AAAAAGTGAA | AGAAGAGTTA | TTTAAAGAAA | AATCTCGTTA | CATTAC | 1744 |
| Asn |            |            |            |            |            |        |      |

|            |        |      |
|------------|--------|------|
| AGGGTTTGTT | TTAATC | 1760 |
|------------|--------|------|

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Asn | His | Ser | His | Ala | Asn | Thr | His | Thr | Asp | Thr | Arg | Thr | Asp |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Asp | Lys | Ser | Thr | Lys | Ile | Val | Arg | Leu | Gly | Leu | Ile | Gly | Gly | Ala |     |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu | Ile | Ala | Leu | Val | Ile | Tyr | Tyr | Ala | Leu | Asn | Ser | Gln | Met | Pro | His |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Ile | Val | Glu | Glu | Ile | Pro | Lys | Leu | Ser | Ser | Leu | Asn | Tyr | Lys | Ala | Met |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Pro | Val | Val | Ala | Gly | Val | Ala | Val | Leu | Met | Gly | Ile | Trp | Trp | Met | Thr |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Glu | Ala | Ile | Asp | Leu | Pro | Ala | Thr | Ala | Leu | Leu | Pro | Leu | Val | Leu | Phe |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ser | Val | Phe | Ser | Val | Asp | Gln | Phe | Ala | Ser | Val | Ser | Ser | Ser | Tyr | Ala |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ser | Pro | Ile | Ile | Phe | Leu | Phe | Met | Gly | Gly | Phe | Ile | Leu | Ala | Leu | Ser |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Met | Gln | Lys | Trp | Asn | Leu | His | Thr | Arg | Ile | Ala | Leu | Ser | Ile | Ile | Leu |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Leu | Val | Gly | Thr | Ser | Pro | Arg | Arg | Leu | Ile | Leu | Gly | Phe | Met | Met | Ala |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Thr | Gly | Phe | Leu | Ser | Met | Trp | Val | Ser | Asn | Thr | Ala | Thr | Ala | Val | Met |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Met | Leu | Pro | Val | Gly | Met | Ser | Val | Leu | Gln | Leu | Val | Ala | Lys | Leu | Val |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Gly | Lys | Glu | Asp | Ala | Ser | Asn | Ser | Trp | His | Gln | Lys | Glu | Glu | Ile | Thr |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Lys | Ala | His | Gly | Gly | Ile | Met | Ser | Asn | Ile | Val | His | Lys | Gly | Lys | Asp |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |





## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

GGTGGCGGCG TATTTTAACG GCGTCCTAT AGAATGCGCT CTTATTAGCG CC ATG GTC 58  
Met Val  
1

ATG GCT AGT GTT ATC GCT TAT CAA AAA GCG CAC CAT AGC GAA GCC ATT 106  
Met Ala Ser Val Ile Ala Tyr Gln Lys Ala His His Ser Glu Ala Ile  
5 10 15

TTA CCC TTT TTG TAT CCG GGC GTT GGG TTT TTT GCG CTT TTT GGG GTT 154  
Leu Pro Phe Leu Tyr Pro Gly Val Gly Phe Phe Ala Leu Phe Gly Val  
20 25 30

TAT AAG GAT TTT GGT GCA GTA GCG ATC ATT TGG CTT TTA GTC GTG GTG 202  
Tyr Lys Asp Phe Gly Ala Val Ala Ile Ile Trp Leu Leu Val Val Val  
35 40 45 50

GTT GCA AGC GAT GTG GGG GCG TTT TTT GGA GGC AAG CTT TTA GGC AAA 250  
Val Ala Ser Asp Val Gly Ala Phe Phe Gly Gly Lys Leu Leu Gly Lys  
55 60 65

ACC CCT TTC ACG CCC ACT TCG CCG AAT AAA ACC TTA GAG GGC GCG TTG 298  
Thr Pro Phe Thr Pro Thr Ser Pro Asn Lys Thr Leu Glu Gly Ala Leu  
70 75 80

ATT GGC GTG GTT TTG GCG AGC GTT TTA GGA TCG TTT GTG GGC ATG GGG 346  
Ile Gly Val Val Leu Ala Ser Val Leu Gly Ser Phe Val Gly Met Gly  
85 90 95

AAA TTG AGC GGA GGC TTT TTT ATG GCG CTC TTT TTT AGT TTT TTA ATC 394  
Lys Leu Ser Gly Gly Phe Phe Met Ala Leu Phe Phe Ser Phe Leu Ile  
100 105 110

GCT CTT GTG GCG GTG TTT GGG GAT TTG TAT GAA AGC TAT TTG AAA AGA 442  
Ala Leu Val Ala Val Phe Gly Asp Leu Tyr Glu Ser Tyr Leu Lys Arg  
115 120 125 130

AAG GTC GGT ATC AAA GAT AGC GGT AAG ATT TTA CCC GGG CAT GGG GGC 490  
Lys Val Gly Ile Lys Asp Ser Gly Lys Ile Leu Pro Gly His Gly Gly  
135 140 145

GTT TTA GAC CGG TTG GAT TCC ATG CTT TTT GGG GCT TTA GGC TTG CAT 538  
Val Leu Asp Arg Leu Asp Ser Met Leu Phe Gly Ala Leu Gly Leu His  
150 155 160

GCG CTG TTG TAT TTT TTA GAA ATT TGG AAA GAA ACG GCG GTG TTT TTA 586  
Ala Leu Leu Tyr Phe Leu Glu Ile Trp Lys Glu Thr Ala Val Phe Leu  
165 170 175

GGG GAT TGAATGGTTG TTTTAGGAAG CACCGGCTCT ATTGGGAAAA ACGCCCTAAA AA 644  
Gly Asp  
180

TCGCAAAAAA ATTTGGC 661

## (2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

Met Val Met Ala Ser Val Ile Ala Tyr Gln Lys Ala His His Ser Glu  
1 5 10 15  
Ala Ile Leu Pro Phe Leu Tyr Pro Gly Val Gly Phe Phe Ala Leu Phe  
20 25 30  
Gly Val Tyr Lys Asp Phe Gly Ala Val Ala Ile Ile Trp Leu Leu Val  
35 40 45  
Val Val Val Ala Ser Asp Val Gly Ala Phe Phe Gly Gly Lys Leu Leu  
50 55 60  
Gly Lys Thr Pro Phe Thr Pro Thr Ser Pro Asn Lys Thr Leu Glu Gly  
65 70 75 80  
Ala Leu Ile Gly Val Val Leu Ala Ser Val Leu Gly Ser Phe Val Gly  
85 90 95  
Met Gly Lys Leu Ser Gly Gly Phe Phe Met Ala Leu Phe Phe Ser Phe  
100 105 110  
Leu Ile Ala Leu Val Ala Val Phe Gly Asp Leu Tyr Glu Ser Tyr Leu  
115 120 125  
Lys Arg Lys Val Gly Ile Lys Asp Ser Gly Lys Ile Leu Pro Gly His  
130 135 140  
Gly Gly Val Leu Asp Arg Leu Asp Ser Met Leu Phe Gly Ala Leu Gly  
145 150 155 160  
Leu His Ala Leu Leu Tyr Phe Leu Glu Ile Trp Lys Glu Thr Ala Val  
165 170 175  
Phe Leu Gly Asp  
180

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 12...1115
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

TAGGGGATTG A ATG GTT GTT TTA GGA AGC ACC GGC TCT ATT GGG AAA AAC 50  
Met Val Val Leu Gly Ser Thr Gly Ser Ile Gly Lys Asn  
1 5 10  
GCC CTA AAA ATC GCA AAA AAA TTT GGC ATA GAA ATA GAG GCC TTA AGC 98

|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |            |                   |                   |     |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-----|
| Ala<br>15         | Leu               | Lys               | Ile               | Ala               | Lys               | Lys<br>20         | Phe               | Gly               | Ile               | Glu               | Ile<br>25         | Glu               | Ala        | Leu               | Ser               |     |
| TGT<br>Cys<br>30  | GGG<br>Gly        | AAA<br>Lys        | AAT<br>Asn        | ATC<br>Ile        | GCT<br>Ala<br>35  | TTA<br>Leu        | ATC<br>Ile        | AAT<br>Asn        | GAA<br>Glu        | CAA<br>Gln<br>40  | ATC<br>Ile        | CAA<br>Gln        | GTT<br>Val | TTC<br>Phe        | AAA<br>Lys<br>45  | 146 |
| CCC<br>Pro        | AAG<br>Lys        | AAA<br>Lys        | GTG<br>Val        | GCG<br>Ala<br>50  | ATT<br>Ile        | TTA<br>Leu        | GAT<br>Asp        | CCT<br>Pro        | AGC<br>Ser<br>55  | GAT<br>Asp        | TTG<br>Leu        | AAT<br>Asn        | GAT<br>Asp | TTA<br>Leu<br>60  | GAG<br>Glu        | 194 |
| CCT<br>Pro        | TTG<br>Leu        | GGT<br>Gly        | GCG<br>Ala<br>65  | GAA<br>Glu        | GTG<br>Val        | TTT<br>Phe        | GTG<br>Val        | GGG<br>Gly<br>70  | TTA<br>Leu        | GAG<br>Glu        | GGC<br>Gly        | ATT<br>Ile<br>75  | GAT<br>Asp | GCG<br>Ala        | ATG<br>Met        | 242 |
| ATA<br>Ile        | GAA<br>Glu        | GAG<br>Glu<br>80  | TGC<br>Cys        | ACC<br>Thr        | TCA<br>Ser        | AAT<br>Asn        | TTA<br>Leu<br>85  | GTC<br>Val        | CTT<br>Leu        | AAC<br>Asn        | GCC<br>Ala<br>90  | ATT<br>Ile        | GTG<br>Val | GGC<br>Gly        | GTG<br>Val        | 290 |
| GCA<br>Ala        | GGA<br>Gly<br>95  | TTG<br>Leu        | AAA<br>Lys        | GCG<br>Ala        | AGC<br>Ser        | TTT<br>Phe<br>100 | AAA<br>Lys        | AGC<br>Ser        | TTA<br>Leu        | CAA<br>Gln<br>105 | AGG<br>Arg        | AAT<br>Asn        | AAA<br>Lys | AAA<br>Lys        | CTG<br>Leu        | 338 |
| GCC<br>Ala<br>110 | CTA<br>Leu        | GCG<br>Ala        | AAT<br>Asn        | AAA<br>Lys        | GAA<br>Glu<br>115 | AGC<br>Ser        | TTA<br>Leu        | GTG<br>Val        | AGC<br>Ser        | GCG<br>Ala<br>120 | GGG<br>Gly        | CAT<br>His        | TTA<br>Leu | TTA<br>Leu        | GAC<br>Asp<br>125 | 386 |
| ATT<br>Ile        | TCA<br>Ser        | CAA<br>Gln        | ATC<br>Ile<br>130 | ACG<br>Thr        | CCC<br>Pro        | ATT<br>Ile        | GAT<br>Asp        | AGC<br>Ser        | GAG<br>Glu<br>135 | CAT<br>His        | TTT<br>Phe        | GGT<br>Gly        | TTG<br>Leu | TGG<br>Trp<br>140 | GCG<br>Ala        | 434 |
| TTG<br>Leu        | TTG<br>Leu        | CAA<br>Gln<br>145 | AAC<br>Asn        | AAG<br>Lys        | ACT<br>Thr        | TTA<br>Leu        | AAG<br>Lys        | CCT<br>Pro<br>150 | AAA<br>Lys        | TCC<br>Ser        | TTA<br>Leu        | ATC<br>Ile<br>155 | ATT<br>Ile | AGC<br>Ser        | GCG<br>Ala        | 482 |
| AGT<br>Ser        | GGG<br>Gly        | GGG<br>Gly<br>160 | GCT<br>Ala        | TTC<br>Phe        | AGG<br>Arg        | GAC<br>Asp        | ACG<br>Thr<br>165 | CCT<br>Pro        | TTA<br>Leu        | GAA<br>Glu        | TTT<br>Phe<br>170 | ATT<br>Ile        | CCT<br>Pro | ATT<br>Ile        | CAA<br>Gln        | 530 |
| AAC<br>Asn        | GCG<br>Ala<br>175 | CAA<br>Gln        | AAT<br>Asn        | GCG<br>Ala        | CTC<br>Leu        | AAG<br>Lys<br>180 | CAC<br>His        | CCT<br>Pro        | AAT<br>Asn        | TGG<br>Trp<br>185 | AGC<br>Ser        | ATG<br>Met        | GGA<br>Gly | TCT<br>Ser        | AAA<br>Lys        | 578 |
| ATC<br>Ile<br>190 | ACC<br>Thr        | ATT<br>Ile        | GAT<br>Asp        | TCA<br>Ser        | GCG<br>Ala<br>195 | AGC<br>Ser        | ATG<br>Met        | GTC<br>Val        | AAT<br>Asn        | AAG<br>Lys<br>200 | CTT<br>Leu        | TTT<br>Phe        | GAA<br>Glu | ATC<br>Ile        | CTA<br>Leu<br>205 | 626 |
| GAA<br>Glu        | ACT<br>Thr        | TAT<br>Tyr        | TGG<br>Trp        | CTT<br>Leu<br>210 | TTT<br>Phe        | GGC<br>Gly        | GCG<br>Ala        | TCT<br>Ser        | TTA<br>Leu<br>215 | AAG<br>Lys        | ATT<br>Ile        | GAT<br>Asp        | GCG<br>Ala | CTG<br>Leu<br>220 | ATT<br>Ile        | 674 |
| GAA<br>Glu        | AGG<br>Arg        | AGT<br>Ser        | TCT<br>Ser<br>225 | ATC<br>Ile        | GTG<br>Val        | CAT<br>His        | GCT<br>Ala        | TTG<br>Leu<br>230 | GTG<br>Val        | GAG<br>Glu        | TTT<br>Phe        | GAA<br>Glu<br>235 | GAC<br>Asp | AAC<br>Asn        | TCT<br>Ser        | 722 |
| ATC<br>Ile        | ATC<br>Ile        | GCG<br>Ala<br>240 | CAT<br>His        | TTA<br>Leu        | GCG<br>Ala        | AGC<br>Ser        | GCA<br>Ala<br>245 | GAT<br>Asp        | ATG<br>Met        | CAA<br>Gln<br>250 | TTA<br>Leu        | CCC<br>Pro<br>255 | ATA<br>Ile | AGC<br>Ser        | TAT<br>Tyr        | 770 |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Lys | Glu | Ser | Leu | Val | Ser | Ala | Gly | His | Leu | Leu | Asp | Ile | Ser | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Thr | Pro | Ile | Asp | Ser | Glu | His | Phe | Gly | Leu | Trp | Ala | Leu | Leu | Gln |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Lys | Thr | Leu | Lys | Pro | Lys | Ser | Leu | Ile | Ile | Ser | Ala | Ser | Gly | Gly |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Phe | Arg | Asp | Thr | Pro | Leu | Glu | Phe | Ile | Pro | Ile | Gln | Asn | Ala | Gln |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asn | Ala | Leu | Lys | His | Pro | Asn | Trp | Ser | Met | Gly | Ser | Lys | Ile | Thr | Ile |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asp | Ser | Ala | Ser | Met | Val | Asn | Lys | Leu | Phe | Glu | Ile | Leu | Glu | Thr | Tyr |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Trp | Leu | Phe | Gly | Ala | Ser | Leu | Lys | Ile | Asp | Ala | Leu | Ile | Glu | Arg | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Ile | Val | His | Ala | Leu | Val | Glu | Phe | Glu | Asp | Asn | Ser | Ile | Ile | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| His | Leu | Ala | Ser | Ala | Asp | Met | Gln | Leu | Pro | Ile | Ser | Tyr | Ala | Ile | Asp |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Pro | Lys | Leu | Ala | Ser | Leu | Ser | Ala | Ser | Ile | Lys | Pro | Leu | Asp | Leu | Tyr |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ala | Leu | Ser | Ala | Ile | Lys | Phe | Glu | Pro | Ile | Ser | Met | Glu | Arg | Tyr | Thr |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Trp | Cys | Tyr | Lys | Asp | Leu | Leu | Leu | Glu | Asn | Pro | Lys | Leu | Gly | Val |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Val | Leu | Asn | Ala | Ser | Asn | Glu | Val | Ala | Met | Glu | Lys | Phe | Leu | Asn | Lys |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Glu | Ile | Ala | Phe | Gly | Gly | Leu | Ile | Gln | Thr | Ile | Ser | Gln | Ala | Leu | Glu |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ser | Tyr | Asp | Lys | Met | Pro | Phe | Lys | Leu | Ser | Ser | Leu | Glu | Glu | Val | Leu |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |
| Glu | Leu | Asp | Lys | Glu | Val | Arg | Glu | Arg | Phe | Lys | Asn | Val | Ala | Gly | Val |
|     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1025 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...999
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

|                                                                 |    |
|-----------------------------------------------------------------|----|
| AAAGAATATA AAGGAATCAA A ATG GCA AAA CAT GAT TTA GTG GGT TCG GTT | 51 |
| Met Ala Lys His Asp Leu Val Gly Ser Val                         |    |
| 1 5 10                                                          |    |
| CTC TGG GAC GCA TAT TCT AAA GAA GTT CAA AGG CGC ATG GAC AAC CCC | 99 |
| Leu Trp Asp Ala Tyr Ser Lys Glu Val Gln Arg Arg Met Asp Asn Pro |    |

| 15  |     |     |     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| ACG | CAT | TTA | GGG | GTC | ATC | ACC | GAA | GAG | CAG | GCT | AAA | GCC | AAA | AAC | GCT | 147 |  |
| Thr | His | Leu | Gly | Val | Ile | Thr | Glu | Glu | Gln | Ala | Lys | Ala | Lys | Asn | Ala |     |  |
|     |     |     | 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |  |
| AAG | CTC | ATT | GTG | GCG | GAT | TAT | GGC | GCA | GAG | GCA | TGC | GGT | GAT | GCG | GTG | 195 |  |
| Lys | Leu | Ile | Val | Ala | Asp | Tyr | Gly | Ala | Glu | Ala | Cys | Gly | Asp | Ala | Val |     |  |
|     |     | 45  |     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |  |
| AGG | TTG | TAT | TGG | CTT | GTA | GAT | GAA | AGC | ACG | GAT | AGA | ATT | GTT | GAC | GCG | 243 |  |
| Arg | Leu | Tyr | Trp | Leu | Val | Asp | Glu | Ser | Thr | Asp | Arg | Ile | Val | Asp | Ala |     |  |
|     | 60  |     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     |     |  |
| AAG | TTT | AAA | AGC | TTT | GGT | TGC | GGA | ACA | GCG | ATC | GCA | AGC | TCA | GAC | ATG | 291 |  |
| Lys | Phe | Lys | Ser | Phe | Gly | Cys | Gly | Thr | Ala | Ile | Ala | Ser | Ser | Asp | Met |     |  |
| 75  |     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |     |  |
| ATG | GTA | GAG | TTG | TGC | TTG | AAT | AAA | AGA | GTC | CAA | GAT | GCG | GTA | AAA | ATC | 339 |  |
| Met | Val | Glu | Leu | Cys | Leu | Asn | Lys | Arg | Val | Gln | Asp | Ala | Val | Lys | Ile |     |  |
|     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |     |     |  |
| ACG | AAT | TTA | GAT | GTG | GAA | AGA | GGC | TTG | AGA | GAC | GAT | CCG | GAC | ACG | CCG | 387 |  |
| Thr | Asn | Leu | Asp | Val | Glu | Arg | Gly | Leu | Arg | Asp | Asp | Pro | Asp | Thr | Pro |     |  |
|     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |     |     |     |  |
| GCG | GTG | CCT | GGG | CAA | AAA | ATG | CAC | TGC | TCG | GTG | ATG | GCG | TAT | GAT | GTG | 435 |  |
| Ala | Val | Pro | Gly | Gln | Lys | Met | His | Cys | Ser | Val | Met | Ala | Tyr | Asp | Val |     |  |
|     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |     |     |     |     |  |
| ATC | AAA | AAA | GCT | GCC | GGC | ATG | TAT | TTG | GGG | AAA | AAC | GCT | GAA | GAT | TTT | 483 |  |
| Ile | Lys | Lys | Ala | Ala | Gly | Met | Tyr | Leu | Gly | Lys | Asn | Ala | Glu | Asp | Phe |     |  |
|     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |     |     |     |     |     |  |
| GAA | GAA | GAA | ATC | ATC | GTG | TGC | GAG | TGC | GCT | AGG | GTG | AGT | TTA | GGT | ACG | 531 |  |
| Glu | Glu | Glu | Ile | Ile | Val | Cys | Glu | Cys | Ala | Arg | Val | Ser | Leu | Gly | Thr |     |  |
| 155 |     |     |     |     | 160 |     |     |     |     | 165 |     |     |     |     | 170 |     |  |
| ATT | AAA | GAA | GTG | ATT | AAG | CTC | AAT | GAT | TTA | AAA | AGC | GTT | GAA | GAA | ATC | 579 |  |
| Ile | Lys | Glu | Val | Ile | Lys | Leu | Asn | Asp | Leu | Lys | Ser | Val | Glu | Glu | Ile |     |  |
|     |     |     |     | 175 |     |     |     |     | 180 |     |     |     |     | 185 |     |     |  |
| ACT | AAC | TAC | ACC | AAA | GCC | GGT | GCT | TTT | TGT | AAA | AGC | TGT | GTG | AGG | CCT | 627 |  |
| Thr | Asn | Tyr | Thr | Lys | Ala | Gly | Ala | Phe | Cys | Lys | Ser | Cys | Val | Arg | Pro |     |  |
|     |     |     | 190 |     |     |     |     | 195 |     |     |     |     | 200 |     |     |     |  |
| GGA | GGG | CAT | GAA | AAA | AGG | GAT | TAT | TAC | TTG | GTG | GAT | ATT | CTT | AAA | GAA | 675 |  |
| Gly | Gly | His | Glu | Lys | Arg | Asp | Tyr | Tyr | Leu | Val | Asp | Ile | Leu | Lys | Glu |     |  |
|     |     | 205 |     |     |     |     | 210 |     |     |     |     | 215 |     |     |     |     |  |
| GTG | CGC | GAA | GAA | ATG | GAA | GCT | GAA | AAA | CTT | AAA | GCG | ACC | GCT | AAT | AAA | 723 |  |
| Val | Arg | Glu | Glu | Met | Glu | Ala | Glu | Lys | Leu | Lys | Ala | Thr | Ala | Asn | Lys |     |  |
|     | 220 |     |     |     |     | 225 |     |     |     |     | 230 |     |     |     |     |     |  |
| TCC | CAA | AGC | GGA | GAA | TTG | GCT | TTC | AGG | GAA | ATG | ACT | ATG | GTT | CAA | AAG | 771 |  |
| Ser | Gln | Ser | Gly | Glu | Leu | Ala | Phe | Arg | Glu | Met | Thr | Met | Val | Gln | Lys |     |  |
| 235 |     |     |     |     | 240 |     |     |     |     | 245 |     |     |     |     | 250 |     |  |







Glu Met Ile Phe Pro Lys Pro Cys Ala Leu Val Ser Leu Phe Leu Ser  
80 85 90

CTC ACG CCG TCT TTT AAA ATC ACA TCT AAA GTT TTA GCC GTC AAT AAG 339  
Leu Thr Pro Ser Phe Lys Ile Thr Ser Lys Val Leu Ala Val Asn Lys  
95 100 105

CTT TCT ATC GTT CCC ACT AGT GCT AAA GAA AGA GCG TAAGGCAACA ACTCTA 391  
Leu Ser Ile Val Pro Thr Ser Ala Lys Glu Arg Ala  
110 115

TCATTATTTT AAAATCCAAA TTT 414

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

Met Leu Ile Met Asp Trp Lys Leu Lys Val Val Lys Glu Ile Ile Thr  
1 5 10 15  
Ile Thr Ala Thr Thr Ala Thr Met Gly Ile Leu Thr Thr Tyr Ser Leu  
20 25 30  
Asn Thr Asn Met Ser Thr Ile Lys Glu Lys Pro Ala Lys Lys Val Glu  
35 40 45  
Ser Leu Val Leu Ala Pro Asp Phe Ala Leu Met Ile Asp Cys Pro Thr  
50 55 60  
Lys Ala His Pro Val Ile Pro Pro Lys Ser Pro Glu Met Ile Phe Pro  
65 70 75 80  
Lys Pro Cys Ala Leu Val Ser Leu Phe Leu Ser Leu Thr Pro Ser Phe  
85 90 95  
Lys Ile Thr Ser Lys Val Leu Ala Val Asn Lys Leu Ser Ile Val Pro  
100 105 110  
Thr Ser Ala Lys Glu Arg Ala  
115

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...660
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TATAAGGTTG CTCTC ATG AAA AAA CCC TAT AGG AAG ATT TCT GAT TAT GCG  | 51  |
| Met Lys Lys Pro Tyr Arg Lys Ile Ser Asp Tyr Ala                   |     |
| 1 5 10                                                            |     |
| ATC GTG GGT GGT TTG AGC GCG TTA GTG ATG GTG AGC ATT GTG GGG TGT   | 99  |
| Ile Val Gly Gly Leu Ser Ala Leu Val Met Val Ser Ile Val Gly Cys   |     |
| 15 20 25                                                          |     |
| AAG AGC AAT GCT GAT GAC AAA CCA AAA GAG CAA AGC TCT TTA AGT CAA   | 147 |
| Lys Ser Asn Ala Asp Asp Lys Pro Lys Glu Gln Ser Ser Leu Ser Gln   |     |
| 30 35 40                                                          |     |
| AGC GTT CAA AAA GGC GCG TTT GTG ATT TTA GAA GAG CAA AAG GAT AAA   | 195 |
| Ser Val Gln Lys Gly Ala Phe Val Ile Leu Glu Glu Gln Lys Asp Lys   |     |
| 45 50 55 60                                                       |     |
| TCT TAC AAG GTT GTT GAA GAA TAC CCC AGC TCA AGA ACC CAC ATT ATA   | 243 |
| Ser Tyr Lys Val Val Glu Glu Tyr Pro Ser Ser Arg Thr His Ile Ile   |     |
| 65 70 75                                                          |     |
| GTG CGC GAT TTG CAA GGC AAT GAA CGC GTG TTA AGC AAT GAA GAG ATT   | 291 |
| Val Arg Asp Leu Gln Gly Asn Glu Arg Val Leu Ser Asn Glu Glu Ile   |     |
| 80 85 90                                                          |     |
| CAA AAG CTC ATC AAA GAA GAA GAA GCT AAA ATT GAT AAC GGC ACG AGC   | 339 |
| Gln Lys Leu Ile Lys Glu Glu Glu Ala Lys Ile Asp Asn Gly Thr Ser   |     |
| 95 100 105                                                        |     |
| AAG CTT GTC CAG CCT AAT AAT GGA GGG AGT AAT GAA GGC TCA GGC TTT   | 387 |
| Lys Leu Val Gln Pro Asn Asn Gly Gly Ser Asn Glu Gly Ser Gly Phe   |     |
| 110 115 120                                                       |     |
| GGC TTG GGG AGC GCG ATT TTA GGG AGC GCG GCG GGG GCG ATT TTA GGG   | 435 |
| Gly Leu Gly Ser Ala Ile Leu Gly Ser Ala Ala Gly Ala Ile Leu Gly   |     |
| 125 130 135 140                                                   |     |
| AGT TAT ATT GGT AAT AAG CTT TTC AAT AAC CCT AAT TAC CAG CAA AAC   | 483 |
| Ser Tyr Ile Gly Asn Lys Leu Phe Asn Asn Pro Asn Tyr Gln Gln Asn   |     |
| 145 150 155                                                       |     |
| GCC CAA CGG ACC TAC AAA TCC CCA CAA GCT TAC CAA CGC TCT CAA AAT   | 531 |
| Ala Gln Arg Thr Tyr Lys Ser Pro Gln Ala Tyr Gln Arg Ser Gln Asn   |     |
| 160 165 170                                                       |     |
| TCC TTT TCT AAA AGT GCG CCC AGT GCT TCA AGC ATG GGC GGA GCG AGT   | 579 |
| Ser Phe Ser Lys Ser Ala Pro Ser Ala Ser Ser Met Gly Gly Ala Ser   |     |
| 175 180 185                                                       |     |
| AAG GGA CAG AGC GGG TTT TTT GGC TCT AGT AGG CCT ACT AGT TCA CCG   | 627 |
| Lys Gly Gln Ser Gly Phe Phe Gly Ser Ser Arg Pro Thr Ser Ser Pro   |     |
| 190 195 200                                                       |     |
| GCG GTA AGC TCT GGG ACA AGG GGC TTT AAC TCA TAATTTAATT GATTCAAGGC | 680 |
| Ala Val Ser Ser Gly Thr Arg Gly Phe Asn Ser                       |     |
| 205 210 215                                                       |     |

## (2) INFORMATION FOR SEQ ID NO:506:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

```

Met Lys Lys Pro Tyr Arg Lys Ile Ser Asp Tyr Ala Ile Val Gly Gly
 1 5 10 15
Leu Ser Ala Leu Val Met Val Ser Ile Val Gly Cys Lys Ser Asn Ala
 20 25 30
Asp Asp Lys Pro Lys Glu Gln Ser Ser Leu Ser Gln Ser Val Gln Lys
 35 40 45
Gly Ala Phe Val Ile Leu Glu Gln Lys Asp Lys Ser Tyr Lys Val
 50 55 60
Val Glu Glu Tyr Pro Ser Arg Thr His Ile Ile Val Arg Asp Leu
 65 70 75 80
Gln Gly Asn Glu Arg Val Leu Ser Asn Glu Glu Ile Gln Lys Leu Ile
 85 90 95
Lys Glu Glu Glu Ala Lys Ile Asp Asn Gly Thr Ser Lys Leu Val Gln
 100 105 110
Pro Asn Asn Gly Gly Ser Asn Glu Gly Ser Gly Phe Gly Leu Gly Ser
 115 120 125
Ala Ile Leu Gly Ser Ala Ala Gly Ala Ile Leu Gly Ser Tyr Ile Gly
 130 135 140
Asn Lys Leu Phe Asn Asn Pro Asn Tyr Gln Gln Asn Ala Gln Arg Thr
 145 150 155 160
Tyr Lys Ser Pro Gln Ala Tyr Gln Arg Ser Gln Asn Ser Phe Ser Lys
 165 170 175
Ser Ala Pro Ser Ala Ser Ser Met Gly Gly Ala Ser Lys Gly Gln Ser
 180 185 190
Gly Phe Phe Gly Ser Ser Arg Pro Thr Ser Ser Pro Ala Val Ser Ser
 195 200 205
Gly Thr Arg Gly Phe Asn Ser
 210 215

```

## (2) INFORMATION FOR SEQ ID NO:507:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...1362
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| TTATAGGACT TTTTA ATG GAG TTA GAA ACT CAT TTG TCA AAA TAT TTC ACC | 51  |
| Met Glu Leu Glu Thr His Leu Ser Lys Tyr Phe Thr                  |     |
| 1 5 10                                                           |     |
| CTA GCC TTT ACG CAT AAA AGC ATG AGC TTA GAA ATG CGA GAA AAA CTC  | 99  |
| Leu Ala Phe Thr His Lys Ser Met Ser Leu Glu Met Arg Glu Lys Leu  |     |
| 15 20 25                                                         |     |
| GCT ATT AAT TCG AAT GCA ACG CTT AAA GAA TTT TTA CAA ACC ATT AAA  | 147 |
| Ala Ile Asn Ser Asn Ala Thr Leu Lys Glu Phe Leu Gln Thr Ile Lys  |     |
| 30 35 40                                                         |     |
| AAC CAT TGC CCT AAC ATC AAA GAG TGC ATG GTG TTA TCC ACA TGC AAT  | 195 |
| Asn His Cys Pro Asn Ile Lys Glu Cys Met Val Leu Ser Thr Cys Asn  |     |
| 45 50 55 60                                                      |     |
| CGC TTT GAA ATC TAT GCG AGC CTA AAA CAC GGC GCT AAT ACT AAT GAA  | 243 |
| Arg Phe Glu Ile Tyr Ala Ser Leu Lys His Gly Ala Asn Thr Asn Glu  |     |
| 65 70 75                                                         |     |
| CAA AAA AAC GCA CTA TTA AAG ATT TTG GCT CAA AAT AAA AAA ATG AGC  | 291 |
| Gln Lys Asn Ala Leu Leu Lys Ile Leu Ala Gln Asn Lys Lys Met Ser  |     |
| 80 85 90                                                         |     |
| GTG TCT GAT TTA GAA AAA TGC GTT TTA ATG AAC ACT GAT GAA AGC GCA  | 339 |
| Val Ser Asp Leu Glu Lys Cys Val Leu Met Asn Thr Asp Glu Ser Ala  |     |
| 95 100 105                                                       |     |
| GTC CAT CAT GTC TTT AGC GTG TGC AGC AGT TTG GAT AGC TTG GTG GTT  | 387 |
| Val His His Val Phe Ser Val Cys Ser Ser Leu Asp Ser Leu Val Val  |     |
| 110 115 120                                                      |     |
| GGG GAA ACT CAA ATC ACA GGG CAG ATG AAA AAC GCT TAT AAA TTC GCT  | 435 |
| Gly Glu Thr Gln Ile Thr Gly Gln Met Lys Asn Ala Tyr Lys Phe Ala  |     |
| 125 130 135 140                                                  |     |
| TTT GAA GAG AAA TTT TGC TCT AAA GAT TTA ACC CGA TTG CTC CAT TTT  | 483 |
| Phe Glu Glu Lys Phe Cys Ser Lys Asp Leu Thr Arg Leu Leu His Phe  |     |
| 145 150 155                                                      |     |
| GCT TTC AAA TGC GCC GCT AAA GTG CGC AAT TTA ACC GGC ATT TCC AAG  | 531 |
| Ala Phe Lys Cys Ala Ala Lys Val Arg Asn Leu Thr Gly Ile Ser Lys  |     |
| 160 165 170                                                      |     |
| CAA GGG GTT TCC ATC TCT TCA GTG GCG GTC AAA GAA GCG CTT AAT ATT  | 579 |
| Gln Gly Val Ser Ile Ser Ser Val Ala Val Lys Glu Ala Leu Asn Ile  |     |
| 175 180 185                                                      |     |
| TTT GAA AAA GAA AGG ATT AAG GAT AAA AAA GCC CTT GTG ATA GGG CTT  | 627 |
| Phe Glu Lys Glu Arg Ile Lys Asp Lys Lys Ala Leu Val Ile Gly Leu  |     |
| 190 195 200                                                      |     |
| GGC GAG ATG GCT CAA TTA GTC ATC AAG CAC CTT TTA AAC AAG CAA TTT  | 675 |
| Gly Glu Met Ala Gln Leu Val Ile Lys His Leu Leu Asn Lys Gln Phe  |     |
| 205 210 215 220                                                  |     |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| GAA GCG CTT ATC TTA GGG CGT AAT GCG GCT AAA TTT GAA GAT TTC ATC<br>Glu Ala Leu Ile Leu Gly Arg Asn Ala Ala Lys Phe Glu Asp Phe Ile<br>225 230 235     | 723  |
| AAA GAA TTA GAA GAA CCT AAA AAA GTA AGC TTT CAA AAT ATA GAA AAT<br>Lys Glu Leu Glu Glu Pro Lys Lys Val Ser Phe Gln Asn Ile Glu Asn<br>240 245 250     | 771  |
| TTA AAC GCT TAT ATC AAT GAA TAC GAA CTG CTT TTT TGC GCC ACT TCT<br>Leu Asn Ala Tyr Ile Asn Glu Tyr Glu Leu Leu Phe Cys Ala Thr Ser<br>255 260 265     | 819  |
| TCG CCG CAT TTT ATC GTG CAA AAT CGC ATG TTA AAA GAA ACG ATT TTC<br>Ser Pro His Phe Ile Val Gln Asn Arg Met Leu Lys Glu Thr Ile Phe<br>270 275 280     | 867  |
| AGG CGT TTT TGG TTT GAT TTA GCC GTG CCA CGG AAT ATT GAA AAG CCG<br>Arg Arg Phe Trp Phe Asp Leu Ala Val Pro Arg Asn Ile Glu Lys Pro<br>285 290 295 300 | 915  |
| GTA TTG GAT AAT ATT TTC TTA TAC AGC GTT GAT GAT TTA GAG CCT ATG<br>Val Leu Asp Asn Ile Phe Leu Tyr Ser Val Asp Asp Leu Glu Pro Met<br>305 310 315     | 963  |
| GTG AGA GAA AAT GTG GAA AAC AGG CAA GAG AGC AGA ATG AGA GCT TAT<br>Val Arg Glu Asn Val Glu Asn Arg Gln Glu Ser Arg Met Arg Ala Tyr<br>320 325 330     | 1011 |
| GAG ATT GTA GGG CTT GCC ACA ATG GAG TTT TAC CAA TGG ATT CAA AGT<br>Glu Ile Val Gly Leu Ala Thr Met Glu Phe Tyr Gln Trp Ile Gln Ser<br>335 340 345     | 1059 |
| TTA GAA GTA GAG CCT GTG ATT AAG GAT TTA AGG GAA TTG GCT AGG ATT<br>Leu Glu Val Glu Pro Val Ile Lys Asp Leu Arg Glu Leu Ala Arg Ile<br>350 355 360     | 1107 |
| TCA GCC CAA AAA GAA TTG CAA AAA GCG CTT AAA AAA CGC TAT GTG CCT<br>Ser Ala Gln Lys Glu Leu Gln Lys Ala Leu Lys Lys Arg Tyr Val Pro<br>365 370 375 380 | 1155 |
| AAA GAA TAC GAA AAC AAC ATT GAA AAG ATC TTG CAC AAC GCT TTC AAC<br>Lys Glu Tyr Glu Asn Asn Ile Glu Lys Ile Leu His Asn Ala Phe Asn<br>385 390 395     | 1203 |
| ACT TTT TTG CAT AAC CCT ACC ATC GCC TTA AAA AAG AAC GCT CAA AAA<br>Thr Phe Leu His Asn Pro Thr Ile Ala Leu Lys Lys Asn Ala Gln Lys<br>400 405 410     | 1251 |
| GAA GAA TCC GAT GTG CTT GTG GGT GCG ATT AAA AAC TTG TTT AAT TTA<br>Glu Glu Ser Asp Val Leu Val Gly Ala Ile Lys Asn Leu Phe Asn Leu<br>415 420 425     | 1299 |
| GAC AAA TCT AAC GCT AAC CAT GCC CAG AAT TTG AAT CTC TAT AAA TGC<br>Asp Lys Ser Asn Ala Asn His Ala Gln Asn Leu Asn Leu Tyr Lys Cys<br>430 435 440     | 1347 |
| GAA TAT TAC GAG GAA TAATGCATGC TATTTTCAAA ACTCTTTGCC CCCACTCTCA A<br>Glu Tyr Tyr Glu Glu                                                              | 1403 |

## (2) INFORMATION FOR SEQ ID NO:508:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

```

Met Glu Leu Glu Thr His Leu Ser Lys Tyr Phe Thr Leu Ala Phe Thr
 1 5 10 15
His Lys Ser Met Ser Leu Glu Met Arg Glu Lys Leu Ala Ile Asn Ser
 20 25 30
Asn Ala Thr Leu Lys Glu Phe Leu Gln Thr Ile Lys Asn His Cys Pro
 35 40 45
Asn Ile Lys Glu Cys Met Val Leu Ser Thr Cys Asn Arg Phe Glu Ile
 50 55 60
Tyr Ala Ser Leu Lys His Gly Ala Asn Thr Asn Glu Gln Lys Asn Ala
 65 70 75 80
Leu Leu Lys Ile Leu Ala Gln Asn Lys Lys Met Ser Val Ser Asp Leu
 85 90 95
Glu Lys Cys Val Leu Met Asn Thr Asp Glu Ser Ala Val His His Val
100 105 110
Phe Ser Val Cys Ser Ser Leu Asp Ser Leu Val Val Gly Glu Thr Gln
115 120 125
Ile Thr Gly Gln Met Lys Asn Ala Tyr Lys Phe Ala Phe Glu Glu Lys
130 135 140
Phe Cys Ser Lys Asp Leu Thr Arg Leu Leu His Phe Ala Phe Lys Cys
145 150 155 160
Ala Ala Lys Val Arg Asn Leu Thr Gly Ile Ser Lys Gln Gly Val Ser
165 170 175
Ile Ser Ser Val Ala Val Lys Glu Ala Leu Asn Ile Phe Glu Lys Glu
180 185 190
Arg Ile Lys Asp Lys Lys Ala Leu Val Ile Gly Leu Gly Glu Met Ala
195 200 205
Gln Leu Val Ile Lys His Leu Leu Asn Lys Gln Phe Glu Ala Leu Ile
210 215 220
Leu Gly Arg Asn Ala Ala Lys Phe Glu Asp Phe Ile Lys Glu Leu Glu
225 230 235 240
Glu Pro Lys Lys Val Ser Phe Gln Asn Ile Glu Asn Leu Asn Ala Tyr
245 250 255
Ile Asn Glu Tyr Glu Leu Leu Phe Cys Ala Thr Ser Ser Pro His Phe
260 265 270
Ile Val Gln Asn Arg Met Leu Lys Glu Thr Ile Phe Arg Arg Phe Trp
275 280 285
Phe Asp Leu Ala Val Pro Arg Asn Ile Glu Lys Pro Val Leu Asp Asn
290 295 300
Ile Phe Leu Tyr Ser Val Asp Asp Leu Glu Pro Met Val Arg Glu Asn
305 310 315 320
Val Glu Asn Arg Gln Glu Ser Arg Met Arg Ala Tyr Glu Ile Val Gly
325 330 335

```

Leu Ala Thr Met Glu Phe Tyr Gln Trp Ile Gln Ser Leu Glu Val Glu  
 340 345 350  
 Pro Val Ile Lys Asp Leu Arg Glu Leu Ala Arg Ile Ser Ala Gln Lys  
 355 360 365  
 Glu Leu Gln Lys Ala Leu Lys Lys Arg Tyr Val Pro Lys Glu Tyr Glu  
 370 375 380  
 Asn Asn Ile Glu Lys Ile Leu His Asn Ala Phe Asn Thr Phe Leu His  
 385 390 395 400  
 Asn Pro Thr Ile Ala Leu Lys Lys Asn Ala Gln Lys Glu Glu Ser Asp  
 405 410 415  
 Val Leu Val Gly Ala Ile Lys Asn Leu Phe Asn Leu Asp Lys Ser Asn  
 420 425 430  
 Ala Asn His Ala Gln Asn Leu Asn Leu Tyr Lys Cys Glu Tyr Tyr Glu  
 435 440 445  
 Glu

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 40...1125
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AAAACCCAAA CGCCGTTAAA ATATTTAAAA AGGAAATTC ATG CCC ATT GAT TTG  | 54  |
| Met Pro Ile Asp Leu                                             |     |
| 1 5                                                             |     |
| AAC GAA CAT TTA AAA AAG AAA AAT TCT CAA AGA GAA ACC CCC ACG CCT | 102 |
| Asn Glu His Leu Lys Lys Lys Asn Ser Gln Arg Glu Thr Pro Thr Pro |     |
| 10 15 20                                                        |     |
| AAT ACG CCT AAT AAT GGG GGG CGT TTC ATC CCG CCG TCT AAT TCT TTT | 150 |
| Asn Thr Pro Asn Asn Gly Gly Arg Phe Ile Pro Pro Ser Asn Ser Phe |     |
| 25 30 35                                                        |     |
| AAT TCT AAA AAA CTA TCG GTT TTA ATT GTC ATT GTC CTT TTA GGC GTT | 198 |
| Asn Ser Lys Lys Leu Ser Val Leu Ile Val Ile Val Leu Leu Gly Val |     |
| 40 45 50                                                        |     |
| ATC GCT TTT TTG GCC AAG CCT TTT GAA GTG ATT AGC TCA GGA GAA ATT | 246 |
| Ile Ala Phe Leu Ala Lys Pro Phe Glu Val Ile Ser Ser Gly Glu Ile |     |
| 55 60 65                                                        |     |
| GGC ATT AAA ATC ACC GCC GGG AAA TAC GAA CCC ACC CCC TTA CAG CCA | 294 |
| Gly Ile Lys Ile Thr Ala Gly Lys Tyr Glu Pro Thr Pro Leu Gln Pro |     |
| 70 75 80 85                                                     |     |

|                |                |                |                |                |                |                |                 |                |                |                |                |                |                |                |         |     |
|----------------|----------------|----------------|----------------|----------------|----------------|----------------|-----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|---------|-----|
| GGG Gly        | ATC Ile        | CAC His        | TTC Phe        | TTT Phe<br>90  | GTG Val        | CCT Pro        | ATC Ile         | ATT Ile        | CAA Gln<br>95  | GAC Asp        | ATT Ile        | CTC Leu        | ATT Ile        | GTG Val<br>100 | GAT Asp | 342 |
| ACA Thr        | AGG Arg        | ATT Ile        | AGG Arg<br>105 | AAT Asn        | ATC Ile        | AAT Asn        | TTT Phe         | TCA Ser<br>110 | CGC Arg        | ACC Thr        | GAA Glu        | GAC Asp        | ATG Met<br>115 | GGC Gly        | GTG Val | 390 |
| GCG Ala        | GGT Gly        | AAA Lys<br>120 | AAC Asn        | CAA Gln        | GGG Gly        | ATT Ile        | TTT Phe<br>125  | AGA Arg        | AAC Asn        | GAC Asp        | GCT Ala        | ATT Ile<br>130 | AAT Asn        | GTG Val        | ATG Met | 438 |
| GAT Asp        | AGT Ser<br>135 | AGG Arg        | GGT Gly        | TTG Leu        | ACC Thr        | GTT Val<br>140 | TCT Ser         | ATT Ile        | GAA Glu        | CTC Leu        | ACC Thr<br>145 | GTG Val        | CAA Gln        | TAC Tyr        | CGC Arg | 486 |
| TTA Leu<br>150 | AAC Asn        | CCC Pro        | CAA Gln        | ACC Thr<br>155 | ACC Thr        | CCC Pro        | CAA Gln         | ACG Thr        | ATC Ile<br>160 | GCT Ala        | ACT Thr        | TAT Tyr        | GGC Gly        | TTG Leu<br>165 | TCT Ser | 534 |
| TGG Trp        | GAG Glu        | CAA Gln        | AAA Lys<br>170 | ATC Ile        | ATC Ile        | AAC Asn        | CCT Pro         | GTG Val<br>175 | GTG Val        | CGC Arg        | GAT Asp        | GTG Val        | GTG Val<br>180 | CGC Arg        | TCT Ser | 582 |
| GTC Val        | GTG Val        | GGG Gly<br>185 | CGC Arg        | TAT Tyr<br>185 | CCG Pro        | GCT Ala        | GAA Glu<br>190  | GAT Asp        | TTA Leu        | CCC Pro        | ATT Ile        | AAG Lys<br>195 | CGC Arg        | AAT Asn        | GAA Glu | 630 |
| ATC Ile        | GCC Ala<br>200 | GCT Ala        | CTT Leu        | ATT Ile        | AAT Asn        | AGC Ser<br>205 | GGT Gly         | ATC Ile        | AAT Asn        | AAA Lys        | GAA Glu<br>210 | GTT Val        | TCT Ser        | AAG Lys        | CTC Leu | 678 |
| CCT Pro        | AAC Asn<br>215 | ACC Thr        | CCT Pro        | GTG Val        | GAA Glu        | TTA Leu<br>220 | AGC Ser         | TCT Ser        | ATC Ile        | CAA Gln<br>225 | TTG Leu        | AGA Arg        | GAA Glu        | ATC Ile        | GTC Val | 726 |
| TTG Leu<br>230 | CCC Pro        | GCT Ala        | AAG Lys        | ATT Ile        | AAA Lys<br>235 | GAG Glu        | CAA Gln         | ATA Ile        | GAA Glu<br>240 | AAA Lys        | GTC Val        | CAA Gln        | ATC Ile        | GCG Ala<br>245 | CGC Arg | 774 |
| CAA Gln        | GAA Glu        | TCA Ser        | GAA Glu<br>250 | AGG Arg        | GTG Val        | AAA Lys        | TAC Tyr         | GAG Glu<br>255 | GTG Val        | GAG Glu        | CGC Arg        | TCC Ser        | AAG Lys        | CAA Gln<br>260 | GAA Glu | 822 |
| GCT Ala        | CAA Gln        | AAA Lys<br>265 | CAA Gln        | GCC Ala        | GCT Ala        | CTG Leu        | GCT Ala<br>270  | AAA Lys        | GGG Gly        | GAA Glu        | GCG Ala        | GAC Asp<br>275 | GCT Ala        | AAC Asn        | AGG Arg | 870 |
| ATT Ile        | AAG Lys<br>280 | GCT Ala        | CAG Gln        | GGC Gly        | GTG Val        | GCT Ala        | GAT Asp<br>285  | GCG Ala        | ATT Ile        | GTG Val        | ATT Ile<br>290 | GAG Glu        | GCT Ala        | AAG Lys        | GCA Ala | 918 |
| AAA Lys        | TCT Ser<br>295 | CAA Gln        | GCT Ala        | AAT Asn        | TTA Leu        | AGC Ser<br>300 | ATT Ile         | TCG Ser        | CAA Gln        | AGC Ser<br>305 | TTG Leu        | AGC Ser        | GAC Asp        | AAG Lys        | CTT Leu | 966 |
| TTA Leu        | AGA Arg        | CTG Leu        | CGC Arg        | CAA Gln        | ATT Ile        | GAA Glu        | GTT Val<br>1014 | CAA Gln        | GGC Gly        | CAG Gln        | TTT Phe        | AAT Asn        | GAA Glu        | GCG Ala        | TTA Leu |     |





(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Ile | Asp | Leu | Asn | Glu | His | Leu | Lys | Lys | Lys | Asn | Ser | Gln | Arg | 1   | 5   | 10  | 15  |
| Glu | Thr | Pro | Thr | Pro | Asn | Thr | Pro | Asn | Asn | Gly | Gly | Arg | Phe | Ile | Pro | 20  | 25  | 30  |     |
| Pro | Ser | Asn | Ser | Phe | Asn | Ser | Lys | Lys | Leu | Ser | Val | Leu | Ile | Val | Ile | 35  | 40  | 45  |     |
| Val | Leu | Leu | Gly | Val | Ile | Ala | Phe | Leu | Ala | Lys | Pro | Phe | Glu | Val | Ile | 50  | 55  | 60  |     |
| Ser | Ser | Gly | Glu | Ile | Gly | Ile | Lys | Ile | Thr | Ala | Gly | Lys | Tyr | Glu | Pro | 65  | 70  | 75  | 80  |
| Thr | Pro | Leu | Gln | Pro | Gly | Ile | His | Phe | Phe | Val | Pro | Ile | Ile | Gln | Asp | 85  | 90  | 95  |     |
| Ile | Leu | Ile | Val | Asp | Thr | Arg | Ile | Arg | Asn | Ile | Asn | Phe | Ser | Arg | Thr | 100 | 105 | 110 |     |
| Glu | Asp | Met | Gly | Val | Ala | Gly | Lys | Asn | Gln | Gly | Ile | Phe | Arg | Asn | Asp | 115 | 120 | 125 |     |
| Ala | Ile | Asn | Val | Met | Asp | Ser | Arg | Gly | Leu | Thr | Val | Ser | Ile | Glu | Leu | 130 | 135 | 140 |     |
| Thr | Val | Gln | Tyr | Arg | Leu | Asn | Pro | Gln | Thr | Thr | Pro | Gln | Thr | Ile | Ala | 145 | 150 | 155 | 160 |
| Thr | Tyr | Gly | Leu | Ser | Trp | Glu | Gln | Lys | Ile | Ile | Asn | Pro | Val | Val | Arg | 165 | 170 | 175 |     |
| Asp | Val | Val | Arg | Ser | Val | Val | Gly | Arg | Tyr | Pro | Ala | Glu | Asp | Leu | Pro | 180 | 185 | 190 |     |
| Ile | Lys | Arg | Asn | Glu | Ile | Ala | Ala | Leu | Ile | Asn | Ser | Gly | Ile | Asn | Lys | 195 | 200 | 205 |     |
| Glu | Val | Ser | Lys | Leu | Pro | Asn | Thr | Pro | Val | Glu | Leu | Ser | Ser | Ile | Gln | 210 | 215 | 220 |     |
| Leu | Arg | Glu | Ile | Val | Leu | Pro | Ala | Lys | Ile | Lys | Glu | Gln | Ile | Glu | Lys | 225 | 230 | 235 | 240 |
| Val | Gln | Ile | Ala | Arg | Gln | Glu | Ser | Glu | Arg | Val | Lys | Tyr | Glu | Val | Glu | 245 | 250 | 255 |     |
| Arg | Ser | Lys | Gln | Glu | Ala | Gln | Lys | Gln | Ala | Ala | Leu | Ala | Lys | Gly | Glu | 260 | 265 | 270 |     |
| Ala | Asp | Ala | Asn | Arg | Ile | Lys | Ala | Gln | Gly | Val | Ala | Asp | Ala | Ile | Val | 275 | 280 | 285 |     |
| Ile | Glu | Ala | Lys | Ala | Lys | Ser | Gln | Ala | Asn | Leu | Ser | Ile | Ser | Gln | Ser | 290 | 295 | 300 |     |
| Leu | Ser | Asp | Lys | Leu | Leu | Arg | Leu | Arg | Gln | Ile | Glu | Val | Gln | Gly | Gln | 305 | 310 | 315 | 320 |
| Phe | Asn | Glu | Ala | Leu | Lys | Thr | Asn | Asn | Asn | Ala | Gln | Ile | Met | Leu | Thr | 325 | 330 | 335 |     |
| Pro | Gly | Gly | Ala | Val | Pro | Asn | Ile | Trp | Ile | Asp | Thr | Lys | Ser | Lys | Val | 340 | 345 | 350 |     |
| Lys | Ser | Ser | Ile | Ala | Glu | Thr | Lys | Glu | Pro |     |     |     |     |     |     | 355 | 360 |     |     |

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 23...559
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| GACTAAAGAG CCTTAAAAAC GC ATG GCA TCT CTT GCC TTT ATC CAA GCT TTT | 52  |
| Met Ala Ser Leu Ala Phe Ile Gln Ala Phe                          |     |
| 1 5 10                                                           |     |
| TTG GAG TCT TTT AAG GGA TTT TTA AGT CAA GCG ACT CTA ATC AGC GTT  | 100 |
| Leu Glu Ser Phe Lys Gly Phe Leu Ser Gln Ala Thr Leu Ile Ser Val  |     |
| 15 20 25                                                         |     |
| TTA ATA GCG AGC GTT TTA ATC CTT TTT TGC GCG ATT TTG CTC CTT TTG  | 148 |
| Leu Ile Ala Ser Val Leu Ile Leu Phe Cys Ala Ile Leu Leu Leu Leu  |     |
| 30 35 40                                                         |     |
| GCT CTG CTT TTG AGA AAC CGC TTA GCT AGC TAT ATA GCA ACA GCA GCT  | 196 |
| Ala Leu Leu Leu Arg Asn Arg Leu Ala Ser Tyr Ile Ala Thr Ala Ala  |     |
| 45 50 55                                                         |     |
| TTT TTG GGT GCG TTT TTA AGC ATG CCT TTT GTT TTG AAC ATT TTA CTC  | 244 |
| Phe Leu Gly Ala Phe Leu Ser Met Pro Phe Val Leu Asn Ile Leu Leu  |     |
| 60 65 70                                                         |     |
| ACT CAA GCG ATT TAC CCC ATA GAA ACA CGC ATC TTA CAC GCT AAC CCT  | 292 |
| Thr Gln Ala Ile Tyr Pro Ile Glu Thr Arg Ile Leu His Ala Asn Pro  |     |
| 75 80 85 90                                                      |     |
| TTA AGT TAC AGC AAC GCC TTT TCT TTG CAA GTG GGA GTC AAA AAC CAT  | 340 |
| Leu Ser Tyr Ser Asn Ala Phe Ser Leu Gln Val Gly Val Lys Asn His  |     |
| 95 100 105                                                       |     |
| TCC AAA TTT ACT CTA AAC AAA TGC GTT TTA CGC CTA GAA GTG CTT AAA  | 388 |
| Ser Lys Phe Thr Leu Asn Lys Cys Val Leu Arg Leu Glu Val Leu Lys  |     |
| 110 115 120                                                      |     |
| AAC CCT CAC AAT TTT GTA GAA GAG CAT GCT TTT AAA TGG TTT GTC AAA  | 436 |
| Asn Pro His Asn Phe Val Glu Glu His Ala Phe Lys Trp Phe Val Lys  |     |
| 125 130 135                                                      |     |
| AAA AGC TAT GAA AAA ATT TTT AAA GAA AAG ATT TTG CCC AAA GAA TCT  | 484 |
| Lys Ser Tyr Glu Lys Ile Phe Lys Glu Lys Ile Leu Pro Lys Glu Ser  |     |
| 140 145 150                                                      |     |

AAG GTC TTT TCA TTC TTT ATT GAC AAC TAC CCT TAT TCA AAA ACG GCC 532  
 Lys Val Phe Ser Phe Phe Ile Asp Asn Tyr Pro Tyr Ser Lys Thr Ala  
 155 160 165 170

CCT TAT CAA GTT TCT TTG TTT TGT TTA TAAAAAATA AAAGATAACG CCCAAGA 586  
 Pro Tyr Gln Val Ser Leu Phe Cys Leu  
 175

TAACATTTCAT TAAAAAGCGA TTAAAAACGC TTAAAGGCAT AGAT 630

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Leu | Ala | Phe | Ile | Gln | Ala | Phe | Leu | Glu | Ser | Phe | Lys | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Leu | Ser | Gln | Ala | Thr | Leu | Ile | Ser | Val | Leu | Ile | Ala | Ser | Val | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Leu | Phe | Cys | Ala | Ile | Leu | Leu | Leu | Leu | Ala | Leu | Leu | Leu | Arg | Asn |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Leu | Ala | Ser | Tyr | Ile | Ala | Thr | Ala | Ala | Phe | Leu | Gly | Ala | Phe | Leu |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ser | Met | Pro | Phe | Val | Leu | Asn | Ile | Leu | Leu | Thr | Gln | Ala | Ile | Tyr | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Glu | Thr | Arg | Ile | Leu | His | Ala | Asn | Pro | Leu | Ser | Tyr | Ser | Asn | Ala |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Phe | Ser | Leu | Gln | Val | Gly | Val | Lys | Asn | His | Ser | Lys | Phe | Thr | Leu | Asn |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Lys | Cys | Val | Leu | Arg | Leu | Glu | Val | Leu | Lys | Asn | Pro | His | Asn | Phe | Val |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Glu | His | Ala | Phe | Lys | Trp | Phe | Val | Lys | Lys | Ser | Tyr | Glu | Lys | Ile |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Lys | Glu | Lys | Ile | Leu | Pro | Lys | Glu | Ser | Lys | Val | Phe | Ser | Phe | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ile | Asp | Asn | Tyr | Pro | Tyr | Ser | Lys | Thr | Ala | Pro | Tyr | Gln | Val | Ser | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe | Cys | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 47...1273  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AAAGAATGAT CTTAAAAGGG CAAACCACAT TTATTAAGGA GAATGC ATG CAA GAA  | 55  |
| Met Gln Glu                                                     |     |
| 1                                                               |     |
| ATC ATA GGA GCG TCT TTA GTT TTT TTG TGC AAT GAA AAG TGC GAA GTG | 103 |
| Ile Ile Gly Ala Ser Leu Val Phe Leu Cys Asn Glu Lys Cys Glu Val |     |
| 5 10 15                                                         |     |
| TTA GAA GAT TAT GGC GTA GTC TTT GAT GAA AAG ATT GTT GAA ATA GGC | 151 |
| Leu Glu Asp Tyr Gly Val Val Phe Asp Glu Lys Ile Val Glu Ile Gly |     |
| 20 25 30 35                                                     |     |
| GAT TAT CAA AGT TTA ACG CTT AAA TAC CCT CAC TTA AAG GCG CAG TTT | 199 |
| Asp Tyr Gln Ser Leu Thr Leu Lys Tyr Pro His Leu Lys Ala Gln Phe |     |
| 40 45 50                                                        |     |
| TTT GAA AAT TCC GTT CTG TTG CCC GCT TTT ATC AAC GCG CAC ACC CAT | 247 |
| Phe Glu Asn Ser Val Leu Leu Pro Ala Phe Ile Asn Ala His Thr His |     |
| 55 60 65                                                        |     |
| TTT GAA TTT TCC AAC AAC AAG GCG AGT TTT GAT TAC GGG AGT TTT TCT | 295 |
| Phe Glu Phe Ser Asn Asn Lys Ala Ser Phe Asp Tyr Gly Ser Phe Ser |     |
| 70 75 80                                                        |     |
| GGC TGG TTA GGG AGC GTG TTA AAC AAT GGG GGG GCG ATT TTA GAA AAT | 343 |
| Gly Trp Leu Gly Ser Val Leu Asn Asn Gly Gly Ala Ile Leu Glu Asn |     |
| 85 90 95                                                        |     |
| TGC CAA GGG GCT ATT CAA AAC GCT ATC AGC ACG CAA TTA AAA AGC GGG | 391 |
| Cys Gln Gly Ala Ile Gln Asn Ala Ile Ser Thr Gln Leu Lys Ser Gly |     |
| 100 105 110 115                                                 |     |
| GTG GGG AGC GTG GGA GCG ATT TCT AAC CAC CTG ATA GAA GTT AAT TTG | 439 |
| Val Gly Ser Val Gly Ala Ile Ser Asn His Leu Ile Glu Val Asn Leu |     |
| 120 125 130                                                     |     |
| TTA AAA GAA AGC CCT TTG AAT GCT GTC GTG TTT TTA GAG TTT TTA GGG | 487 |
| Leu Lys Glu Ser Pro Leu Asn Ala Val Val Phe Leu Glu Phe Leu Gly |     |
| 135 140 145                                                     |     |
| AGC AGT TAT TCT TTA GAA AAA TTA AAA GCG TTT GAG GCC AAA TTT AAG | 535 |
| Ser Ser Tyr Ser Leu Glu Lys Leu Lys Ala Phe Glu Ala Lys Phe Lys |     |
| 150 155 160                                                     |     |
| GAA TTA AAA GAT TTA GAA GAT AAA AAA CTT AAA GCG GCT CTC GCT GTG | 583 |
| Glu Leu Lys Asp Leu Glu Asp Lys Lys Leu Lys Ala Ala Leu Ala Val |     |
| 165 170 175                                                     |     |
| CAT GCC CCT TAT TCG GTC CAA AAA GAC ATG GCT TTG AGC GTC ATC CAA | 631 |
| His Ala Pro Tyr Ser Val Gln Lys Asp Met Ala Leu Ser Val Ile Gln |     |
| 180 185 190 195                                                 |     |

|     |     |     |     |     |     |     |     |     |     |     |       |     |     |     |     |  |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-------|-----|-----|-----|-----|--|------|
| TTA | GCC | AAA | GAT | TCA | CAA | AGC | CTG | CTT | TCT | ACG | CAT   | TTT | TTA | GAA | TCG |  | 679  |
| Leu | Ala | Lys | Asp | Ser | Gln | Ser | Leu | Leu | Ser | Thr | His   | Phe | Leu | Glu | Ser |  |      |
|     |     |     |     | 200 |     |     |     |     | 205 |     |       |     |     | 210 |     |  |      |
| CTT | GAA | GAA | TTA | GAA | TGG | GTA | GAA | AAC | TCT | AAA | GGG   | TGG | TTT | GAA | AAT |  | 727  |
| Leu | Glu | Glu | Leu | Glu | Trp | Val | Glu | Asn | Ser | Lys | Gly   | Trp | Phe | Glu | Asn |  |      |
|     |     |     | 215 |     |     |     |     | 220 |     |     |       |     | 225 |     |     |  |      |
| TTT | TAC | CAG | CAT | TTT | TTA | AAG | GAG | TCT | CAT | TTC | AAA   | TCG | CTC | TAT | AAG |  | 775  |
| Phe | Tyr | Gln | His | Phe | Leu | Lys | Glu | Ser | His | Phe | Lys   | Ser | Leu | Tyr | Lys |  |      |
|     |     | 230 |     |     |     |     | 235 |     |     |     |       | 240 |     |     |     |  |      |
| GGC | GCG | AAC | GAT | TAC | ATT | GAC | ATG | TTT | AAA | GAC | ACG   | CAC | ACT | TTA | TTC |  | 823  |
| Gly | Ala | Asn | Asp | Tyr | Ile | Asp | Met | Phe | Lys | Asp | Thr   | His | Thr | Leu | Phe |  |      |
|     | 245 |     |     |     |     | 250 |     |     |     |     | 255   |     |     |     |     |  |      |
| GTG | CAT | AAC | CAG | TTC | GCT | TCT | TTA | GAA | GCG | TTA | AAA   | AGG | ATT | AAA | TCT |  | 871  |
| Val | His | Asn | Gln | Phe | Ala | Ser | Leu | Glu | Ala | Leu | Lys   | Arg | Ile | Lys | Ser |  |      |
| 260 |     |     |     | 265 |     |     |     | 270 |     |     |       |     |     | 275 |     |  |      |
| CAA | GTC | AAA | AAC | GCT | TTT | TTA | ATC | ACA | TGC | CCC | TTT   | TCT | AAC | CGC | CTA |  | 919  |
| Gln | Val | Lys | Asn | Ala | Phe | Leu | Ile | Thr | Cys | Pro | Phe   | Ser | Asn | Arg | Leu |  |      |
|     |     |     | 280 |     |     |     |     | 285 |     |     |       |     |     | 290 |     |  |      |
| TTG | AGC | GGG | CAA | GCG | TTG | GAT | TTA | GAA | AGA | ACT | AAA   | GAA | GCC | GGT | TTG |  | 967  |
| Leu | Ser | Gly | Gln | Ala | Leu | Asp | Leu | Glu | Arg | Thr | Lys   | Glu | Ala | Gly | Leu |  |      |
|     |     | 295 |     |     |     |     | 300 |     |     |     |       | 305 |     |     |     |  |      |
| AGC | GTG | AGC | GTG | GCC | ACT | GAT | GGC | TTG | AGT | TCT | AAC   | ATT | TCG | CTG | AGC |  | 1015 |
| Ser | Val | Ser | Val | Ala | Thr | Asp | Gly | Leu | Ser | Ser | Asn   | Ile | Ser | Leu | Ser |  |      |
|     | 310 |     |     |     |     | 315 |     |     |     |     |       | 320 |     |     |     |  |      |
| CTT | TTA | GAC | GAA | TTA | AGA | GCG | TTT | TTG | CTC | ACC | CAT   | AAC | ATG | CCG | TTA |  | 1063 |
| Leu | Leu | Asp | Glu | Leu | Arg | Ala | Phe | Leu | Leu | Thr | His   | Asn | Met | Pro | Leu |  |      |
|     | 325 |     |     |     |     | 330 |     |     |     |     | 335   |     |     |     |     |  |      |
| TTA | GAA | TTA | GCT | AAA | ATA | GCC | CTT | TTA | GGG | GCG | ACT   | AGG | CAT | GGG | GCT |  | 1111 |
| Leu | Glu | Leu | Ala | Lys | Ile | Ala | Leu | Leu | Gly | Ala | Thr   | Arg | His | Gly | Ala |  |      |
| 340 |     |     |     | 345 |     |     |     |     | 350 |     |       |     |     | 355 |     |  |      |
| AAA | GCT | TTA | GCT | TTG | AAT | AAT | GGC | GAG | ATA | GAA | GCC   | AAC | AAA | AGG | GCG |  | 1159 |
| Lys | Ala | Leu | Ala | Leu | Asn | Asn | Gly | Glu | Ile | Glu | Ala   | Asn | Lys | Arg | Ala |  |      |
|     |     |     | 360 |     |     |     | 365 |     |     |     |       |     | 370 |     |     |  |      |
| GAT | TTG | AGC | GTG | TTT | GGT | TTT | AAT | GAA | AAA | TTC | ACT   | AAA | GAG | CAA | GCG |  | 1207 |
| Asp | Leu | Ser | Val | Phe | Gly | Phe | Asn | Glu | Lys | Phe | Thr   | Lys | Glu | Gln | Ala |  |      |
|     |     | 375 |     |     |     |     | 380 |     |     |     |       | 385 |     |     |     |  |      |
| ATT | TTG | CAA | TTT | TTA | TTG | CAT | GCT | AAA | GAA | GTG | GAG   | TGC | TTG | TTT | TTA |  | 1255 |
| Ile | Leu | Gln | Phe | Leu | Leu | His | Ala | Lys | Glu | Val | Glu</ |     |     |     |     |  |      |

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Gln | Glu | Ile | Ile | Gly | Ala | Ser | Leu | Val | Phe | Leu | Cys | Asn | Glu | Lys | 1   | 5   | 10  | 15 |
| Cys | Glu | Val | Leu | Glu | Asp | Tyr | Gly | Val | Val | Phe | Asp | Glu | Lys | Ile | Val | 20  | 25  | 30  |    |
| Glu | Ile | Gly | Asp | Tyr | Gln | Ser | Leu | Thr | Leu | Lys | Tyr | Pro | His | Leu | Lys | 35  | 40  | 45  |    |
| Ala | Gln | Phe | Phe | Glu | Asn | Ser | Val | Leu | Leu | Pro | Ala | Phe | Ile | Asn | Ala | 50  | 55  | 60  |    |
| His | Thr | His | Phe | Glu | Phe | Ser | Asn | Asn | Lys | Ala | Ser | Phe | Asp | Tyr | Gly | 65  | 70  | 75  |    |
| Ser | Phe | Ser | Gly | Trp | Leu | Gly | Ser | Val | Leu | Asn | Asn | Gly | Gly | Ala | Ile | 85  | 90  | 95  |    |
| Leu | Glu | Asn | Cys | Gln | Gly | Ala | Ile | Gln | Asn | Ala | Ile | Ser | Thr | Gln | Leu | 100 | 105 | 110 |    |
| Lys | Ser | Gly | Val | Gly | Ser | Val | Gly | Ala | Ile | Ser | Asn | His | Leu | Ile | Glu | 115 | 120 | 125 |    |
| Val | Asn | Leu | Leu | Lys | Glu | Ser | Pro | Leu | Asn | Ala | Val | Val | Phe | Leu | Glu | 130 | 135 | 140 |    |
| Phe | Leu | Gly | Ser | Ser | Tyr | Ser | Leu | Glu | Lys | Leu | Lys | Ala | Phe | Glu | Ala | 145 | 150 | 155 |    |
| Lys | Phe | Lys | Glu | Leu | Lys | Asp | Leu | Glu | Asp | Lys | Lys | Leu | Lys | Ala | Ala | 165 | 170 | 175 |    |
| Leu | Ala | Val | His | Ala | Pro | Tyr | Ser | Val | Gln | Lys | Asp | Met | Ala | Leu | Ser | 180 | 185 | 190 |    |
| Val | Ile | Gln | Leu | Ala | Lys | Asp | Ser | Gln | Ser | Leu | Leu | Ser | Thr | His | Phe | 195 | 200 | 205 |    |
| Leu | Glu | Ser | Leu | Glu | Glu | Leu | Glu | Trp | Val | Glu | Asn | Ser | Lys | Gly | Trp | 210 | 215 | 220 |    |
| Phe | Glu | Asn | Phe | Tyr | Gln | His | Phe | Leu | Lys | Glu | Ser | His | Phe | Lys | Ser | 225 | 230 | 235 |    |
| Leu | Tyr | Lys | Gly | Ala | Asn | Asp | Tyr | Ile | Asp | Met | Phe | Lys | Asp | Thr | His | 245 | 250 | 255 |    |
| Thr | Leu | Phe | Val | His | Asn | Gln | Phe | Ala | Ser | Leu | Glu | Ala | Leu | Lys | Arg | 260 | 265 | 270 |    |
| Ile | Lys | Ser | Gln | Val | Lys | Asn | Ala | Phe | Leu | Ile | Thr | Cys | Pro | Phe | Ser | 275 | 280 | 285 |    |
| Asn | Arg | Leu | Leu | Ser | Gly | Gln | Ala | Leu | Asp | Leu | Glu | Arg | Thr | Lys | Glu | 290 | 295 | 300 |    |
| Ala | Gly | Leu | Ser | Val | Ser | Val | Ala | Thr | Asp | Gly | Leu | Ser | Ser | Asn | Ile | 305 | 310 | 315 |    |
| Ser | Leu | Ser | Leu | Leu | Asp | Glu | Leu | Arg | Ala | Phe | Leu | Leu | Thr | His | Asn | 325 | 330 | 335 |    |
| Met | Pro | Leu | Leu | Glu | Leu | Ala | Lys | Ile | Ala | Leu | Leu | Gly | Ala | Thr | Arg | 340 | 345 | 350 |    |
| His | Gly | Ala | Lys | Ala | Leu | Ala | Leu | Asn | Asn | Gly | Glu | Ile | Glu | Ala | Asn | 355 | 360 | 365 |    |





|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| Ala               | Phe               | Glu               | Phe               | Phe<br>125        | Glu               | Lys               | Lys               | Ala               | Gln<br>130        | Ile               | Arg               | Ser               | Leu               | Leu<br>135        | Asn               |      |
| ATC<br>Ile        | TCT<br>Ser        | ATA<br>Ile        | GGG<br>Gly<br>140 | TGC<br>Cys        | GAT<br>Asp        | AAG<br>Lys        | AAA<br>Lys        | TGC<br>Cys<br>145 | GCT<br>Ala        | TAT<br>Tyr        | TGC<br>Cys        | ATC<br>Ile        | GTC<br>Val<br>150 | CCG<br>Pro        | CAC<br>His        | 486  |
| ACT<br>Thr        | AGG<br>Arg        | GGG<br>Gly<br>155 | AAA<br>Lys        | GAA<br>Glu        | ATT<br>Ile        | TCT<br>Ser        | ATC<br>Ile<br>160 | CCT<br>Pro        | ATG<br>Met        | GAT<br>Asp        | TTG<br>Leu        | ATT<br>Ile<br>165 | TTA<br>Leu        | AAA<br>Lys        | GAA<br>Glu        | 534  |
| GCT<br>Ala        | GAG<br>Glu<br>170 | AAA<br>Lys        | TTA<br>Leu        | GCG<br>Ala        | AAT<br>Asn        | AAC<br>Asn<br>175 | GGC<br>Gly        | ACC<br>Thr        | AAA<br>Lys        | GAG<br>Glu        | CTT<br>Leu<br>180 | ATG<br>Met        | CTT<br>Leu        | TTA<br>Leu        | GGG<br>Gly        | 582  |
| CAG<br>Gln<br>185 | AAT<br>Asn        | GTG<br>Val        | AAT<br>Asn        | AAT<br>Asn        | TAC<br>Tyr<br>190 | GGC<br>Gly        | GCG<br>Ala        | CGT<br>Arg        | TTC<br>Phe<br>195 | AGC<br>Ser        | AGC<br>Ser        | GAG<br>Glu        | CAT<br>His        | GCG<br>Ala        | AAA<br>Lys<br>200 | 630  |
| GTG<br>Val        | GAT<br>Asp        | TTT<br>Phe        | AGC<br>Ser<br>205 | GAT<br>Asp        | TTG<br>Leu        | TTG<br>Leu        | GAT<br>Asp        | AAA<br>Lys<br>210 | TTG<br>Leu        | AGC<br>Ser        | GAA<br>Glu        | ATC<br>Ile        | CAG<br>Gln<br>215 | GGG<br>Gly        | ATT<br>Ile        | 678  |
| GAA<br>Glu        | AGG<br>Arg        | ATA<br>Ile<br>220 | CGA<br>Arg        | TTC<br>Phe        | ACT<br>Thr        | TCG<br>Ser        | CCT<br>Pro        | CAC<br>His<br>225 | CCC<br>Pro        | TTG<br>Leu        | CAC<br>His        | ATG<br>Met<br>230 | AAT<br>Asn<br>230 | GAT<br>Asp        | GGA<br>Gly        | 726  |
| TTT<br>Phe        | TTA<br>Leu<br>235 | GAG<br>Glu        | CGT<br>Arg        | TTT<br>Phe        | GCC<br>Ala        | AAA<br>Lys<br>240 | AAC<br>Asn        | CCT<br>Pro        | AAA<br>Lys        | GTG<br>Val        | TGC<br>Cys<br>245 | AAG<br>Lys<br>245 | AGT<br>Ser        | ATC<br>Ile        | CAC<br>His        | 774  |
| ATG<br>Met        | CCT<br>Pro<br>250 | TTA<br>Leu        | CAG<br>Gln        | AGC<br>Ser        | GGA<br>Gly<br>255 | TCT<br>Ser<br>255 | AGC<br>Ser        | GCG<br>Ala        | GTG<br>Val        | TTA<br>Leu<br>260 | AAG<br>Lys<br>260 | ATG<br>Met        | ATG<br>Met        | CGA<br>Arg        | AGG<br>Arg        | 822  |
| GGT<br>Gly<br>265 | TAT<br>Tyr        | AGT<br>Ser        | AAG<br>Lys        | GAG<br>Glu        | TGG<br>Trp<br>270 | TTT<br>Phe        | TTA<br>Leu        | AAT<br>Asn        | AGG<br>Arg        | GTG<br>Val<br>275 | GAG<br>Glu        | AGG<br>Arg        | TTA<br>Leu        | AAA<br>Lys        | GCT<br>Ala<br>280 | 870  |
| TTA<br>Leu        | GTG<br>Val        | CCT<br>Pro        | GAA<br>Glu<br>285 | GTG<br>Val<br>285 | GGC<br>Gly        | ATT<br>Ile        | AGC<br>Ser        | ACG<br>Thr        | GAT<br>Asp<br>290 | ATT<br>Ile        | ATC<br>Ile        | GTA<br>Val        | GGC<br>Gly<br>295 | TTC<br>Phe<br>295 | CCT<br>Pro        | 918  |
| AAT<br>Asn        | GAG<br>Glu        | AGC<br>Ser<br>300 | GAT<br>Asp        | AAG<br>Lys        | GAT<br>Asp        | TTT<br>Phe        | GAA<br>Glu        | GAC<br>Asp<br>305 | ACA<br>Thr        | ATG<br>Met        | GAG<br>Glu        | GTG<br>Val<br>310 | CTA<br>Leu        | GAA<br>Glu        | AAA<br>Lys        | 966  |
| GTG<br>Val        | CGC<br>Arg<br>315 | TTT<br>Phe        | GAC<br>Asp        | ACG<br>Thr        | CTC<br>Leu        | TAT<br>Tyr<br>320 | AGT<br>Ser        | TTC<br>Phe        | ATT<br>Ile        | TAT<br>Tyr        | TCC<br>Ser<br>325 | CCA<br>Pro<br>325 | CGC<br>Arg        | CCT<br>Pro        | TTC<br>Phe        | 1014 |
| ACT<br>Thr        | GAA<br>Glu<br>330 | GCG<br>Ala        | GGA<br>Gly        | GCT<br>Ala        | TGG<br>Trp<br>335 | AAG<br>Lys<br>335 | GAA<br>Glu        | AGA<br>Arg        | GTG<br>Val        | CCG<br>Pro<br>340 | TTA<br>Leu<br>340 | GAA<br>Glu        | GTT<br>Val        | TCA<br>Ser        | TCT<br>Ser        | 1062 |
| TCA<br>Ser<br>345 | AGG<br>Arg        | TTG<br>Leu        | GAG<br>Glu        | AGG<br>Arg<br>350 | TTG<br>Leu<br>350 | CAA<br>Gln        | AAC<br>Asn        | AGG<br>Arg        | CAC<br>His<br>355 | AAA<br>Lys<br>355 | GAA<br>Glu        | ATT<br>Ile        | TTA<br>Leu        | GAA<br>Glu        | GAA<br>Glu<br>360 | 1110 |





| 20                |                   |                   |                   | 25                |                   |                   |                   | 30                |                   |                   |                   | 35                |                   |                   |                   |     |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| TCT<br>Ser        | AAG<br>Lys        | GTT<br>Val        | AGG<br>Arg        | ATT<br>Ile<br>40  | TCA<br>Ser        | GAG<br>Glu        | GGC<br>Gly        | TGT<br>Cys        | TAT<br>Tyr<br>45  | GCG<br>Ala        | TTT<br>Phe        | AAT<br>Asn        | GGA<br>Gly        | ATC<br>Ile<br>50  | TTG<br>Leu        | 202 |
| CAA<br>Gln        | GAA<br>Glu        | ATC<br>Ile        | CCC<br>Pro<br>55  | ATG<br>Met        | CAA<br>Gln        | CGA<br>Arg        | GCC<br>Ala        | GTT<br>Val<br>60  | AAA<br>Lys        | GCC<br>Ala        | TTG<br>Leu        | AGC<br>Ser        | GAA<br>Glu<br>65  | TTT<br>Phe        | AAA<br>Lys        | 250 |
| GAA<br>Glu        | ATC<br>Ile        | GCT<br>Ala<br>70  | CTC<br>Leu        | AAA<br>Lys        | TAC<br>Tyr        | AAA<br>Lys        | AGC<br>Ser<br>75  | AAA<br>Lys        | AAA<br>Lys        | ATC<br>Ile        | CTG<br>Leu        | TGC<br>Cys<br>80  | GTG<br>Val        | GCG<br>Ala        | ACC<br>Thr        | 298 |
| TCA<br>Ser        | GCG<br>Ala<br>85  | GTG<br>Val        | CGC<br>Arg        | GAT<br>Asp        | GCC<br>Ala        | CCT<br>Pro<br>90  | AAT<br>Asn        | CGG<br>Arg        | CTG<br>Leu        | GAG<br>Glu        | TTT<br>Phe<br>95  | GTA<br>Val        | GCG<br>Ala        | AGG<br>Arg        | GTG<br>Val        | 346 |
| AAA<br>Lys<br>100 | AAG<br>Lys        | GCT<br>Ala        | TGC<br>Cys        | GGT<br>Gly<br>105 | TTG<br>Leu<br>105 | CAA<br>Gln        | ATC<br>Ile        | AAA<br>Lys        | ATC<br>Ile<br>110 | ATT<br>Ile<br>110 | GAT<br>Asp        | GGG<br>Gly        | CAA<br>Gln        | AAA<br>Lys        | GAA<br>Glu<br>115 | 394 |
| GCG<br>Ala        | CTC<br>Leu        | TAT<br>Tyr        | GGC<br>Gly<br>120 | GGG<br>Gly<br>120 | ATT<br>Ile        | GCG<br>Ala        | TGC<br>Cys        | GCG<br>Ala        | AAT<br>Asn<br>125 | TTG<br>Leu<br>125 | TTG<br>Leu        | CAT<br>His        | AAA<br>Lys        | AAT<br>Asn<br>130 | TCA<br>Ser        | 442 |
| GGG<br>Gly        | ATC<br>Ile        | ACG<br>Thr<br>135 | ATA<br>Ile        | GAT<br>Asp<br>135 | ATT<br>Ile        | GGA<br>Gly<br>140 | GGG<br>Gly<br>140 | GGT<br>Gly<br>140 | AGC<br>Ser        | ACC<br>Thr        | GAG<br>Glu<br>145 | TGC<br>Cys<br>145 | GCG<br>Ala<br>145 | TTG<br>Leu        | ATT<br>Ile        | 490 |
| GAA<br>Glu        | AAA<br>Lys        | GGC<br>Gly<br>150 | AAG<br>Lys        | ATT<br>Ile        | AAG<br>Lys        | GAC<br>Asp<br>155 | TTA<br>Leu<br>155 | ATC<br>Ile        | TCG<br>Ser        | CTT<br>Leu        | GAT<br>Asp<br>160 | GTT<br>Val<br>160 | GGG<br>Gly        | ACG<br>Thr        | ATT<br>Ile        | 538 |
| CGC<br>Arg        | ATT<br>Ile<br>165 | AAA<br>Lys        | GAA<br>Glu        | ATG<br>Met        | TTT<br>Phe<br>170 | TTA<br>Leu<br>170 | GAC<br>Asp<br>170 | AAA<br>Lys        | GAC<br>Asp<br>175 | TTA<br>Leu<br>175 | GAG<br>Glu<br>175 | GTC<br>Val<br>175 | AAA<br>Lys        | TTG<br>Leu        | GCT<br>Ala        | 586 |
| AAA<br>Lys<br>180 | GCC<br>Ala        | TTT<br>Phe        | ATC<br>Ile        | CAA<br>Gln<br>185 | AAA<br>Lys<br>185 | GAA<br>Glu<br>185 | GTC<br>Val        | TCT<br>Ser        | AAA<br>Lys<br>190 | CTG<br>Leu<br>190 | CCC<br>Pro        | TTT<br>Phe        | AAA<br>Lys        | CAC<br>His        | AAA<br>Lys<br>195 | 634 |
| AAC<br>Asn        | GCC<br>Ala        | TTT<br>Phe        | GGG<br>Gly<br>200 | GTG<br>Val<br>200 | GGG<br>Gly<br>200 | GGG<br>Gly<br>200 | ACG<br>Thr        | ATC<br>Ile        | AGA<br>Arg<br>205 | GCG<br>Ala<br>205 | TTG<br>Leu        | AGT<br>Ser        | AAG<br>Lys        | GTA<br>Val<br>210 | TTG<br>Leu        | 682 |
| ATG<br>Met        | AAA<br>Lys        | CGC<br>Arg<br>215 | TTT<br>Phe<br>215 | TGT<br>Cys        | TAC<br>Tyr        | CCT<br>Pro        | ATT<br>Ile<br>220 | GAT<br>Asp<br>220 | TCT<br>Ser<br>220 | TTG<br>Leu<br>220 | CAT<br>His        | GGC<br>Gly<br>225 | TAT<br>Tyr<br>225 | GAA<br>Glu        | ATA<br>Ile        | 730 |
| GAT<br>Asp        | GCA<br>Ala        | CAT<br>His<br>230 | AAA<br>Lys        | AAT<br>Asn        | TTA<br>Leu        | GCG<br>Ala        | TTC<br>Phe<br>235 | ATT<br>Ile<br>235 | GAA<br>Glu        | AAA<br>Lys        | ATC<br>Ile<br>240 | GTC<br>Val<br>240 | ATG<br>Met        | CTC<br>Leu        | AAA<br>Lys        | 778 |
| GAA<br>Glu<br>245 | GAT<br>Asp<br>245 | CAA<br>Gln        | TTA<br>Leu        | CGG<br>Arg        | CTT<br>Leu<br>250 | TTA<br>Leu<br>250 | GGG<br>Gly<br>250 | GTG<br>Val        | AAT<br>Asn        | GAA<br>Glu<br>255 | GAG<br>Glu<br>255 | CGT<br>Arg        | TTG<br>Leu        | GAT<br>Asp        | AGC<br>Ser        | 826 |

|     |     |     |     |     |     |     |     |     |     |     |       |     |     |     |     |  |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-------|-----|-----|-----|-----|--|------|
| ATC | AGG | AGC | GGG | GCG | TTG | ATT | TTA | TCA | GTC | GTT | TTG   | GAG | CAT | TTA | AAA |  | 874  |
| Ile | Arg | Ser | Gly | Ala | Leu | Ile | Leu | Ser | Val | Val | Leu   | Glu | His | Leu | Lys |  |      |
| 260 |     |     |     |     | 265 |     |     |     |     | 270 |       |     |     |     | 275 |  |      |
| ACT | TCT | TTA | ATG | ATC | ACT | AGT | GGG | GTG | GGG | GTG | AGA   | GAA | GGC | GTG | TTT |  | 922  |
| Thr | Ser | Leu | Met | Ile | Thr | Ser | Gly | Val | Gly | Val | Arg   | Glu | Gly | Val | Phe |  |      |
|     |     |     |     | 280 |     |     |     |     | 285 |     |       |     |     | 290 |     |  |      |
| TTG | AGC | GAT | TTA | TTG | CGC | CAT | CAT | TAC | CAT | AAA | TTC   | CCC | CCC | AAT | ATC |  | 970  |
| Leu | Ser | Asp | Leu | Leu | Arg | His | His | Tyr | His | Lys | Phe   | Pro | Pro | Asn | Ile |  |      |
|     |     |     | 295 |     |     |     |     | 300 |     |     |       |     | 305 |     |     |  |      |
| AAC | CCC | TCT | CTC | ATC | TCT | TTA | AAA | GAT | CGC | TTT | TTG   | CCC | CAT | GAA | AAG |  | 1018 |
| Asn | Pro | Ser | Leu | Ile | Ser | Leu | Lys | Asp | Arg | Phe | Leu   | Pro | His | Glu | Lys |  |      |
|     |     | 310 |     |     |     |     | 315 |     |     |     |       | 320 |     |     |     |  |      |
| CAC | AGC | CAA | AAG | GTC | AAA | AAA | GAA | TGC | GTG | AAA | TTG   | TTT | GAA | GCC | TTA |  | 1066 |
| His | Ser | Gln | Lys | Val | Lys | Lys | Glu | Cys | Val | Lys | Leu   | Phe | Glu | Ala | Leu |  |      |
|     | 325 |     |     |     |     | 330 |     |     |     |     | 335   |     |     |     |     |  |      |
| TCG | CCT | TTG | CAT | AAA | ATA | GAT | GAA | AAA | TAC | CTT | TTC   | CAT | TTA | AAG | ATT |  | 1114 |
| Ser | Pro | Leu | His | Lys | Ile | Asp | Glu | Lys | Tyr | Leu | Phe   | His | Leu | Lys | Ile |  |      |
| 340 |     |     |     |     | 345 |     |     |     |     | 350 |       |     |     |     | 355 |  |      |
| GCG | GGG | GAA | TTA | GCG | AGC | ATG | GGT | AAG | ATT | TTA | AGC   | GTC | TAT | TTA | GCC |  | 1162 |
| Ala | Gly | Glu | Leu | Ala | Ser | Met | Gly | Lys | Ile | Leu | Ser   | Val | Tyr | Leu | Ala |  |      |
|     |     |     |     | 360 |     |     |     |     | 365 |     |       |     |     | 370 |     |  |      |
| CAC | AAG | CAC | AGC | GCG | TAT | TTT | ATT | TTA | AAC | GCT | TTG   | AGT | TAT | GGC | TTT |  | 1210 |
| His | Lys | His | Ser | Ala | Tyr | Phe | Ile | Leu | Asn | Ala | Leu   | Ser | Tyr | Gly | Phe |  |      |
|     |     |     | 375 |     |     |     |     | 380 |     |     |       |     | 385 |     |     |  |      |
| AGC | CAC | CAG | GAT | AGA | GCG | ATC | ATT | TGC | TTA | TTA | GCC   | CAA | TTC | AGC | CAT |  | 1258 |
| Ser | His | Gln | Asp | Arg | Ala | Ile | Ile | Cys | Leu | Leu | Ala   | Gln | Phe | Ser | His |  |      |
|     |     | 390 |     |     |     |     | 395 |     |     |     |       | 400 |     |     |     |  |      |
| AAA | AAA | ATC | CCT | AAA | GAC | AAC | GCT | ATC | GCC | CAC | ATG   | AGC | GCG | ATG | ATG |  | 1306 |
| Lys | Lys | Ile | Pro | Lys | Asp | Asn | Ala | Ile | Ala | His | Met   | Ser | Ala | Met | Met |  |      |
|     | 405 |     |     |     |     | 410 |     |     |     |     | 415   |     |     |     |     |  |      |
| CCA | AGC | CTT | TTA | ACC | TTA | CAA | TGG | CTG | AGT | TTT | ATC   | CTT | TCT | TTA | GCC |  | 1354 |
| Pro | Ser | Leu | Leu | Thr | Leu | Gln | Trp | Leu | Ser | Phe | Ile   | Leu | Ser | Leu | Ala |  |      |
| 420 |     |     |     |     | 425 |     |     |     |     | 430 |       |     |     |     | 435 |  |      |
| GAA | AAT | TTG | TGC | CTA | ACA | GAC | AGC | CAT | CAT | TTA | AAA   | TAC | ACG | CTA | GAA |  | 1402 |
| Glu | Asn | Leu | Cys | Leu | Thr | Asp | Ser | His | His | Leu | Lys   | Tyr | Thr | Leu | Glu |  |      |
|     |     |     |     | 440 |     |     |     |     | 445 |     |       |     |     | 450 |     |  |      |
| AAA | AAC | AAG | CTT | GTG | ATC | CAT | TCT | AAT | GAC | ACG | CTT   | TAC | TTG | GCT | AAA |  | 1450 |
| Lys | Asn | Lys | Leu | Val | Ile | His | Ser | Asn | Asp | Thr | Leu</ |     |     |     |     |  |      |

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Lys | Ile | Thr | Thr | Val | Ile | Asp | Ile | Gly | Ser | Asn | Ser | Val | Arg | 1   | 5   | 10  | 15  |
| Leu | Ala | Val | Phe | Lys | Lys | Thr | Ser | Gln | Phe | Gly | Phe | Tyr | Leu | Leu | Phe | 20  | 25  | 30  |     |
| Glu | Thr | Lys | Ser | Lys | Val | Arg | Ile | Ser | Glu | Gly | Cys | Tyr | Ala | Phe | Asn | 35  | 40  | 45  |     |
| Gly | Ile | Leu | Gln | Glu | Ile | Pro | Met | Gln | Arg | Ala | Val | Lys | Ala | Leu | Ser | 50  | 55  | 60  |     |
| Glu | Phe | Lys | Glu | Ile | Ala | Leu | Lys | Tyr | Lys | Ser | Lys | Lys | Ile | Leu | Cys | 65  | 70  | 75  | 80  |
| Val | Ala | Thr | Ser | Ala | Val | Arg | Asp | Ala | Pro | Asn | Arg | Leu | Glu | Phe | Val | 85  | 90  | 95  |     |
| Ala | Arg | Val | Lys | Lys | Ala | Cys | Gly | Leu | Gln | Ile | Lys | Ile | Ile | Asp | Gly | 100 | 105 | 110 |     |
| Gln | Lys | Glu | Ala | Leu | Tyr | Gly | Gly | Ile | Ala | Cys | Ala | Asn | Leu | Leu | His | 115 | 120 | 125 |     |
| Lys | Asn | Ser | Gly | Ile | Thr | Ile | Asp | Ile | Gly | Gly | Gly | Ser | Thr | Glu | Cys | 130 | 135 | 140 |     |
| Ala | Leu | Ile | Glu | Lys | Gly | Lys | Ile | Lys | Asp | Leu | Ile | Ser | Leu | Asp | Val | 145 | 150 | 155 | 160 |
| Gly | Thr | Ile | Arg | Ile | Lys | Glu | Met | Phe | Leu | Asp | Lys | Asp | Leu | Glu | Val | 165 | 170 | 175 |     |
| Lys | Leu | Ala | Lys | Ala | Phe | Ile | Gln | Lys | Glu | Val | Ser | Lys | Leu | Pro | Phe | 180 | 185 | 190 |     |
| Lys | His | Lys | Asn | Ala | Phe | Gly | Val | Gly | Gly | Thr | Ile | Arg | Ala | Leu | Ser | 195 | 200 | 205 |     |
| Lys | Val | Leu | Met | Lys | Arg | Phe | Cys | Tyr | Pro | Ile | Asp | Ser | Leu | His | Gly | 210 | 215 | 220 |     |
| Tyr | Glu | Ile | Asp | Ala | His | Lys | Asn | Leu | Ala | Phe | Ile | Glu | Lys | Ile | Val | 225 | 230 | 235 | 240 |
| Met | Leu | Lys | Glu | Asp | Gln | Leu | Arg | Leu | Leu | Gly | Val | Asn | Glu | Glu | Arg | 245 | 250 | 255 |     |
| Leu | Asp | Ser | Ile | Arg | Ser | Gly | Ala | Leu | Ile | Leu | Ser | Val | Val | Leu | Glu | 260 | 265 | 270 |     |
| His | Leu | Lys | Thr | Ser | Leu | Met | Ile | Thr | Ser | Gly | Val | Gly | Val | Arg | Glu | 275 | 280 | 285 |     |
| Gly | Val | Phe | Leu | Ser | Asp | Leu | Leu | Arg | His | His | Tyr | His | Lys | Phe | Pro | 290 | 295 | 300 |     |
| Pro | Asn | Ile | Asn | Pro | Ser | Leu | Ile | Ser | Leu | Lys | Asp | Arg | Phe | Leu | Pro | 305 | 310 | 315 | 320 |
| His | Glu | Lys | His | Ser | Gln | Lys | Val | Lys | Lys | Glu | Cys | Val | Lys | Leu | Phe | 325 | 330 | 335 |     |
| Glu | Ala | Leu | Ser | Pro | Leu | His | Lys | Ile | Asp | Glu | Lys | Tyr | Leu | Phe | His | 340 | 345 | 350 |     |

Leu Lys Ile Ala Gly Glu Leu Ala Ser Met Gly Lys Ile Leu Ser Val  
 355 360 365  
 Tyr Leu Ala His Lys His Ser Ala Tyr Phe Ile Leu Asn Ala Leu Ser  
 370 375 380  
 Tyr Gly Phe Ser His Gln Asp Arg Ala Ile Ile Cys Leu Leu Ala Gln  
 385 390 395 400  
 Phe Ser His Lys Lys Ile Pro Lys Asp Asn Ala Ile Ala His Met Ser  
 405 410 415  
 Ala Met Met Pro Ser Leu Leu Thr Leu Gln Trp Leu Ser Phe Ile Leu  
 420 425 430  
 Ser Leu Ala Glu Asn Leu Cys Leu Thr Asp Ser His His Leu Lys Tyr  
 435 440 445  
 Thr Leu Glu Lys Asn Lys Leu Val Ile His Ser Asn Asp Thr Leu Tyr  
 450 455 460  
 Leu Ala Lys Glu Met Leu Pro Lys Leu Val Lys Pro Ile Pro Leu Thr  
 465 470 475 480  
 Ile Glu Phe Ala

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 60...1073
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

GCCAACTACC ATAAAAAGGA TTTTCTATC CAAAATATAG AGCCTAAAAA AATTAAAGA A 60  
 Me  
  
 TGC GTT TTA AAC ATC TTA AAG GAA AAA GAA TGA CTT ACA AAG AAC GAC 108  
 t Arg Phe Lys His Leu Lys Gly Lys Arg Met Thr Tyr Lys Glu Arg Le  
 1 5 10 15  
  
 TCA TAC ACG AAA AAA TAT TGA AAC AAG ACG ACA AGG GTT TTA AAA CAG 156  
 u Ile His Glu Lys Ile Leu Lys Gln Asp Asp Lys Gly Phe Lys Thr Gl  
 20 25 30  
  
 AAC TGC GCA TTT TGA GTA TTT TTA TCG TGG AAT CTT TAG TGA ATA TTT 204  
 u Leu Arg Ile Leu Ser Ile Phe Ile Val Glu Ser Leu Val Asn Ile Le  
 35 40 45  
  
 TGG GGT TTA TTT TAG CTA AAA TGC CCC ATT CGT GGT TTT TAA GGT GCA 252  
 u Gly Phe Ile Leu Ala Lys Met Pro His Ser Trp Phe Leu Arg Cys Il  
 50 55 60 6  
  
 TTA AAG CGG TGG CGT GGC TCA TGA AAA CTT TTG ATA AGT GCC GTT ATT 300

5 e Lys Ala Val Ala Trp Leu Met Lys Thr Phe Asp Lys Cys Arg Tyr Ph  
70 75 80

TTG ACG CTA AGG CCA ATT TGG ATT TTG TGT TTG GGG ATT CTA AAA GCG 348  
e Asp Ala Lys Ala Asn Leu Asp Phe Val Phe Gly Asp Ser Lys Ser Gl  
85 90 95

AAG AAG AGA AAA AAA GGA TCA TTA AAA AGG GTT ATG AAA ATT TTG CTT 396  
u Glu Glu Lys Lys Arg Ile Ile Lys Lys Gly Tyr Glu Asn Phe Ala Ph  
100 105 110

TCA TTA TTT TAG AAA CTA TTA GAG TGA TCT TTA TCC CTA AAG ATG AAT 444  
e Ile Ile Leu Glu Thr Ile Arg Val Ile Phe Ile Pro Lys Asp Glu Ty  
115 120 125

ACG ACG CTC GTT TCA CGC TCA TCA ATG AAG AAA ATG TGT GGA AAT CTT 492  
r Asp Ala Arg Phe Thr Leu Ile Asn Glu Glu Asn Val Trp Lys Ser Le  
130 135 140 1

TAA ACA AGG AAG GCC AAG CGA TCA CTT TAT GCA TGC ATT TTG GCT ATT 540  
u Asn Lys Glu Gly Gln Ala Ile Thr Leu Cys Met His Phe Gly Tyr Tr  
45 150 155 160

GGG AAG CGG TAG GCA CGA CTT TAG CGC AAT ATT ATG AAA ATT ATG GTA 588  
p Glu Ala Val Gly Thr Thr Leu Ala Gln Tyr Tyr Glu Asn Tyr Gly Ar  
165 170 175

GGG GGT GTT TGG GGC GTT TGA CTA AAT TTG CCC CTA TCA ATC ACA TGA 636  
g Gly Cys Leu Gly Arg Leu Thr Lys Phe Ala Pro Ile Asn His Met Il  
180 185 190

TTA TGA GTA GGC GAG AGG CGT TTG GGG TGC GTT TTG TCA ATA AAA TAG 684  
e Met Ser Arg Arg Glu Ala Phe Gly Val Arg Phe Val Asn Lys Ile Gl  
195 200 205

GGG CGA TGA AAG AAC TCA TTA AAA TGT ATA ATC AAG GCA ATG GTC TGG 732  
y Ala Met Lys Glu Leu Ile Lys Met Tyr Asn Gln Gly Asn Gly Leu Va  
210 215 220 2

TGG GGA TTT TAG TGG ATC AAA ATG TCG TGC CTA AAG ATG GGG TGG TGG 780  
1 Gly Ile Leu Val Asp Gln Asn Val Val Pro Lys Asp Gly Val Val Va  
25 230 235 240

TGA AAT TCT TTG ATA GAG ACG CTA CGC ACA CCA CGA TCG CTT CTA TTT 828  
1 Lys Phe Phe Asp Arg Asp Ala Thr His Thr Thr Ile Ala Ser Ile Le  
245 250 255

TGT CGC GCC GTT ATA ATA TAG ATA TTC AGC CGG TAT TCA TTG ATT TTA 876  
u Ser Arg Arg Tyr Asn Ile Asp Ile Gln Pro Val Phe Ile Asp Phe As  
260 265 270

ATG ACG ATT ATT CGC ATT ATA CAG CGA CCT ATT ATC CGA GTA TCC GCT 924  
n Asp Asp Tyr Ser His Tyr Thr Ala Thr Tyr Tyr Pro Ser Ile Arg Se  
275 280 285

CTC AAA TCA CCG ATA ACG CGC AAA ACG ATA TTT TAG AAT GCA CGC AAG 972  
r Gln Ile Thr Asp Asn Ala Gln Asn Asp Ile Leu Glu Cys Thr Gln Al  
290 295 300 3



CCC AAG CGA GTT TGT GCG AAG AGG TGA TTA GAA ACC ACC CGG AAA GTT 1020  
a Gln Ala Ser Leu Cys Glu Glu Val Ile Arg Asn His Pro Glu Ser Ty  
05 310 315 320

ATT TTT GGT TCC ATA GGC GTT TTA AAA GCA CCC ACC CTG AGA TTT ATC 1068  
r Phe Trp Phe His Arg Arg Phe Lys Ser Thr His Pro Glu Ile Tyr Gl  
325 330 335

AAA GA TAGGGTTTTG TTTTAATCAA AAATTAAAAA CTAAAGCCTT ATTTTAAAGA AAA 1126  
n Arg

CTTT 1130

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Phe | Lys | His | Leu | Lys | Gly | Lys | Arg | Met | Thr | Tyr | Lys | Glu | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ile | His | Glu | Lys | Ile | Leu | Lys | Gln | Asp | Asp | Lys | Gly | Phe | Lys | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Leu | Arg | Ile | Leu | Ser | Ile | Phe | Ile | Val | Glu | Ser | Leu | Val | Asn | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Gly | Phe | Ile | Leu | Ala | Lys | Met | Pro | His | Ser | Trp | Phe | Leu | Arg | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Lys | Ala | Val | Ala | Trp | Leu | Met | Lys | Thr | Phe | Asp | Lys | Cys | Arg | Tyr |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Phe | Asp | Ala | Lys | Ala | Asn | Leu | Asp | Phe | Val | Phe | Gly | Asp | Ser | Lys | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Glu | Glu | Lys | Lys | Arg | Ile | Ile | Lys | Lys | Gly | Tyr | Glu | Asn | Phe | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Ile | Ile | Leu | Glu | Thr | Ile | Arg | Val | Ile | Phe | Ile | Pro | Lys | Asp | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Tyr | Asp | Ala | Arg | Phe | Thr | Leu | Ile | Asn | Glu | Glu | Asn | Val | Trp | Lys | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Asn | Lys | Glu | Gly | Gln | Ala | Ile | Thr | Leu | Cys | Met | His | Phe | Gly | Tyr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Trp | Glu | Ala | Val | Gly | Thr | Thr | Leu | Ala | Gln | Tyr | Tyr | Glu | Asn | Tyr | Gly |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Arg | Gly | Cys | Leu | Gly | Arg | Leu | Thr | Lys | Phe | Ala | Pro | Ile | Asn | His | Met |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Met | Ser | Arg | Arg | Glu | Ala | Phe | Gly | Val | Arg | Phe | Val | Asn | Lys | Ile |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Ala | Met | Lys | Glu | Leu | Ile | Lys | Met | Tyr | Asn | Gln | Gly | Asn | Gly | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Gly | Ile | Leu | Val | Asp | Gln | Asn | Val | Val | Pro | Lys | Asp | Gly | Val | Val |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Val | Lys | Phe | Phe | Asp | Arg | Asp | Ala | Thr | His | Thr | Thr | Ile | Ala | Ser | Ile |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |

Leu Ser Arg Arg Tyr Asn Ile Asp Ile Gln Pro Val Phe Ile Asp Phe  
 260 265 270  
 Asn Asp Asp Tyr Ser His Tyr Thr Ala Thr Tyr Tyr Pro Ser Ile Arg  
 275 280 285  
 Ser Gln Ile Thr Asp Asn Ala Gln Asn Asp Ile Leu Glu Cys Thr Gln  
 290 295 300  
 Ala Gln Ala Ser Leu Cys Glu Glu Val Ile Arg Asn His Pro Glu Ser  
 305 310 315 320  
 Tyr Phe Trp Phe His Arg Arg Phe Lys Ser Thr His Pro Glu Ile Tyr  
 325 330 335  
 Gln Arg

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...8694
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| AGAGGGTAGC ATTTA ATG AAA AAG TTT AAA AAG AAA CCA AAA AGT ATC AAA | 51  |
| Met Lys Lys Phe Lys Lys Lys Pro Lys Ser Ile Lys                  |     |
| 1 5 10                                                           |     |
| CGA TCG CAT CAA AAT CAA AAA ACA ATC TTA AAG CGT CCT TTA TGG CTT  | 99  |
| Arg Ser His Gln Asn Gln Lys Thr Ile Leu Lys Arg Pro Leu Trp Leu  |     |
| 15 20 25                                                         |     |
| ATG CCT TTA CTC ATC AGC GGG TTT GCT AGT GGG GTG TAT GCG AAT AAT  | 147 |
| Met Pro Leu Leu Ile Ser Gly Phe Ala Ser Gly Val Tyr Ala Asn Asn  |     |
| 30 35 40                                                         |     |
| CTG TGG GAT TTG TTA AAC CCA AAA GTG GGG GGT GAG TAT GTG CAT TGG  | 195 |
| Leu Trp Asp Leu Leu Asn Pro Lys Val Gly Gly Glu Tyr Val His Trp  |     |
| 45 50 55 60                                                      |     |
| GTT AAG GGC AGT CAG TAT TGT GCA TGG TGG GAA TTT GCT GGG TGT TTA  | 243 |
| Val Lys Gly Ser Gln Tyr Cys Ala Trp Trp Glu Phe Ala Gly Cys Leu  |     |
| 65 70 75                                                         |     |
| AAG AAT GTA TGG GGG GCA AAT CAT AAA GGC TAT GAT GCT GGA AAC GCC  | 291 |
| Lys Asn Val Trp Gly Ala Asn His Lys Gly Tyr Asp Ala Gly Asn Ala  |     |
| 80 85 90                                                         |     |
| GCT AAC TAT TTG TCT TCT CAA AAC TAT CAA GCT ATT TCG GTG GGT AGT  | 339 |
| Ala Asn Tyr Leu Ser Ser Gln Asn Tyr Gln Ala Ile Ser Val Gly Ser  |     |
| 95 100 105                                                       |     |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| GGG AAT GAA ACG GGG ACT TAT AGT TTA AGC GGT TTT ACC AAT TAT GTT<br>Gly Asn Glu Thr Gly Thr Tyr Ser Leu Ser Gly Phe Thr Asn Tyr Val<br>110 115 120     | 387  |
| GGG GGC AAT CTC ACG ATC AAT CTA GGC AAT AGC GTT GTT TTA GAT TTA<br>Gly Gly Asn Leu Thr Ile Asn Leu Gly Asn Ser Val Val Leu Asp Leu<br>125 130 135 140 | 435  |
| AGC GGT TCT AAT AGT TTC ACT TCG TAT CAA GGT TAT AAT CAA GGC AAA<br>Ser Gly Ser Asn Ser Phe Thr Ser Tyr Gln Gly Tyr Asn Gln Gly Lys<br>145 150 155     | 483  |
| GAT GAT GTA ACA TTT ACG GTT GGC GCA ATC AAT TTA AAC GGC ACT TTA<br>Asp Asp Val Thr Phe Thr Val Gly Ala Ile Asn Leu Asn Gly Thr Leu<br>160 165 170     | 531  |
| GAA GTG GGT AAT CGT GTG GGA TCG GGA GCT GGC ACG CAC ACC GGC ACA<br>Glu Val Gly Asn Arg Val Gly Ser Gly Ala Gly Thr His Thr Gly Thr<br>175 180 185     | 579  |
| GCC ACT TTA AAC TTG AAC GCT AAT AAG GTC AAT ATC AAT TCC AAT ATC<br>Ala Thr Leu Asn Leu Asn Ala Asn Lys Val Asn Ile Asn Ser Asn Ile<br>190 195 200     | 627  |
| AAC GCG TAT AAA ACT TCG CAA GTG AAT ATA GGC AAC GCT AAC AGC GTT<br>Asn Ala Tyr Lys Thr Ser Gln Val Asn Ile Gly Asn Ala Asn Ser Val<br>205 210 215 220 | 675  |
| ATT ACC ATT GGT TCG GTT TCT TTG AGT GGG GAT GTT TGC AGT TCT TTA<br>Ile Thr Ile Gly Ser Val Ser Leu Ser Gly Asp Val Cys Ser Ser Leu<br>225 230 235     | 723  |
| GCT AGC GTT GGG ATA GGG GCT AAT TGC TCC ACT TCT GGG CCT AGC TAT<br>Ala Ser Val Gly Ile Gly Ala Asn Cys Ser Thr Ser Gly Pro Ser Tyr<br>240 245 250     | 771  |
| TCT TTT AAA GGG ACG ACT AAC GCT ACT AAC ACG GCG TTT AGT AAT GCA<br>Ser Phe Lys Gly Thr Thr Asn Ala Thr Asn Thr Ala Phe Ser Asn Ala<br>255 260 265     | 819  |
| AGC GGC AGT TTC ACT TTT GAA GAG AAC GCC ACT TTT AGC GGG GCG AAA<br>Ser Gly Ser Phe Thr Phe Glu Glu Asn Ala Thr Phe Ser Gly Ala Lys<br>270 275 280     | 867  |
| TGG AAT GGG GGG ACT TAT ACC TTT AAT AAA GAG TTT AGC GCT ACC AAT<br>Trp Asn Gly Gly Thr Tyr Thr Phe Asn Lys Glu Phe Ser Ala Thr Asn<br>285 290 295 300 | 915  |
| AAC ACC GCC TTT AGT AGC GGT AGT TTT AAT TTT AAA GGT GTA AGC TCT<br>Asn Thr Ala Phe Ser Ser Gly Ser Phe Asn Phe Lys Gly Val Ser Ser<br>305 310 315     | 963  |
| TTT AAT GGT ACT TCG TTT AGT AAC GCT TCT TAT ACT TTT GAC AAT CAA<br>Phe Asn Gly Thr Ser Phe Ser Asn Ala Ser Tyr Thr Phe Asp Asn Gln<br>320 325 330     | 1011 |
| GCC ACT TTC CAA AAC AGC TCC TTT AAT GGG GGG ACT TTT ACT TTT AAT<br>Ala Thr Phe Gln Asn Ser Ser Phe Asn Gly Gly Thr Phe Thr Phe Asn<br>1059            |      |

|         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |      |
|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|------|
|         | 335     |         |         |         |         | 340     |         |         |         |         | 345     |         |         |         |         |      |
| AAC Asn | CAA Gln | ACT Thr | AAT Asn | CCA Pro | ACT Thr | AAC Asn | AAC Asn | GCT Ala | CAG Gln | CAC His | CCC Pro | CAA Gln | ATT Ile | CAA Gln | AAC Asn | 1107 |
|         | 350     |         |         |         |         | 355     |         |         |         |         | 360     |         |         |         |         |      |
| AGC Ser | TCT Ser | TTT Phe | AGT Ser | GGT Gly | AAC Asn | GCT Ala | ACC Thr | ACT Thr | CTT Leu | AAG Lys | GGC Gly | TTT Phe | GTG Val | AAT Asn | TTC Phe | 1155 |
| 365     |         |         |         |         | 370     |         |         |         |         | 375     |         |         |         |         | 380     |      |
| CAG Gln | CAA Gln | GCC Ala | TTT Phe | AAC Asn | AAT Asn | TCA Ser | AAC Asn | CAC His | CAA Gln | CTA Leu | ACG Thr | ATC Ile | CAA Gln | AAC Asn | GCT Ala | 1203 |
|         |         |         |         | 385     |         |         |         |         | 390     |         |         |         |         | 395     |         |      |
| TCC Ser | TTT Phe | AAT Asn | AAC Asn | GCC Ala | ACT Thr | TTT Phe | AAC Asn | AAT Asn | ACC Thr | GGT Gly | AAA Lys | ATC Ile | ACT Thr | ATA Ile | GAA Glu | 1251 |
|         |         |         | 400     |         |         |         |         | 405     |         |         |         |         | 410     |         |         |      |
| AAA Lys | GAT Asp | GCG Ala | AGT Ser | TTT Phe | AAT Asn | AAC Asn | ACG Thr | ACA Thr | TTC Phe | AAC Asn | ACT Thr | TCT Ser | GTT Val | GAT Asp | ACA Thr | 1299 |
|         | 415     |         |         |         |         | 420     |         |         |         |         |         | 425     |         |         |         |      |
| AAC Asn | AAC Asn | ATG Met | AGT Ser | GTT Val | ACC Thr | GGT Gly | GGC Gly | GTT Val | ACT Thr | TTA Leu | AGC Ser | GGT Gly | AAA Lys | AAT Asn | GAC Asp | 1347 |
|         | 430     |         |         |         |         | 435     |         |         |         |         | 440     |         |         |         |         |      |
| TTG Leu | AAA Lys | AAT Asn | GGC Gly | TCA Ser | ACC Thr | CTT Leu | GAT Asp | TTT Phe | GGG Gly | AGT Ser | TCT Ser | AAA Lys | ATC Ile | ACT Thr | CTC Leu | 1395 |
| 445     |         |         |         | 450     |         |         |         |         | 455     |         |         |         |         |         | 460     |      |
| GCT Ala | CAA Gln | GGG Gly | ACG Thr | ACT Thr | TTC Phe | AAC Asn | CTC Leu | ACA Thr | AGT Ser | TTA Leu | GGC Gly | AGT Ser | GAG Glu | AAG Lys | AGC Ser | 1443 |
|         |         |         | 465     |         |         |         |         | 470     |         |         |         |         | 475     |         |         |      |
| GTA Val | ACG Thr | ATT Ile | TTA Leu | AAT Asn | TCT Ser | AGC Ser | GGT Gly | GGG Gly | ATC Ile | ACT Thr | TAT Tyr | AGT Ser | AAC Asn | CTT Leu | TTA Leu | 1491 |
|         |         |         | 480     |         |         |         | 485     |         |         |         |         | 490     |         |         |         |      |
| AAC Asn | CAT His | GCA Ala | ATC Ile | AAC Asn | GGC Gly | TTG Leu | ACA Thr | AGT Ser | GCC Ala | TTA Leu | AAA Lys | ACG Thr | AAC Asn | GAA Glu | AGC Ser | 1539 |
|         | 495     |         |         |         |         | 500     |         |         |         |         | 505     |         |         |         |         |      |
| CTT Leu | TCA Ser | AAT Asn | CCG Pro | CAA Gln | AGT Ser | TTC Phe | GCT Ala | CAA Gln | GGT Gly | TTG Leu | TGG Trp | GAT Asp | ATA Ile | ATC Ile | ACT Thr | 1587 |
|         | 510     |         |         |         |         | 515     |         |         |         |         | 520     |         |         |         |         |      |
| TAC Tyr | AAT Asn | GGG Gly | GTT Val | ACC Thr | GGG Gly | CAG Gln | CTT Leu | TTG Leu | AAT Asn | GAA Glu | AAC Asn | GCT Ala | GCA Ala | ACA Thr | TCT Ser | 1635 |
| 525     |         |         |         |         | 530     |         |         |         | 535     |         |         |         |         |         | 540     |      |
| AAA Lys | CCC Pro | ACT Thr | GAC Asp | TCT Ser | TCG Ser | CCC Pro | TCT Ser | AAA Lys | TCC Ser | TCT Ser | ACA Thr | AAC Asn | TCT Ser | ACG Thr | CAA Gln | 1683 |
|         |         |         | 545     |         |         |         |         | 550     |         |         |         |         |         | 555     |         |      |
| GTC Val | TAT Tyr | CAA Gln | GTG Val | GGT Gly | TAC Tyr | AAA Lys | ATA Ile | GGG Gly | GAT Asp | ACT Thr | ATC Ile | TAC Tyr | AAA Lys | CTG Leu | CAA Gln | 1731 |
|         |         |         | 560     |         |         |         |         | 565     |         |         |         | 570     |         |         |         |      |

|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| GAA<br>Glu        | ACT<br>Thr        | TTC<br>Phe<br>575 | AGC<br>Ser        | CAC<br>His        | AAT<br>Asn        | TCC<br>Ser        | ATT<br>Ile<br>580 | ATT<br>Ile        | ATT<br>Ile        | CAG<br>Gln        | GCT<br>Ala        | TTA<br>Leu<br>585 | GAG<br>Glu        | AGC<br>Ser        | GGG<br>Gly        | 1779 |
| ACT<br>Thr        | TAC<br>Tyr<br>590 | ACG<br>Thr        | CCA<br>Pro        | CCC<br>Pro        | CCT<br>Pro        | GTC<br>Val<br>595 | ATT<br>Ile        | AAC<br>Asn        | GGC<br>Gly        | TCC<br>Ser        | AAA<br>Lys<br>600 | TTT<br>Phe        | GAC<br>Asp        | TTA<br>Leu        | TCC<br>Ser        | 1827 |
| GCT<br>Ala<br>605 | TCA<br>Ser        | AAT<br>Asn        | TAT<br>Tyr        | ATC<br>Ile        | AAT<br>Asn<br>610 | GCT<br>Ala        | GAC<br>Asp        | ATG<br>Met        | CCT<br>Pro        | TGG<br>Trp<br>615 | TAT<br>Tyr        | GAC<br>Asp        | CAT<br>His        | AAA<br>Lys        | TAT<br>Tyr<br>620 | 1875 |
| TAC<br>Tyr        | ATC<br>Ile        | CCT<br>Pro        | AAA<br>Lys        | TCC<br>Ser<br>625 | CAA<br>Gln        | AAT<br>Asn        | TTT<br>Phe        | ACA<br>Thr        | GAG<br>Glu<br>630 | AGC<br>Ser        | GGG<br>Gly        | ACT<br>Thr        | TAT<br>Tyr        | TAC<br>Tyr<br>635 | TTG<br>Leu        | 1923 |
| CCG<br>Pro        | AGC<br>Ser        | GTC<br>Val        | CAA<br>Gln<br>640 | ATA<br>Ile        | TGG<br>Trp        | GGG<br>Gly        | AGC<br>Ser        | TAC<br>Tyr<br>645 | ACT<br>Thr        | AAC<br>Asn        | TCG<br>Ser        | TTT<br>Phe<br>650 | AAA<br>Lys        | CAA<br>Gln        | ACT<br>Thr        | 1971 |
| TTT<br>Phe        | AGC<br>Ser<br>655 | GCA<br>Ala        | AAT<br>Asn        | GGT<br>Gly        | AGT<br>Ser        | AAT<br>Asn        | CTG<br>Leu<br>660 | GTG<br>Val        | ATT<br>Ile        | GGG<br>Gly        | TAT<br>Tyr<br>665 | AAC<br>Asn        | TCA<br>Ser        | ACA<br>Thr        | TGG<br>Trp        | 2019 |
| ACT<br>Thr<br>670 | GAT<br>Asp        | CAT<br>His        | AAT<br>Asn        | GTC<br>Val        | TCT<br>Ser        | TCT<br>Ser<br>675 | AGC<br>Ser        | GGC<br>Gly        | ACG<br>Thr        | GTG<br>Val<br>680 | TCT<br>Ser        | TTT<br>Phe        | GGG<br>Gly        | GAC<br>Asp        | ACT<br>Thr        | 2067 |
| TCA<br>Ser<br>685 | GGG<br>Gly        | AGC<br>Ser        | GCT<br>Ala        | CTT<br>Leu        | AAT<br>Asn<br>690 | GGG<br>Gly        | CAT<br>His        | TGC<br>Cys        | GGA<br>Gly        | CCT<br>Pro<br>695 | TGG<br>Trp        | CCG<br>Pro        | TAT<br>Tyr        | TAC<br>Tyr        | CAA<br>Gln<br>700 | 2115 |
| TGC<br>Cys        | ACA<br>Thr        | GGC<br>Gly        | ACG<br>Thr        | ACT<br>Thr<br>705 | AAC<br>Asn        | GGC<br>Gly        | ACT<br>Thr        | TAT<br>Tyr        | AGC<br>Ser<br>710 | GCC<br>Ala        | TAT<br>Tyr        | CAT<br>His        | GTG<br>Val<br>715 | TAT<br>Tyr        | ATC<br>Ile        | 2163 |
| ACA<br>Thr        | GCG<br>Ala        | AAT<br>Asn        | CTG<br>Leu<br>720 | CGT<br>Arg        | TCT<br>Ser        | GGC<br>Gly        | AAT<br>Asn        | CGT<br>Arg<br>725 | ATA<br>Ile        | GGC<br>Gly        | ACC<br>Thr        | GGT<br>Gly        | GGG<br>Gly<br>730 | GCA<br>Ala        | GCT<br>Ala        | 2211 |
| AAT<br>Asn        | CTA<br>Leu        | ATC<br>Ile<br>735 | TTT<br>Phe        | AAT<br>Asn        | GGG<br>Gly        | GTA<br>Val        | GAT<br>Asp<br>740 | AGT<br>Ser        | ATC<br>Ile        | AAT<br>Asn        | ATC<br>Ile<br>745 | GCT<br>Ala        | AAC<br>Asn        | GCT<br>Ala        | ACC<br>Thr        | 2259 |
| ATC<br>Ile<br>750 | ACG<br>Thr        | CAA<br>Gln        | CAT<br>His        | AAC<br>Asn        | GCC<br>Ala        | GGA<br>Gly<br>755 | ATC<br>Ile        | TAT<br>Tyr        | TCA<br>Ser        | AGC<br>Ser        | TCT<br>Ser<br>760 | ATG<br>Met        | ACT<br>Thr        | TTT<br>Phe        | TCC<br>Ser        | 2307 |
| ACG<br>Thr<br>765 | CAA<br>Gln        | AGC<br>Ser        | ATG<br>Met        | GAT<br>Asp        | AAT<br>Asn<br>770 | TCG<br>Ser        | CAG<br>Gln        | AAT<br>Asn        | TTG<br>Leu        | AAT<br>Asn<br>775 | GGT<br>Gly        | CTA<br>Leu        | AAT<br>Asn        | TCT<br>Ser        | AAC<br>Asn<br>780 | 2355 |
| GGC<br>Gly        | AAA<br>Lys        | CTT<br>Leu        | TCG<br>Ser        | GTG<br>Val<br>785 | TAT<br>Tyr        | GGC<br>Gly        | ACC<br>Thr        | ACT<br>Thr        | TTC<br>Phe<br>790 | ACT<br>Thr        | AAC<br>Asn        | GAA<br>Glu        | GCT<br>Ala        | AAA<br>Lys<br>795 | GAT<br>Asp        | 2403 |
| GGG<br>Gly        | AAA<br>Lys        | TTC<br>Phe        | ATT<br>Ile        | TTC<br>Phe        | AAT<br>Asn        | GCA<br>Ala        | GGG<br>Gly        | CAA<br>Gln        | GCG<br>Ala        | GTT<br>Val        | TTT<br>Phe        | GAA<br>Glu        | AAC<br>Asn        | ACC<br>Thr        | AAC<br>Asn        | 2451 |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |  |  |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|--|--|
| 800        |            |            |            |            |            | 805        |            |            |            |            |            | 810        |            |            |            |      |  |  |
| TTT<br>Phe | AAT<br>Asn | GGA<br>Gly | GGG<br>Gly | AGT<br>Ser | TAC<br>Tyr | CAA<br>Gln | TTC<br>Phe | AGC<br>Ser | GGC<br>Gly | GAT<br>Asp | AGC<br>Ser | TTG<br>Leu | AAT<br>Asn | TTT<br>Phe | TCA<br>Ser | 2499 |  |  |
| 815        |            |            |            |            |            | 820        |            |            |            |            |            | 825        |            |            |            |      |  |  |
| AAC<br>Asn | AAC<br>Asn | AAC<br>Asn | CAG<br>Gln | TTC<br>Phe | AAT<br>Asn | AGC<br>Ser | GGT<br>Gly | TCG<br>Ser | TTT<br>Phe | GAA<br>Glu | ATT<br>Ile | AGC<br>Ser | GCA<br>Ala | AAA<br>Lys | AAC<br>Asn | 2547 |  |  |
| 830        |            |            |            |            |            | 835        |            |            |            |            |            | 840        |            |            |            |      |  |  |
| GCT<br>Ala | TCG<br>Ser | TTC<br>Phe | AAT<br>Asn | AAC<br>Asn | GCT<br>Ala | AAC<br>Asn | TTT<br>Phe | AAC<br>Asn | AAC<br>Asn | AGC<br>Ser | GCT<br>Ala | TCT<br>Ser | TTT<br>Phe | AAT<br>Asn | TTC<br>Phe | 2595 |  |  |
| 845        |            |            |            |            |            | 850        |            |            |            |            |            | 855        |            |            |            |      |  |  |
| AAT<br>Asn | AAT<br>Asn | TCT<br>Ser | AAC<br>Asn | GCG<br>Ala | ACC<br>Thr | ACT<br>Thr | TCG<br>Ser | TTT<br>Phe | GTG<br>Val | GGG<br>Gly | GAT<br>Asp | TTC<br>Phe | ACT<br>Thr | AAC<br>Asn | GCT<br>Ala | 2643 |  |  |
| 865        |            |            |            |            |            | 870        |            |            |            |            |            | 875        |            |            |            |      |  |  |
| AAT<br>Asn | TCA<br>Ser | AAT<br>Asn | TTG<br>Leu | CAA<br>Gln | ATC<br>Ile | GCC<br>Ala | GGG<br>Gly | AAC<br>Asn | GCT<br>Ala | GTT<br>Val | TTT<br>Phe | GGG<br>Gly | AAC<br>Asn | TCT<br>Ser | ACT<br>Thr | 2691 |  |  |
| 880        |            |            |            |            |            | 885        |            |            |            |            |            | 890        |            |            |            |      |  |  |
| AAT<br>Asn | GGC<br>Gly | TCT<br>Ser | CAA<br>Gln | AAT<br>Asn | ACC<br>Thr | GCT<br>Ala | AAT<br>Asn | TTT<br>Phe | AAT<br>Asn | AAT<br>Asn | ACC<br>Thr | GGC<br>Gly | TCT<br>Ser | GTT<br>Val | AAT<br>Asn | 2739 |  |  |
| 895        |            |            |            |            |            | 900        |            |            |            |            |            | 905        |            |            |            |      |  |  |
| ATT<br>Ile | TCA<br>Ser | GGG<br>Gly | AAT<br>Asn | GCA<br>Ala | ACC<br>Thr | TTT<br>Phe | GAT<br>Asp | AAT<br>Asn | GTG<br>Val | GTG<br>Val | TTT<br>Phe | AAT<br>Asn | GGC<br>Gly | CCT<br>Pro | ACG<br>Thr | 2787 |  |  |
| 910        |            |            |            |            |            | 915        |            |            |            |            |            | 920        |            |            |            |      |  |  |
| AAC<br>Asn | ACG<br>Thr | AGC<br>Ser | GTG<br>Val | AAA<br>Lys | GGG<br>Gly | CAG<br>Gln | GTT<br>Val | ACT<br>Thr | TTA<br>Leu | AAT<br>Asn | AAC<br>Asn | ATC<br>Ile | ACT<br>Thr | TTA<br>Leu | AAA<br>Lys | 2835 |  |  |
| 925        |            |            |            |            |            | 930        |            |            |            |            |            | 935        |            |            |            |      |  |  |
| AAC<br>Asn | CTG<br>Leu | AAC<br>Asn | GCC<br>Ala | CCT<br>Pro | TTG<br>Leu | TCT<br>Ser | TTT<br>Phe | GGC<br>Gly | GAT<br>Asp | GGG<br>Gly | ACG<br>Thr | ATT<br>Ile | ACT<br>Thr | TTT<br>Phe | AAC<br>Asn | 2883 |  |  |
| 945        |            |            |            |            |            | 950        |            |            |            |            |            | 955        |            |            |            |      |  |  |
| GCT<br>Ala | CAT<br>His | TCG<br>Ser | GTG<br>Val | ATT<br>Ile | AAT<br>Asn | ATT<br>Ile | GCT<br>Ala | GAA<br>Glu | TCT<br>Ser | ATC<br>Ile | ACT<br>Thr | AAT<br>Asn | GGC<br>Gly | AAC<br>Asn | CCT<br>Pro | 2931 |  |  |
| 960        |            |            |            |            |            | 965        |            |            |            |            |            | 970        |            |            |            |      |  |  |
| ATC<br>Ile | ACT<br>Thr | CTT<br>Leu | GTA<br>Val | AGC<br>Ser | TCT<br>Ser | TCT<br>Ser | AAA<br>Lys | GAA<br>Glu | ATT<br>Ile | GAA<br>Glu | TAC<br>Tyr | AAC<br>Asn | AAC<br>Asn | GCT<br>Ala | TTC<br>Phe | 2979 |  |  |
| 975        |            |            |            |            |            | 980        |            |            |            |            |            | 985        |            |            |            |      |  |  |
| AGT<br>Ser | AAA<br>Lys | AAT<br>Asn | CTA<br>Leu | TGG<br>Trp | CAG<br>Gln | CTC<br>Leu | ATC<br>Ile | AAC<br>Asn | TAC<br>Tyr | CAA<br>Gln | GGG<br>Gly | CAT<br>His | GGG<br>Gly | GCA<br>Ala | AGC<br>Ser | 3027 |  |  |
| 990        |            |            |            |            |            | 995        |            |            |            |            |            | 1000       |            |            |            |      |  |  |
| AGT<br>Ser | GAA<br>Glu | AAG<br>Lys | CTC<br>Leu | GTC<br>Val | TCT<br>Ser | AGC<br>Ser | GCG<br>Ala | GGT<br>Gly | AAT<br>Asn | GGC<br>Gly | GTT<br>Val | TAT<br>Tyr | GAT<br>Asp | GTG<br>Val | GTG<br>Val | 3075 |  |  |
| 1005       |            |            |            |            |            | 1010       |            |            |            |            |            | 1015       |            |            |            |      |  |  |
| TAT<br>Tyr | TCT<br>Ser | TTC<br>Phe | AAT<br>Asn | AAC<br>Asn | CAA<br>Gln | ACC<br>Thr | TAC<br>Tyr | AAT<br>Asn | TTC<br>Phe | CAA<br>Gln | GAG<br>Glu | GTT<br>Val | TTT<br>Phe | TCA<br>Ser | CAA<br>Gln | 3123 |  |  |
| 1025       |            |            |            |            |            | 1030       |            |            |            |            |            | 1035       |            |            |            |      |  |  |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |  |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|--|
| AAC<br>Asn | AGC<br>Ser | ATT<br>Ile | TCT<br>Ser | ATC<br>Ile | CGG<br>Arg | CGT<br>Arg | TTG<br>Leu | GGC<br>Gly | GTT<br>Val | AAC<br>Asn | ATG<br>Met | GTG<br>Val | TTT<br>Phe | GAT<br>Asp | TAT<br>Tyr | 3171 |  |
|            |            |            | 1040       |            |            |            |            |            | 1045       |            |            | 1050       |            |            |            |      |  |
| GTG<br>Val | GAT<br>Asp | ATG<br>Met | GAA<br>Glu | AAA<br>Lys | TCG<br>Ser | GAT<br>Asp | CAT<br>His | TTA<br>Leu | TAT<br>Tyr | TAT<br>Tyr | CAA<br>Gln | AAC<br>Asn | GCT<br>Ala | CTC<br>Leu | GGT<br>Gly | 3219 |  |
|            |            |            | 1055       |            |            |            |            |            | 1060       |            |            | 1065       |            |            |            |      |  |
| TTT<br>Phe | ATG<br>Met | ACC<br>Thr | TAC<br>Tyr | ATG<br>Met | CCT<br>Pro | AAT<br>Asn | AGC<br>Ser | TAT<br>Tyr | AAC<br>Asn | AAT<br>Asn | AAT<br>Asn | TTA<br>Leu | GGG<br>Gly | AAT<br>Asn | GCA<br>Ala | 3267 |  |
|            |            |            | 1070       |            |            |            |            |            | 1075       |            |            | 1080       |            |            |            |      |  |
| AAC<br>Asn | AAC<br>Asn | ACC<br>Thr | ATT<br>Ile | TAC<br>Tyr | TAT<br>Tyr | TAC<br>Tyr | GAC<br>Asp | AAG<br>Lys | AGC<br>Ser | ATT<br>Ile | GAT<br>Asp | TTT<br>Phe | TAT<br>Tyr | GCG<br>Ala | AGC<br>Ser | 3315 |  |
| 1085       |            |            |            |            |            | 1090       |            |            |            |            |            | 1095       |            |            | 1100       |      |  |
| GGG<br>Gly | AAA<br>Lys | ACT<br>Thr | CTA<br>Leu | TTC<br>Phe | ACT<br>Thr | AAA<br>Lys | GCG<br>Ala | GAA<br>Glu | TTT<br>Phe | TCT<br>Ser | CAA<br>Gln | ACA<br>Thr | TTC<br>Phe | ACC<br>Thr | GGG<br>Gly | 3363 |  |
|            |            |            | 1105       |            |            |            |            |            | 1110       |            |            | 1115       |            |            |            |      |  |
| CAA<br>Gln | AAC<br>Asn | AGC<br>Ser | GCG<br>Ala | ATC<br>Ile | GTT<br>Val | TTT<br>Phe | GGG<br>Gly | GCT<br>Ala | AAA<br>Lys | AGC<br>Ser | ATA<br>Ile | TGG<br>Trp | ACG<br>Thr | AGC<br>Ser | TTA<br>Leu | 3411 |  |
|            |            |            | 1120       |            |            |            |            |            | 1125       |            |            | 1130       |            |            |            |      |  |
| AGC<br>Ser | GAT<br>Asp | GCA<br>Ala | CCG<br>Pro | CAG<br>Gln | TCT<br>Ser | AAC<br>Asn | ACC<br>Thr | ATC<br>Ile | ATT<br>Ile | CGC<br>Arg | TTT<br>Phe | GGG<br>Gly | GAC<br>Asp | AAT<br>Asn | AAG<br>Lys | 3459 |  |
|            |            |            | 1135       |            |            |            |            |            | 1140       |            |            | 1145       |            |            |            |      |  |
| GGA<br>Gly | GCA<br>Ala | GGG<br>Gly | AGT<br>Ser | AAT<br>Asn | GAT<br>Asp | GCG<br>Ala | AGC<br>Ser | GGG<br>Gly | CAT<br>His | TGC<br>Cys | TGG<br>Trp | AAT<br>Asn | TTG<br>Leu | CAA<br>Gln | TGC<br>Cys | 3507 |  |
|            |            |            | 1150       |            |            |            |            |            | 1155       |            |            | 1160       |            |            |            |      |  |
| ATA<br>Ile | GGC<br>Gly | TTT<br>Phe | ATT<br>Ile | ACA<br>Thr | GGG<br>Gly | CAT<br>His | TAT<br>Tyr | GAA<br>Glu | GCG<br>Ala | CAA<br>Gln | AAG<br>Lys | ATT<br>Ile | TAC<br>Tyr | ATC<br>Ile | ACC<br>Thr | 3555 |  |
| 1165       |            |            |            |            |            | 1170       |            |            |            |            |            | 1175       |            |            | 1180       |      |  |
| GGT<br>Gly | AGC<br>Ser | ATT<br>Ile | GAA<br>Glu | AGC<br>Ser | GGG<br>Gly | AAT<br>Asn | CGC<br>Arg | ATT<br>Ile | TCT<br>Ser | AGC<br>Ser | GGT<br>Gly | GGG<br>Gly | GGC<br>Gly | GCG<br>Ala | AGC<br>Ser | 3603 |  |
|            |            |            | 1185       |            |            |            |            |            | 1190       |            |            | 1195       |            |            |            |      |  |
| CTT<br>Leu | AAT<br>Asn | TTT<br>Phe | AAC<br>Asn | GGG<br>Gly | CTT<br>Leu | CAA<br>Gln | GGC<br>Gly | ATT<br>Ile | CTT<br>Leu | TTA<br>Leu | ACG<br>Thr | AAC<br>Asn | GCG<br>Ala | ACT<br>Thr | TTG<br>Leu | 3651 |  |
|            |            |            | 1200       |            |            |            |            |            | 1205       |            |            | 1210       |            |            |            |      |  |
| TAT<br>Tyr | AAC<br>Asn | CGC<br>Arg | GCC<br>Ala | GCT<br>Ala | GGC<br>Gly | ACG<br>Thr | CAA<br>Gln | AGC<br>Ser | TCG<br>Ser | TCT<br>Ser | ATG<br>Met | AAT<br>Asn | TTT<br>Phe | ATC<br>Ile | TCT<br>Ser | 3699 |  |
|            |            |            | 1215       |            |            |            |            |            | 1220       |            |            | 1225       |            |            |            |      |  |
| AAC<br>Asn | AGC<br>Ser | GCG<br>Ala | AAC<br>Asn | ATT<br>Ile | CAG<br>Gln | GCT<br>Ala | CAA<br>Gln | AAC<br>Asn | TCC<br>Ser | TAT<br>Tyr | TTT<br>Phe | ATA<br>Ile | GAC<br>Asp | GAT<br>Asp | ACC<br>Thr | 3747 |  |
|            |            |            | 1230       |            |            |            |            |            | 1235       |            |            | 1240       |            |            |            |      |  |
| GCA<br>Ala | CAA<br>Gln | AAT<br>Asn | GGC<br>Gly | GGT<br>Gly | AAC<br>Asn | CCT<br>Pro | AAT<br>Asn | TTC<br>Phe | AGT<br>Ser | TTC<br>Phe | AAC<br>Asn | GCT<br>Ala | TTG<br>Leu | AAT<br>Asn | CTG<br>Leu | 3795 |  |
| 1245       |            |            |            |            |            | 1250       |            |            |            |            |            | 1255       |            |            | 1260       |      |  |
| GAT<br>Asp | TTT<br>Phe | TCT<br>Ser | AAC<br>Asn | AGC<br>Ser | TCT<br>Ser | TTT<br>Phe | AGA<br>Arg | GGC<br>Gly | TAT<br>Tyr | GTG<br>Val | GGG<br>Gly | AAA<br>Lys | ACG<br>Thr | CAA<br>Gln | TCT<br>Ser | 3843 |  |

| 1265 |     |     |     |     | 1270 |     |     |     |     | 1275 |     |     |     |     |      |      |  |
|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|------|--|
| GTT  | TTT | AAA | TTC | AAT | GCC  | AAG | AAT | GCG | ATC | AGT  | TTC | ACC | AAC | AGC | ACG  | 3891 |  |
| Val  | Phe | Lys | Phe | Asn | Ala  | Lys | Asn | Ala | Ile | Ser  | Phe | Thr | Asn | Ser | Thr  |      |  |
| 1280 |     |     |     |     | 1285 |     |     |     |     | 1290 |     |     |     |     |      |      |  |
| AAT  | TTA | AGC | TCT | GGT | TTG  | TAT | CAA | ATG | CAA | GCT  | AAA | AGC | GTG | TTG | TTT  | 3939 |  |
| Asn  | Leu | Ser | Ser | Gly | Leu  | Tyr | Gln | Met | Gln | Ala  | Lys | Ser | Val | Leu | Phe  |      |  |
| 1295 |     |     |     |     | 1300 |     |     |     |     | 1305 |     |     |     |     |      |      |  |
| GAC  | AAT | TCC | AAT | TTA | AGC  | GTT | TCA | GTG | GGG | ACA  | AGC | AGT | ATT | AAA | GCC  | 3987 |  |
| Asp  | Asn | Ser | Asn | Leu | Ser  | Val | Ser | Val | Gly | Thr  | Ser | Ser | Ile | Lys | Ala  |      |  |
| 1310 |     |     |     |     | 1315 |     |     |     |     | 1320 |     |     |     |     |      |      |  |
| AAT  | GCG | ATC | AAT | CTT | TCT  | CAA | AAT | GCC | TCT | ATT  | AAT | GCG | AGC | AAC | CAT  | 4035 |  |
| Asn  | Ala | Ile | Asn | Leu | Ser  | Gln | Asn | Ala | Ser | Ile  | Asn | Ala | Ser | Asn | His  |      |  |
| 1325 |     |     |     |     | 1330 |     |     |     |     | 1335 |     |     |     |     | 1340 |      |  |
| TCA  | ACC | TTA | GAA | CTT | CAA  | GGC | GAT | TTG | AAT | GTG  | AAC | GAC | ACC | AGC | TCG  | 4083 |  |
| Ser  | Thr | Leu | Glu | Leu | Gln  | Gly | Asp | Leu | Asn | Val  | Asn | Asp | Thr | Ser | Ser  |      |  |
| 1345 |     |     |     |     | 1350 |     |     |     |     | 1355 |     |     |     |     |      |      |  |
| CTC  | AAC | CTC | AAC | CAA | AGC  | ACG | ATT | AAT | GTT | TCC  | AAT | AAC | GCC | ACG | ATC  | 4131 |  |
| Leu  | Asn | Leu | Asn | Gln | Ser  | Thr | Ile | Asn | Val | Ser  | Asn | Asn | Ala | Thr | Ile  |      |  |
| 1360 |     |     |     |     | 1365 |     |     |     |     | 1370 |     |     |     |     |      |      |  |
| AAC  | GAT | TAT | GCG | AGC | TTG  | ATT | GCG | AGT | AAT | GGC  | TCT | CAC | CTT | AAT | TTT  | 4179 |  |
| Asn  | Asp | Tyr | Ala | Ser | Leu  | Ile | Ala | Ser | Asn | Gly  | Ser | His | Leu | Asn | Phe  |      |  |
| 1375 |     |     |     |     | 1380 |     |     |     |     | 1385 |     |     |     |     |      |      |  |
| AAC  | GGG | GCG | GTT | AAT | TTC  | AAT | TCA | GCG | AAT | ATT  | ACT | ACG | AGT | TTG | AAT  | 4227 |  |
| Asn  | Gly | Ala | Val | Asn | Phe  | Asn | Ser | Ala | Asn | Ile  | Thr | Thr | Ser | Leu | Asn  |      |  |
| 1390 |     |     |     |     | 1395 |     |     |     |     | 1400 |     |     |     |     |      |      |  |
| AAT  | TCC | TCT | ATC | GTG | TTT  | AAG | GGG | GCG | GTC | TCT  | TTA | GGA | GGG | CAG | TTT  | 4275 |  |
| Asn  | Ser | Ser | Ile | Val | Phe  | Lys | Gly | Ala | Val | Ser  | Leu | Gly | Gly | Gln | Phe  |      |  |
| 1405 |     |     |     |     | 1410 |     |     |     |     | 1415 |     |     |     |     | 1420 |      |  |
| AAT  | TTA | AGC | AAT | AAC | TCT  | TCT | TTA | GAT | TTC | CAA  | GGC | TCT | AGC | GCT | ATC  | 4323 |  |
| Asn  | Leu | Ser | Asn | Asn | Ser  | Ser | Leu | Asp | Phe | Gln  | Gly | Ser | Ser | Ala | Ile  |      |  |
| 1425 |     |     |     |     | 1430 |     |     |     |     | 1435 |     |     |     |     |      |      |  |
| ACC  | TCT | AAC | ACG | GCG | TTT  | AAT | TTC | TAT | GAT | AAC  | GCT | TTT | TCT | CAA | AGC  | 4371 |  |
| Thr  | Ser | Asn | Thr | Ala | Phe  | Asn | Phe | Tyr | Asp | Asn  | Ala | Phe | Ser | Gln | Ser  |      |  |
| 1440 |     |     |     |     | 1445 |     |     |     |     | 1450 |     |     |     |     |      |      |  |
| CCC  | ATC | ACT | TTC | CAT | CAA  | GCC | CTT | GAC | ATT | AAA  | GCG | CCC | TTA | AGT | TTG  | 4419 |  |
| Pro  | Ile | Thr | Phe | His | Gln  | Ala | Leu | Asp | Ile | Lys  | Ala | Pro | Leu | Ser | Leu  |      |  |
| 1455 |     |     |     |     | 1460 |     |     |     |     | 1465 |     |     |     |     |      |      |  |
| GGA  | GGC | AAC | CTT | TTA | AAC  | CCT | AAC | AAC | AGC | AGC  | GTG | CTG | GAT | TTA | AAA  | 4467 |  |
| Gly  | Gly | Asn | Leu | Leu | Asn  | Pro | Asn | Asn | Ser | Ser  | Val | Leu | Asp | Leu | Lys  |      |  |
| 1470 |     |     |     |     | 1475 |     |     |     |     | 1480 |     |     |     |     |      |      |  |
| AAC  | AGC | CAG | CTT | GTT | TTT  | GGC | GAT | CAA | GGG | AGT  | TTG | AAT | ATC | GCT | AAC  | 4515 |  |
| Asn  | Ser | Gln | Leu | Val | Phe  | Gly | Asp | Gln | Gly | Ser  | Leu | Asn | Ile | Ala | Asn  |      |  |
| 1485 |     |     |     |     | 1490 |     |     |     |     | 1495 |     |     |     |     | 1500 |      |  |



|                     |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
|---------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| ATT<br>Ile          | GAT<br>Asp | TTA<br>Leu | CTA<br>Leu | AGC<br>Ser | GAT<br>Asp | CTA<br>Leu | AAT<br>Asn | GAT<br>Asp | AAT<br>Asn | AAA<br>Lys | AAT<br>Asn | CGT<br>Arg | GTG<br>Val | TAT<br>Tyr | AAC<br>Asn | 4563 |
| 1505 1510 1515      |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| ATC<br>Ile          | ATT<br>Ile | CAA<br>Gln | GCG<br>Ala | GAC<br>Asp | ATG<br>Met | AAT<br>Asn | AGT<br>Ser | AAT<br>Asn | TGG<br>Trp | TAT<br>Tyr | GAG<br>Glu | CGT<br>Arg | ATC<br>Ile | AGC<br>Ser | TTC<br>Phe | 4611 |
| 1520 1525 1530      |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| TTT<br>Phe          | GGC<br>Gly | ATG<br>Met | CAC<br>His | ATC<br>Ile | AAT<br>Asn | GAC<br>Asp | GGG<br>Gly | ATT<br>Ile | TAT<br>Tyr | GAT<br>Asp | GCT<br>Ala | AAA<br>Lys | AAC<br>Asn | CAA<br>Gln | ACT<br>Thr | 4659 |
| 1535 1540 1545      |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| TAT<br>Tyr          | AGT<br>Ser | TTC<br>Phe | ACT<br>Thr | AAC<br>Asn | CCC<br>Pro | CTT<br>Leu | AAT<br>Asn | AAC<br>Asn | GCC<br>Ala | CTA<br>Leu | AAA<br>Lys | ATC<br>Ile | ACC<br>Thr | GAG<br>Glu | AGC<br>Ser | 4707 |
| 1550 1555 1560      |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| TTT<br>Phe          | AAA<br>Lys | GAC<br>Asp | AAC<br>Asn | CAA<br>Gln | CTA<br>Leu | AGC<br>Ser | GTT<br>Val | ACG<br>Thr | CTC<br>Leu | TCT<br>Ser | CAA<br>Gln | ATC<br>Ile | CCG<br>Pro | GGT<br>Gly | ATT<br>Ile | 4755 |
| 1565 1570 1575 1580 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| AAA<br>Lys          | AAC<br>Asn | ACG<br>Thr | CTC<br>Leu | TAT<br>Tyr | AAC<br>Asn | ATT<br>Ile | GGC<br>Gly | TCT<br>Ser | GAA<br>Glu | ATT<br>Ile | TTT<br>Phe | AAC<br>Asn | TAC<br>Tyr | CAA<br>Gln | AAA<br>Lys | 4803 |
| 1585 1590 1595      |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GTT<br>Val          | TAT<br>Tyr | AAC<br>Asn | AAC<br>Asn | GCT<br>Ala | AAT<br>Asn | GGC<br>Gly | GTG<br>Val | TAT<br>Tyr | TCT<br>Ser | TAT<br>Tyr | AGC<br>Ser | GAT<br>Asp | GAT<br>Asp | GCA<br>Ala | CAA<br>Gln | 4851 |
| 1600 1605 1610      |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GGC<br>Gly          | GTG<br>Val | TTT<br>Phe | TAT<br>Tyr | CTC<br>Leu | ACA<br>Thr | AGC<br>Ser | AAC<br>Asn | GTG<br>Val | AAA<br>Lys | GGC<br>Gly | TAT<br>Tyr | TAC<br>Tyr | AAC<br>Asn | CCT<br>Pro | AAC<br>Asn | 4899 |
| 1615 1620 1625      |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| CAA<br>Gln          | TCC<br>Ser | TAT<br>Tyr | CAA<br>Gln | GCC<br>Ala | AGC<br>Ser | GGC<br>Gly | AGT<br>Ser | AAC<br>Asn | AAC<br>Asn | ACC<br>Thr | ACG<br>Thr | AAA<br>Lys | AAT<br>Asn | AAT<br>Asn | AAT<br>Asn | 4947 |
| 1630 1635 1640      |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| CTA<br>Leu          | ACC<br>Thr | TCT<br>Ser | GAA<br>Glu | TCT<br>Ser | TCT<br>Ser | ATC<br>Ile | ATC<br>Ile | TCG<br>Ser | CAA<br>Gln | ACC<br>Thr | TAT<br>Tyr | AAC<br>Asn | GCG<br>Ala | CAA<br>Gln | GGC<br>Gly | 4995 |
| 1645 1650 1655 1660 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| AAC<br>Asn          | CCT<br>Pro | ATT<br>Ile | AGC<br>Ser | GCG<br>Ala | TTG<br>Leu | CAC<br>His | ATC<br>Ile | TAT<br>Tyr | AAC<br>Asn | AAG<br>Lys | GGC<br>Gly | TAT<br>Tyr | AAT<br>Asn | TTC<br>Phe | AAC<br>Asn | 5043 |
| 1665 1670 1675      |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| AAT<br>Asn          | ATC<br>Ile | AAA<br>Lys | GCG<br>Ala | TTA<br>Leu | GGG<br>Gly | CAA<br>Gln | ATG<br>Met | GCT<br>Ala | CTC<br>Leu | AAA<br>Lys | CTC<br>Leu | TAC<br>Tyr | CCT<br>Pro | GAA<br>Glu | ATC<br>Ile | 5091 |
| 1680 1685 1690      |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| AAA<br>Lys          | AAG<br>Lys | GTA<br>Val | TTA<br>Leu | GGG<br>Gly | AAT<br>Asn | GAT<br>Asp | TTT<br>Phe | TCG<br>Ser | CCC<br>Pro | TCA<br>Ser | AGT<br>Ser | TTG<br>Leu | AAC<br>Asn | GCT<br>Ala | TTA<br>Leu | 5139 |
| 1695 1700 1705      |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| AAC<br>Asn          | TCT<br>Ser | AAT<br>Asn | GCG<br>Ala | CTA<br>Leu | AAC<br>Asn | CAA<br>Gln | CTT<br>Leu | ACC<br>Thr | AAA<br>Lys | CTC<br>Leu | ATC<br>Ile | ACG<br>Thr | CCT<br>Pro | AAC<br>Asn | GAC<br>Asp | 5187 |
| 1710 1715 1720      |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| TGG<br>Trp          | AAA<br>Lys | AAC<br>Asn | ATT<br>Ile | AAC<br>Asn | GAG<br>Glu | TTG<br>Leu | ATT<br>Ile | GAT<br>Asp | AAC<br>Asn | GCA<br>Ala | AAC<br>Asn | AAT<br>Asn | TCG<br>Ser | GTG<br>Val | GTG<br>Val | 5235 |

| 1725                                                                                                                               | 1730 |  |  |  |  |  | 1735 |  |  |  |  |  | 1740 |  |  |  |  |  |      |
|------------------------------------------------------------------------------------------------------------------------------------|------|--|--|--|--|--|------|--|--|--|--|--|------|--|--|--|--|--|------|
| CAA AAT TTC AAT AAC GGC ACT TTG ATT GTG GGA GCG ACT CAA ATA GGG<br>Gln Asn Phe Asn Asn Gly Thr Leu Ile Val Gly Ala Thr Gln Ile Gly | 1745 |  |  |  |  |  | 1750 |  |  |  |  |  | 1755 |  |  |  |  |  | 5283 |
| CAA ACA GAC ACC AAT AGC GCG GTT GTT TTT GGG GGC TTG GGC TAT CAA<br>Gln Thr Asp Thr Asn Ser Ala Val Val Phe Gly Gly Leu Tyr Gln     | 1760 |  |  |  |  |  | 1765 |  |  |  |  |  | 1770 |  |  |  |  |  | 5331 |
| ACA CCT TGT GAT TAT ACT GAT ATT GTG TGC CAA AAA TTT AGA GGC ACT<br>Thr Pro Cys Asp Tyr Thr Asp Ile Val Cys Gln Lys Phe Arg Gly Thr | 1775 |  |  |  |  |  | 1780 |  |  |  |  |  | 1785 |  |  |  |  |  | 5379 |
| TAT TTA GGA CAG CTT TTA GAG TCC AGC TCG GCT GAT TTG GGC TAT ATT<br>Tyr Leu Gly Gln Leu Leu Glu Ser Ser Ser Ala Asp Leu Gly Tyr Ile | 1790 |  |  |  |  |  | 1795 |  |  |  |  |  | 1800 |  |  |  |  |  | 5427 |
| GAC ACG ACT TTT AAC GCT AAA GAA ATT TAT CTT ACC GGC ACT TTA GGG<br>Asp Thr Thr Phe Asn Gln Lys Glu Ile Tyr Leu Thr Gly Thr Leu Gly | 1805 |  |  |  |  |  | 1810 |  |  |  |  |  | 1815 |  |  |  |  |  | 5475 |
| AGC GGG AAC GCA TGG GGG ACT GGG GGG AGC GCG AGC GTA ACT TTT AAC<br>Ser Gly Asn Ala Trp Gly Thr Gly Gly Ser Ala Ser Val Thr Phe Asn | 1825 |  |  |  |  |  | 1830 |  |  |  |  |  | 1835 |  |  |  |  |  | 5523 |
| AGC CAA ACT TCG CTC ATT CTC AAT CAG GCT AAT ATC GTA AGC TCG CAA<br>Ser Gln Thr Ser Leu Ile Leu Asn Gln Ala Asn Ile Val Ser Ser Gln | 1840 |  |  |  |  |  | 1845 |  |  |  |  |  | 1850 |  |  |  |  |  | 5571 |
| ACC GAT GGG ATC TTT AGC ATG CTG GGT CAA GAG GGT ATT AAT AAG GTT<br>Thr Asp Gly Ile Phe Ser Met Leu Gly Gln Glu Gly Ile Asn Lys Val | 1855 |  |  |  |  |  | 1860 |  |  |  |  |  | 1865 |  |  |  |  |  | 5619 |
| TTC AAT CAA GCC GGG CTC GCT AAT ATT TTG GGC GAA GTG GCG GTG CAA<br>Phe Asn Gln Ala Gly Leu Ala Asn Ile Leu Gly Glu Val Ala Val Gln | 1870 |  |  |  |  |  | 1875 |  |  |  |  |  | 1880 |  |  |  |  |  | 5667 |
| TCC ATC AAC AAA GCC GGG GGA TTA GGG AAT TTG ATA GTA AAT ACG CTA<br>Ser Ile Asn Lys Ala Gly Gly Leu Gly Asn Leu Ile Val Asn Thr Leu | 1885 |  |  |  |  |  | 1890 |  |  |  |  |  | 1895 |  |  |  |  |  | 5715 |
| GGG AGT AAT AGC GTG ATT GGG GGG TAT TTA ACG CCT GAA CAA AAA AAT<br>Gly Ser Asn Ser Val Ile Gly Gly Tyr Leu Thr Pro Glu Gln Lys Asn | 1905 |  |  |  |  |  | 1910 |  |  |  |  |  | 1915 |  |  |  |  |  | 5763 |
| CAA ACC CTA AGC CAG CTT TTA GGG CAG AAT AAC TTT GAT AAT CTC ATG<br>Gln Thr Leu Ser Gln Leu Leu Gly Gln Asn Asn Phe Asp Asn Leu Met | 1920 |  |  |  |  |  | 1925 |  |  |  |  |  | 1930 |  |  |  |  |  | 5811 |
| AAC GAT AGC GGT TTG AAT ACG GCG ATT AAG GAT TTG ATC AGA CAA AAA<br>Asn Asp Ser Gly Leu Asn Thr Ala Ile Lys Asp Leu Ile Arg Gln Lys | 1935 |  |  |  |  |  | 1940 |  |  |  |  |  | 1945 |  |  |  |  |  | 5859 |
| TTA GGC TTT TGG ACC GGG CTA GTG GGG GGA TTA GCC GGA CTA GGG GGC<br>Leu Gly Phe Trp Thr Gly Leu Val Gly Gly Leu Ala Gly Leu Gly Gly | 1950 |  |  |  |  |  | 1955 |  |  |  |  |  | 1960 |  |  |  |  |  | 5907 |

|                    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
|--------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| ATT<br>Ile<br>1965 | GAT<br>Asp | TTG<br>Leu | CAA<br>Gln | AAC<br>Asn | CCT<br>Pro | GAA<br>Glu | AAG<br>Lys | CTT<br>Leu | ATA<br>Ile | GGC<br>Gly | AGC<br>Ser | ATG<br>Met | TCA<br>Ser | ATC<br>Ile | AAT<br>Asn | 5955 |
| 1970               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 1975               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 1980               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GAT<br>Asp         | TTA<br>Leu | TTG<br>Leu | AGT<br>Ser | AAA<br>Lys | AAA<br>Lys | GGG<br>Gly | TTG<br>Leu | TTC<br>Phe | AAT<br>Asn | CAG<br>Gln | ATC<br>Ile | ACC<br>Thr | GGC<br>Gly | TTT<br>Phe | ATT<br>Ile | 6003 |
| 1985               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 1990               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 1995               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| TCC<br>Ser         | GCT<br>Ala | AAC<br>Asn | GAT<br>Asp | ATA<br>Ile | GGG<br>Gly | CAA<br>Gln | GTC<br>Val | ATA<br>Ile | AGC<br>Ser | GTA<br>Val | ATG<br>Met | TTG<br>Leu | CAA<br>Gln | GAT<br>Asp | ATT<br>Ile | 6051 |
| 2000               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2005               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2010               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GTC<br>Val         | AAA<br>Lys | CCG<br>Pro | AGC<br>Ser | AAC<br>Asn | GCT<br>Ala | TTA<br>Leu | AAA<br>Lys | AAC<br>Asn | GAT<br>Asp | GTA<br>Val | GCG<br>Ala | GCT<br>Ala | TTA<br>Leu | GGC<br>Gly | AAG<br>Lys | 6099 |
| 2015               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2020               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2025               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| CAA<br>Gln         | ATG<br>Met | ATT<br>Ile | GGC<br>Gly | GAA<br>Glu | TTT<br>Phe | TTA<br>Leu | GGC<br>Gly | CAA<br>Gln | GAC<br>Asp | ACG<br>Thr | CTC<br>Leu | AAT<br>Asn | TCT<br>Ser | TTA<br>Leu | GAA<br>Glu | 6147 |
| 2030               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2035               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2040               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| AGC<br>Ser         | TTG<br>Leu | TTG<br>Leu | CAA<br>Gln | AAC<br>Asn | CAG<br>Gln | CAG<br>Gln | ATT<br>Ile | AAA<br>Lys | AGC<br>Ser | GTT<br>Val | TTA<br>Leu | GAC<br>Asp | AAA<br>Lys | GTC<br>Val | CTA<br>Leu | 6195 |
| 2045               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2050               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2055               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2060               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GCG<br>Ala         | GCT<br>Ala | AAA<br>Lys | GGT<br>Gly | TTA<br>Leu | GGG<br>Gly | CCT<br>Pro | ATT<br>Ile | TAT<br>Tyr | GAA<br>Glu | CAA<br>Gln | GGC<br>Gly | TTG<br>Leu | GGG<br>Gly | GAT<br>Asp | TTG<br>Leu | 6243 |
| 2065               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2070               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2075               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| ATA<br>Ile         | CCT<br>Pro | AAT<br>Asn | CTT<br>Leu | GGT<br>Gly | AAA<br>Lys | AAA<br>Lys | GGG<br>Gly | CTT<br>Leu | TTC<br>Phe | GCT<br>Ala | CCT<br>Pro | TAT<br>Tyr | GGC<br>Gly | TTG<br>Leu | AGT<br>Ser | 6291 |
| 2080               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2085               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2090               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| CAA<br>Gln         | GTG<br>Val | TGG<br>Trp | CAA<br>Gln | AAA<br>Lys | GGG<br>Gly | GAT<br>Asp | TTT<br>Phe | AGT<br>Ser | TTC<br>Phe | AAC<br>Asn | GCA<br>Ala | CAA<br>Gln | GGC<br>Gly | AAT<br>Asn | GTT<br>Val | 6339 |
| 2095               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2100               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2105               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| TTT<br>Phe         | GTG<br>Val | CAA<br>Gln | AAT<br>Asn | TCC<br>Ser | ACT<br>Thr | TTC<br>Phe | TCT<br>Ser | AAC<br>Asn | GCC<br>Ala | AAT<br>Asn | GGA<br>Gly | GGC<br>Gly | ACG<br>Thr | CTC<br>Leu | TCT<br>Ser | 6387 |
| 2110               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2115               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2120               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| TTT<br>Phe         | AAC<br>Asn | GCA<br>Ala | GGA<br>Gly | AAT<br>Asn | TCG<br>Ser | CTC<br>Leu | ATT<br>Ile | TTT<br>Phe | GCC<br>Ala | GGA<br>Gly | AAC<br>Asn | AAT<br>Asn | CAT<br>His | ATT<br>Ile | GCA<br>Ala | 6435 |
| 2125               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2130               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2135               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2140               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| TTC<br>Phe         | ACT<br>Thr | AAC<br>Asn | CAC<br>His | GCT<br>Ala | GGA<br>Gly | ACT<br>Thr | CTT<br>Leu | CAA<br>Gln | TTA<br>Leu | TTG<br>Leu | TCC<br>Ser | GAT<br>Asp | CAA<br>Gln | GTT<br>Val | TCT<br>Ser | 6483 |
| 2145               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2150               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2155               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| AAC<br>Asn         | ATT<br>Ile | AAC<br>Asn | ATC<br>Ile | ACC<br>Thr | ACG<br>Thr | CTT<br>Leu | AAC<br>Asn | GCT<br>Ala | AGC<br>Ser | AAC<br>Asn | GGC<br>Gly | CTT<br>Leu | AAG<br>Lys | ATT<br>Ile | AAC<br>Asn | 6531 |
| 2160               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2165               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2170               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GCC<br>Ala         | GCT<br>Ala | AAT<br>Asn | AAC<br>Asn | AAT<br>Asn | GTT<br>Val | TCT<br>Ser | GTG<br>Val | TCT<br>Ser | CAA<br>Gln | GGC<br>Gly | AAT<br>Asn | CTG<br>Leu | TTT<br>Phe | GTC<br>Val | AGC<br>Ser | 6579 |
| 2175               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2180               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| 2185               |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GCT<br>Ala         | AGC<br>Ser | TGC<br>Cys | GCG<br>Ala | CAA<br>Gln | CAA<br>Gln | AGC<br>Ser | GAT<br>Asp | CCA<br>Pro | ACT<br>Thr | ACA<br>Thr | GCT<br>Ala | AAT<br>Asn | ATT<br>Ile | GCA<br>Ala | AAC<br>Asn | 6627 |

| 2190               |            |            |            |            |            | 2195       |            |            |            |            |            | 2200       |            |            |            |      |      |      |
|--------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|------|------|
| CCT<br>Pro<br>2205 | TGC<br>Cys | GCG<br>Ala | CTT<br>Leu | AGC<br>Ser | GCC<br>Ala | CAA<br>Gln | AGC<br>Ser | ACG<br>Thr | AAT<br>Asn | GGC<br>Gly | GCT<br>Ala | TCT<br>Ser | TCT<br>Ser | AAT<br>Asn | AAT<br>Asn | 6675 |      |      |
|                    |            |            |            |            | 2210       |            |            |            |            |            | 2215       |            |            |            |            |      | 2220 |      |
| GCG<br>Ala         | TCA<br>Ser | AAT<br>Asn | AAC<br>Asn | GCG<br>Ala | CCA<br>Pro | ATC<br>Ile | GCC<br>Ala | TTG<br>Leu | AGT<br>Ser | AAT<br>Asn | AAC<br>Asn | GAT<br>Asp | GAA<br>Glu | AGC<br>Ser | TTG<br>Leu | 6723 |      |      |
|                    |            |            |            |            | 2225       |            |            |            |            |            | 2230       |            |            |            |            |      | 2235 |      |
| ATG<br>Met         | GTT<br>Val | GCG<br>Ala | GCG<br>Ala | AAT<br>Asn | GAT<br>Asp | TTC<br>Phe | AAT<br>Asn | TTT<br>Phe | TCA<br>Ser | GGC<br>Gly | AAT<br>Asn | ATT<br>Ile | TAC<br>Tyr | GCT<br>Ala | AAT<br>Asn | 6771 |      |      |
|                    |            |            |            |            | 2240       |            |            |            |            |            | 2245       |            |            |            |            |      | 2250 |      |
| GGG<br>Gly         | GTG<br>Val | GTT<br>Val | GAT<br>Asp | TTT<br>Phe | TCA<br>Ser | AAG<br>Lys | ATT<br>Ile | AAA<br>Lys | GGC<br>Gly | TCT<br>Ser | GCA<br>Ala | AAC<br>Asn | ATT<br>Ile | AAA<br>Lys | AAC<br>Asn | 6819 |      |      |
|                    |            |            |            |            | 2255       |            |            |            |            |            | 2260       |            |            |            |            |      | 2265 |      |
| CTG<br>Leu         | TAT<br>Tyr | CTT<br>Leu | TAC<br>Tyr | AAT<br>Asn | AAC<br>Asn | GCT<br>Ala | CAA<br>Gln | TTC<br>Phe | CAA<br>Gln | GCC<br>Ala | AAC<br>Asn | AAT<br>Asn | CTC<br>Leu | ACT<br>Thr | ATT<br>Ile | 6867 |      |      |
|                    |            |            |            |            | 2270       |            |            |            |            |            | 2275       |            |            |            |            |      | 2280 |      |
| TCC<br>Ser         | AAT<br>Asn | CAA<br>Gln | GCG<br>Ala | GTG<br>Val | TTA<br>Leu | GAA<br>Glu | AAA<br>Lys | AAC<br>Asn | GCC<br>Ala | AGC<br>Ser | TTT<br>Phe | GTA<br>Val | ACG<br>Thr | AAT<br>Asn | AAT<br>Asn | 6915 |      |      |
|                    |            |            |            |            | 2285       |            |            |            |            |            | 2290       |            |            |            |            |      | 2295 | 2300 |
| TTA<br>Leu         | AAC<br>Asn | ATT<br>Ile | CAA<br>Gln | GGA<br>Gly | GCG<br>Ala | TTT<br>Phe | AAC<br>Asn | AAC<br>Asn | AAC<br>Asn | GCC<br>Ala | ACG<br>Thr | CAA<br>Gln | AAA<br>Lys | ATA<br>Ile | GAG<br>Glu | 6963 |      |      |
|                    |            |            |            |            | 2305       |            |            |            |            |            | 2310       |            |            |            |            |      | 2315 |      |
| GTG<br>Val         | CTT<br>Leu | CAA<br>Gln | AAT<br>Asn | TTA<br>Leu | GTG<br>Val | ATC<br>Ile | GCT<br>Ala | TCA<br>Ser | AAC<br>Asn | GCT<br>Ala | TCT<br>Ser | TTA<br>Leu | AGC<br>Ser | ACC<br>Thr | GGG<br>Gly | 7011 |      |      |
|                    |            |            |            |            | 2320       |            |            |            |            |            | 2325       |            |            |            |            |      | 2330 |      |
| ATT<br>Ile         | TAT<br>Tyr | GGG<br>Gly | TTA<br>Leu | GAA<br>Glu | GTA<br>Val | GGG<br>Gly | GGG<br>Gly | GCT<br>Ala | TTG<br>Leu | AAT<br>Asn | AAT<br>Asn | TCT<br>Ser | GGA<br>Gly | GCG<br>Ala | ATC<br>Ile | 7059 |      |      |
|                    |            |            |            |            | 2335       |            |            |            |            |            | 2340       |            |            |            |            |      | 2345 |      |
| CAT<br>His         | TTT<br>Phe | AAT<br>Asn | TTA<br>Leu | GAA<br>Glu | AAT<br>Asn | ACC<br>Thr | CAA<br>Gln | ACG<br>Thr | CCA<br>Pro | ACG<br>Thr | CCG<br>Pro | CTC<br>Leu | ATT<br>Ile | CAA<br>Gln | GCA<br>Ala | 7107 |      |      |
|                    |            |            |            |            | 2350       |            |            |            |            |            | 2355       |            |            |            |            |      | 2360 |      |
| GAG<br>Glu         | GGG<br>Gly | ATC<br>Ile | ATT<br>Ile | AAC<br>Asn | CTC<br>Leu | AAC<br>Asn | ACC<br>Thr | ACC<br>Thr | CAA<br>Gln | ACG<br>Thr | CCT<br>Pro | TTT<br>Phe | ATG<br>Met | AAT<br>Asn | GTC<br>Val | 7155 |      |      |
|                    |            |            |            |            | 2365       |            |            |            |            |            | 2370       |            |            |            |            |      | 2375 | 2380 |
| AAT<br>Asn         | AAC<br>Asn | AGC<br>Ser | ATG<br>Met | GCC<br>Ala | AAT<br>Asn | AAT<br>Asn | ACG<br>Thr | ACT<br>Thr | TAC<br>Tyr | ACT<br>Thr | TTA<br>Leu | TTA<br>Leu | AAA<br>Lys | AGC<br>Ser | AGC<br>Ser | 7203 |      |      |
|                    |            |            |            |            | 2385       |            |            |            |            |            | 2390       |            |            |            |            |      | 2395 |      |
| CGT<br>Arg         | TAC<br>Tyr | ATT<br>Ile | GAT<br>Asp | TAC<br>Tyr | AAT<br>Asn | ATC<br>Ile | AAC<br>Asn | CCC<br>Pro | AAC<br>Asn | AGC<br>Ser | TTG<br>Leu | CAA<br>Gln | TCG<br>Ser | TAT<br>Tyr | TTG<br>Leu | 7251 |      |      |
|                    |            |            |            |            | 2400       |            |            |            |            |            | 2405       |            |            |            |            |      | 2410 |      |
| AAT<br>Asn         | CTC<br>Leu | TAC<br>Tyr | ACT<br>Thr | TTA<br>Leu | ATC<br>Ile | AAT<br>Asn | ATC<br>Ile | AAC<br>Asn | GGG<br>Gly | AAC<br>Asn | CAC<br>His | ATA<br>Ile | GAG<br>Glu | GAA<br>Glu | AAA<br>Lys | 7299 |      |      |
|                    |            |            |            |            | 2415       |            |            |            |            |            | 2420       |            |            |            |            |      | 2425 |      |

|                                                                                                                                        |      |
|----------------------------------------------------------------------------------------------------------------------------------------|------|
| AAC GGC GCA TTG ACT TAT TTG GGC CAA CGG GTT TTG TTA CAA GAT AAG<br>Asn Gly Ala Leu Thr Tyr Leu Gly Gln Arg Val Leu Leu Gln Asp Lys     | 7347 |
| 2430 2435 2440                                                                                                                         |      |
| GGG TTA TTG TTA AGC GTA GCG CTG CCC AAC TCA AAC AAC GCT TCT CAA<br>Gly Leu Leu Leu Ser Val Ala Leu Pro Asn Ser Asn Asn Ala Ser Gln     | 7395 |
| 2445 2450 2455 2460                                                                                                                    |      |
| AAC AAC ATT TTA AGC CTT TCT GTC CTT TAT AAC CAA GTT AAA ATG TCT<br>Asn Asn Ile Leu Ser Leu Ser Val Leu Tyr Asn Asn Gln Val Lys Met Ser | 7443 |
| 2465 2470 2475                                                                                                                         |      |
| TGC GGC GAT AAA GCG ATG GAT TTT ACC CCC CCT ACC TTA CAA GAT TAC<br>Cys Gly Asp Lys Ala Met Asp Phe Thr Pro Pro Thr Leu Gln Asp Tyr     | 7491 |
| 2480 2485 2490                                                                                                                         |      |
| ATT GTG GGC ATT CAA GGG CAA AGC GCG CTC AAT CAA ATT GAA GCT GTT<br>Ile Val Gly Ile Gln Gly Gln Ser Ala Leu Asn Gln Ile Glu Ala Val     | 7539 |
| 2495 2500 2505                                                                                                                         |      |
| GGG GGC AAC GCT ATC AAG TGG CTT TCA ACA TTG ATG ATG GAG ACT AAA<br>Gly Gly Asn Ala Ile Lys Trp Leu Ser Thr Leu Met Met Glu Thr Lys     | 7587 |
| 2510 2515 2520                                                                                                                         |      |
| GAA AAC CCG TTT TTT GCG CCG ATT TAT TTA AAA AAC CAC TCT TTG AAT<br>Glu Asn Pro Phe Phe Ala Pro Ile Tyr Leu Lys Asn His Ser Leu Asn     | 7635 |
| 2525 2530 2535 2540                                                                                                                    |      |
| GAA ATC TTA GGC GTA ACA AAA GAT CTT CAA AAC ACC GCA AGC TTG ATT<br>Glu Ile Leu Gly Val Thr Lys Asp Leu Gln Asn Thr Ala Ser Leu Ile     | 7683 |
| 2545 2550 2555                                                                                                                         |      |
| TCT AAC CCT AAT TTT AGA GAT AAC GCT ACC AAT CTT TTA GAA TTG GCG<br>Ser Asn Pro Asn Phe Arg Asp Asn Ala Thr Asn Leu Leu Glu Leu Ala     | 7731 |
| 2560 2565 2570                                                                                                                         |      |
| AGT TAC ACC CAA CAA ACC AGC CGT TTA ACA AAA CTC TCT GAT TTT AGA<br>Ser Tyr Thr Gln Gln Thr Ser Arg Leu Thr Lys Leu Ser Asp Phe Arg     | 7779 |
| 2575 2580 2585                                                                                                                         |      |
| TCT AGA GAG GGA GAG TCT GAT TTT TCT TTG TTA GAG CTT AAA AAC AAG<br>Ser Arg Glu Gly Glu Ser Asp Phe Ser Leu Leu Glu Leu Lys Asn Lys     | 7827 |
| 2590 2595 2600                                                                                                                         |      |
| CGT TTT AGC GAT CCT AAT CCA GAG GTT TTT GTC AAA TAC TCT CAA CTT<br>Arg Phe Ser Asp Pro Asn Pro Glu Val Phe Val Lys Tyr Ser Gln Leu     | 7875 |
| 2605 2610 2615 2620                                                                                                                    |      |
| AGC AAA CAC CCA AAT AAC CTT TGG GTT CAA GGG GTG GGA GGA GCG AGC<br>Ser Lys His Pro Asn Asn Leu Trp Val Gln Gly Val Gly Gly Ala Ser     | 7923 |
| 2625 2630 2635                                                                                                                         |      |
| TTT ATT TCT GGG GGC AAT GGC ACG CTT TAT GGC TTG AAT GCG GGC TAT<br>Phe Ile Ser Gly Gly Asn Gly Thr Leu Tyr Gly Leu Asn Ala Gly Tyr     | 7971 |
| 2640 2645 2650                                                                                                                         |      |
| GAC AGG TTG GTT AAA AAT GTG ATC CTT GGG GGT TAT GTG GCT TAT GGC<br>Asp Arg Leu Val Lys Asn Val Ile Leu Gly Gly Tyr Val Ala Tyr Gly     | 8019 |

| 2655 |     |     |     |     | 2660 |     |     |     |     | 2665 |     |     |     |     |      |      |
|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|-----|------|------|
| TAT  | AGC | GAC | TTT | AAT | GGG  | AAC | ATC | ATG | CAT | TCT  | TTG | GGT | AAT | AAT | GTG  | 8067 |
| Tyr  | Ser | Asp | Phe | Asn | Gly  | Asn | Ile | Met | His | Ser  | Leu | Gly | Asn | Asn | Val  |      |
| 2670 |     |     |     |     | 2675 |     |     |     |     | 2680 |     |     |     |     |      |      |
| GAT  | GTG | GGG | ATG | TAT | GCG  | AGG | GCT | TTT | TTA | AAA  | AGG | AAC | GAA | TTC | ACT  | 8115 |
| Asp  | Val | Gly | Met | Tyr | Ala  | Arg | Ala | Phe | Leu | Lys  | Arg | Asn | Glu | Phe | Thr  |      |
| 2685 |     |     |     |     | 2690 |     |     |     |     | 2695 |     |     |     |     | 2700 |      |
| TTG  | AGC | GCG | AAT | GAA | ACT  | TAT | GGA | GGC | AAT | GCA  | ACT | AGT | ATC | AAT | TCT  | 8163 |
| Leu  | Ser | Ala | Asn | Glu | Thr  | Tyr | Gly | Gly | Asn | Ala  | Thr | Ser | Ile | Asn | Ser  |      |
| 2705 |     |     |     |     | 2710 |     |     |     |     | 2715 |     |     |     |     |      |      |
| TCT  | AAT | TCT | TTG | CTC | TCT  | GTG | TTG | AAC | CAA | CGC  | TAC | AAC | TAC | AAC | ACC  | 8211 |
| Ser  | Asn | Ser | Leu | Leu | Ser  | Val | Leu | Asn | Gln | Arg  | Tyr | Asn | Tyr | Asn | Thr  |      |
| 2720 |     |     |     |     | 2725 |     |     |     |     | 2730 |     |     |     |     |      |      |
| TGG  | ACA | ACG | AGC | GTG | AAC  | GGG | AAT | TAC | GGC | TAT  | GAT | TTC | ATG | TTC | AAA  | 8259 |
| Trp  | Thr | Thr | Ser | Val | Asn  | Gly | Asn | Tyr | Gly | Tyr  | Asp | Phe | Met | Phe | Lys  |      |
| 2735 |     |     |     |     | 2740 |     |     |     |     | 2745 |     |     |     |     |      |      |
| CAA  | AAA | AGC | GTG | GTG | CTA  | AAA | CCT | CAA | GTG | GGT  | TTG | AGC | TAT | CAT | TTC  | 8307 |
| Gln  | Lys | Ser | Val | Val | Leu  | Lys | Pro | Gln | Val | Gly  | Leu | Ser | Tyr | His | Phe  |      |
| 2750 |     |     |     |     | 2755 |     |     |     |     | 2760 |     |     |     |     |      |      |
| ATA  | GGT | CTA | AGT | GGG | ATG  | AAA | GGC | AAT | GAT | GCC  | GCT | TAC | AAA | CAA | TTC  | 8355 |
| Ile  | Gly | Leu | Ser | Gly | Met  | Lys | Gly | Asn | Asp | Ala  | Ala | Tyr | Lys | Gln | Phe  |      |
| 2765 |     |     |     |     | 2770 |     |     |     |     | 2775 |     |     |     |     | 2780 |      |
| CTC  | ATG | CAT | TCA | AAC | CCC  | TCT | AAC | GAA | TCG | GTT  | TTA | ACG | CTC | AAC | ATG  | 8403 |
| Leu  | Met | His | Ser | Asn | Pro  | Ser | Asn | Glu | Ser | Val  | Leu | Thr | Leu | Asn | Met  |      |
| 2785 |     |     |     |     | 2790 |     |     |     |     | 2795 |     |     |     |     |      |      |
| GGG  | TTG | GAG | AGC | CGT | AAA  | TAT | TTT | GGT | AAA | AAT  | TCC | TAT | TAT | TTT | GTA  | 8451 |
| Gly  | Leu | Glu | Ser | Arg | Lys  | Tyr | Phe | Gly | Lys | Asn  | Ser | Tyr | Tyr | Phe | Val  |      |
| 2800 |     |     |     |     | 2805 |     |     |     |     | 2810 |     |     |     |     |      |      |
| ACG  | GCG | AGA | CTA | GGT | AGG  | GAT | CTT | TTG | ATC | AAA  | TCT | AAA | GGC | AGC | AAT  | 8499 |
| Thr  | Ala | Arg | Leu | Gly | Arg  | Asp | Leu | Leu | Ile | Lys  | Ser | Lys | Gly | Ser | Asn  |      |
| 2815 |     |     |     |     | 2820 |     |     |     |     | 2825 |     |     |     |     |      |      |
| ACG  | GTG | CGT | TTT | GTG | GGC  | GAA | AAC | ACT | TTA | TTG  | TAT | CGC | AAG | GGG | GAA  | 8547 |
| Thr  | Val | Arg | Phe | Val | Gly  | Glu | Asn | Thr | Leu | Leu  | Tyr | Arg | Lys | Gly | Glu  |      |
| 2830 |     |     |     |     | 2835 |     |     |     |     | 2840 |     |     |     |     |      |      |
| GTT  | TTT | AAC | ACT | TTT | GCG  | AGC | GTG | ATT | ACA | GGG  | GGC | GAA | ATG | CAT | TTG  | 8595 |
| Val  | Phe | Asn | Thr | Phe | Ala  | Ser | Val | Ile | Thr | Gly  | Gly | Glu | Met | His | Leu  |      |
| 2845 |     |     |     |     | 2850 |     |     |     |     | 2855 |     |     |     |     | 2860 |      |
| TGG  | CGT | TTG | GTG | TAT | GTG  | AAT | GCG | GGG | GTG | GGG  | CTT | AAG | ATG | GGC | TTG  | 8643 |
| Trp  | Arg | Leu | Val | Tyr | Val  | Asn | Ala | Gly | Val | Gly  | Leu | Lys | Met | Gly | Leu  |      |
| 2865 |     |     |     |     | 2870 |     |     |     |     | 2875 |     |     |     |     |      |      |
| CAA  | TAC | CAA | GAT | ATT | AAT  | ATA | ACC | GGG | AAT | GTG  | GGC | ATG | CGA | GTG | GCG  | 8691 |
| Gln  | Tyr | Gln | Asp | Ile | Asn  | Ile | Thr | Gly | Asn | Val  | Gly | Met | Arg | Val | Ala  |      |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 325 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 330 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 335 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Asn | Ser | Ser | Phe | Asn | Gly | Gly | Thr | Phe | Thr | Phe | Asn | Asn | Gln | Thr | Asn | 340 | 345 | 350 | 355 | 360 | 365 | 370 | 375 | 380 | 385 | 390 | 395 | 400 | 405 | 410 | 415 | 420 | 425 | 430 | 435 | 440 | 445 | 450 | 455 | 460 | 465 | 470 | 475 | 480 | 485 | 490 | 495 | 500 | 505 | 510 | 515 | 520 | 525 | 530 | 535 | 540 | 545 | 550 | 555 | 560 | 565 | 570 | 575 | 580 | 585 | 590 | 595 | 600 | 605 | 610 | 615 | 620 | 625 | 630 | 635 | 640 | 645 | 650 | 655 | 660 | 665 | 670 | 675 | 680 | 685 | 690 | 695 | 700 | 705 | 710 | 715 | 720 | 725 | 730 | 735 | 740 | 745 | 750 | 755 | 760 | 765 | 770 | 775 | 780 |
| Pro | Thr | Asn | Asn | Ala | Gln | His | Pro | Gln | Ile | Gln | Asn | Ser | Ser | Phe | Ser | 340 | 345 | 350 | 355 | 360 | 365 | 370 | 375 | 380 | 385 | 390 | 395 | 400 | 405 | 410 | 415 | 420 | 425 | 430 | 435 | 440 | 445 | 450 | 455 | 460 | 465 | 470 | 475 | 480 | 485 | 490 | 495 | 500 | 505 | 510 | 515 | 520 | 525 | 530 | 535 | 540 | 545 | 550 | 555 | 560 | 565 | 570 | 575 | 580 | 585 | 590 | 595 | 600 | 605 | 610 | 615 | 620 | 625 | 630 | 635 | 640 | 645 | 650 | 655 | 660 | 665 | 670 | 675 | 680 | 685 | 690 | 695 | 700 | 705 | 710 | 715 | 720 | 725 | 730 | 735 | 740 | 745 | 750 | 755 | 760 | 765 | 770 | 775 | 780 |
| Gly | Asn | Ala | Thr | Thr | Leu | Lys | Gly | Phe | Val | Asn | Phe | Gln | Gln | Ala | Phe | 370 | 375 | 380 | 385 | 390 | 395 | 400 | 405 | 410 | 415 | 420 | 425 | 430 | 435 | 440 | 445 | 450 | 455 | 460 | 465 | 470 | 475 | 480 | 485 | 490 | 495 | 500 | 505 | 510 | 515 | 520 | 525 | 530 | 535 | 540 | 545 | 550 | 555 | 560 | 565 | 570 | 575 | 580 | 585 | 590 | 595 | 600 | 605 | 610 | 615 | 620 | 625 | 630 | 635 | 640 | 645 | 650 | 655 | 660 | 665 | 670 | 675 | 680 | 685 | 690 | 695 | 700 | 705 | 710 | 715 | 720 | 725 | 730 | 735 | 740 | 745 | 750 | 755 | 760 | 765 | 770 | 775 | 780 |     |     |     |     |     |     |
| Asn | Asn | Ser | Asn | His | Gln | Leu | Thr | Ile | Gln | Asn | Ala | Ser | Phe | Asn | Asn | 385 | 390 | 395 | 400 | 405 | 410 | 415 | 420 | 425 | 430 | 435 | 440 | 445 | 450 | 455 | 460 | 465 | 470 | 475 | 480 | 485 | 490 | 495 | 500 | 505 | 510 | 515 | 520 | 525 | 530 | 535 | 540 | 545 | 550 | 555 | 560 | 565 | 570 | 575 | 580 | 585 | 590 | 595 | 600 | 605 | 610 | 615 | 620 | 625 | 630 | 635 | 640 | 645 | 650 | 655 | 660 | 665 | 670 | 675 | 680 | 685 | 690 | 695 | 700 | 705 | 710 | 715 | 720 | 725 | 730 | 735 | 740 | 745 | 750 | 755 | 760 | 765 | 770 | 775 | 780 |     |     |     |     |     |     |     |     |     |
| Ala | Thr | Phe | Asn | Asn | Thr | Gly | Lys | Ile | Thr | Ile | Glu | Lys | Asp | Ala | Ser | 405 | 410 | 415 | 420 | 425 | 430 | 435 | 440 | 445 | 450 | 455 | 460 | 465 | 470 | 475 | 480 | 485 | 490 | 495 | 500 | 505 | 510 | 515 | 520 | 525 | 530 | 535 | 540 | 545 | 550 | 555 | 560 | 565 | 570 | 575 | 580 | 585 | 590 | 595 | 600 | 605 | 610 | 615 | 620 | 625 | 630 | 635 | 640 | 645 | 650 | 655 | 660 | 665 | 670 | 675 | 680 | 685 | 690 | 695 | 700 | 705 | 710 | 715 | 720 | 725 | 730 | 735 | 740 | 745 | 750 | 755 | 760 | 765 | 770 | 775 | 780 |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Phe | Asn | Asn | Thr | Thr | Phe | Asn | Thr | Ser | Val | Asp | Thr | Asn | Asn | Met | Ser | 420 | 425 | 430 | 435 | 440 | 445 | 450 | 455 | 460 | 465 | 470 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |



|     |      |      |      |     |      |      |      |      |      |      |      |      |      |      |
|-----|------|------|------|-----|------|------|------|------|------|------|------|------|------|------|
| 785 |      |      |      |     | 790  |      |      |      |      | 795  |      |      |      | 800  |
| Phe | Asn  | Ala  | Gly  | Gln | Ala  | Val  | Phe  | Glu  | Asn  | Thr  | Asn  | Phe  | Asn  | Gly  |
|     |      |      |      | 805 |      |      |      |      | 810  |      |      |      |      | 815  |
| Ser | Tyr  | Gln  | Phe  | Ser | Gly  | Asp  | Ser  | Leu  | Asn  | Phe  | Ser  | Asn  | Asn  | Gln  |
|     |      |      | 820  |     |      |      |      | 825  |      |      |      |      | 830  |      |
| Phe | Asn  | Ser  | Gly  | Ser | Phe  | Glu  | Ile  | Ser  | Ala  | Lys  | Asn  | Ala  | Ser  | Phe  |
|     |      | 835  |      |     |      |      | 840  |      |      |      |      | 845  |      |      |
| Asn | Ala  | Asn  | Phe  | Asn | Asn  | Ser  | Ala  | Ser  | Phe  | Asn  | Phe  | Asn  | Asn  | Ser  |
|     | 850  |      |      |     |      | 855  |      |      |      |      | 860  |      |      |      |
| Ala | Thr  | Thr  | Ser  | Phe | Val  | Gly  | Asp  | Phe  | Thr  | Asn  | Ala  | Asn  | Ser  | Asn  |
| 865 |      |      |      |     | 870  |      |      |      |      | 875  |      |      |      | 880  |
| Gln | Ile  | Ala  | Gly  | Asn | Ala  | Val  | Phe  | Gly  | Asn  | Ser  | Thr  | Asn  | Gly  | Ser  |
|     |      |      | 885  |     |      |      |      | 890  |      |      |      |      |      | 895  |
| Asn | Thr  | Ala  | Asn  | Phe | Asn  | Asn  | Thr  | Gly  | Ser  | Val  | Asn  | Ile  | Ser  | Gly  |
|     |      | 900  |      |     |      |      |      | 905  |      |      |      |      | 910  |      |
| Ala | Thr  | Phe  | Asp  | Asn | Val  | Val  | Phe  | Asn  | Gly  | Pro  | Thr  | Asn  | Thr  | Ser  |
|     |      | 915  |      |     |      |      | 920  |      |      |      |      | 925  |      |      |
| Lys | Gly  | Gln  | Val  | Thr | Leu  | Asn  | Asn  | Ile  | Thr  | Leu  | Lys  | Asn  | Leu  | Asn  |
|     | 930  |      |      |     |      | 935  |      |      |      |      | 940  |      |      |      |
| Pro | Leu  | Ser  | Phe  | Gly | Asp  | Gly  | Thr  | Ile  | Thr  | Phe  | Asn  | Ala  | His  | Ser  |
| 945 |      |      |      |     | 950  |      |      |      |      | 955  |      |      |      | 960  |
| Ile | Asn  | Ile  | Ala  | Glu | Ser  | Ile  | Thr  | Asn  | Gly  | Asn  | Pro  | Ile  | Thr  | Leu  |
|     |      |      | 965  |     |      |      |      |      | 970  |      |      |      |      | 975  |
| Ser | Ser  | Ser  | Lys  | Glu | Ile  | Glu  | Tyr  | Asn  | Asn  | Ala  | Phe  | Ser  | Lys  | Asn  |
|     |      |      | 980  |     |      |      |      | 985  |      |      |      |      | 990  |      |
| Trp | Gln  | Leu  | Ile  | Asn | Tyr  | Gln  | Gly  | His  | Gly  | Ala  | Ser  | Ser  | Glu  | Lys  |
|     | 995  |      |      |     |      | 1000 |      |      |      |      |      | 1005 |      |      |
| Val | Ser  | Ser  | Ala  | Gly | Asn  | Gly  | Val  | Tyr  | Asp  | Val  | Val  | Tyr  | Ser  | Phe  |
|     | 1010 |      |      |     |      | 1015 |      |      |      |      | 1020 |      |      |      |
| Asn | Gln  | Thr  | Tyr  | Asn | Phe  | Gln  | Glu  | Val  | Phe  | Ser  | Gln  | Asn  | Ser  | Ile  |
| 025 |      |      |      |     | 1030 |      |      |      |      | 1035 |      |      |      | 1040 |
| Ile | Arg  | Arg  | Leu  | Gly | Val  | Asn  | Met  | Val  | Phe  | Asp  | Tyr  | Val  | Asp  | Met  |
|     |      |      | 1045 |     |      |      |      |      | 1050 |      |      |      |      | 1055 |
| Lys | Ser  | Asp  | His  | Leu | Tyr  | Tyr  | Gln  | Asn  | Ala  | Leu  | Gly  | Phe  | Met  | Thr  |
|     |      | 1060 |      |     |      |      |      | 1065 |      |      |      |      | 1070 |      |
| Met | Pro  | Asn  | Ser  | Tyr | Asn  | Asn  | Asn  | Leu  | Gly  | Asn  | Ala  | Asn  | Asn  | Thr  |
|     |      | 1075 |      |     |      |      | 1080 |      |      |      |      | 1085 |      |      |
| Tyr | Tyr  | Tyr  | Asp  | Lys | Ser  | Ile  | Asp  | Phe  | Tyr  | Ala  | Ser  | Gly  | Lys  | Thr  |
|     | 1090 |      |      |     |      | 1095 |      |      |      |      | 1100 |      |      |      |
| Phe | Thr  | Lys  | Ala  | Glu | Phe  | Ser  | Gln  | Thr  | Phe  | Thr  | Gly  | Gln  | Asn  | Ser  |
| 105 |      |      |      |     | 1110 |      |      |      |      | 1115 |      |      |      | 1120 |
| Ile | Val  | Phe  | Gly  | Ala | Lys  | Ser  | Ile  | Trp  | Thr  | Ser  | Leu  | Ser  | Asp  | Ala  |
|     |      |      | 1125 |     |      |      |      | 1130 |      |      |      |      |      | 1135 |
| Gln | Ser  | Asn  | Thr  | Ile | Ile  | Arg  | Phe  | Gly  | Asp  | Asn  | Lys  | Gly  | Ala  | Gly  |
|     |      | 1140 |      |     |      |      |      | 1145 |      |      |      |      | 1150 |      |
| Asn | Asp  | Ala  | Ser  | Gly | His  | Cys  | Trp  | Asn  | Leu  | Gln  | Cys  | Ile  | Gly  | Phe  |
|     | 1155 |      |      |     |      |      | 1160 |      |      |      |      | 1165 |      |      |
| Thr | Gly  | His  | Tyr  | Glu | Ala  | Gln  | Lys  | Ile  | Tyr  | Ile  | Thr  | Gly  | Ser  | Ile  |
|     | 1170 |      |      |     |      | 1175 |      |      |      |      | 1180 |      |      |      |
| Ser | Gly  | Asn  | Arg  | Ile | Ser  | Ser  | Gly  | Gly  | Gly  | Ala  | Ser  | Leu  | Asn  | Phe  |
| 185 |      |      |      |     | 1190 |      |      |      |      | 1195 |      |      |      | 1200 |
| Gly | Leu  | Gln  | Gly  | Ile | Leu  | Leu  | Thr  | Asn  | Ala  | Thr  | Leu  | Tyr  | Asn  | Arg  |
|     |      |      | 1205 |     |      |      |      |      | 1210 |      |      |      |      | 1215 |
| Ala | Gly  | Thr  | Gln  | Ser | Ser  | Ser  | Met  | Asn  | Phe  | Ile  | Ser  | Asn  | Ser  | Ala  |
|     |      | 1220 |      |     |      |      |      | 1225 |      |      |      |      | 1230 |      |
| Ile | Gln  | Ala  | Gln  | Asn | Ser  | Tyr  | Phe  | Ile  | Asp  | Asp  | Thr  | Ala  | Gln  | Asn  |
|     | 1235 |      |      |     |      |      | 1240 |      |      |      |      | 1245 |      |      |
| Gly | Asn  | Pro  | Asn  | Phe | Ser  | Phe  | Asn  | Ala  | Leu  | Asn  | Leu  | Asp  | Phe  | Ser  |

|         |      |     |     |     |      |      |     |     |     |      |      |     |     |     |     |
|---------|------|-----|-----|-----|------|------|-----|-----|-----|------|------|-----|-----|-----|-----|
| 1250    |      |     |     |     | 1255 |      |     |     |     | 1260 |      |     |     |     |     |
| Ser 265 | Ser  | Phe | Arg | Gly | Tyr  | Val  | Gly | Lys | Thr | Gln  | Ser  | Val | Phe | Lys | Phe |
| Asn     | Ala  | Lys | Asn | Ala | Ile  | Ser  | Phe | Thr | Asn | Ser  | Thr  | Asn | Leu | Ser | Ser |
| 1285    |      |     |     |     | 1290 |      |     |     |     | 1295 |      |     |     |     |     |
| Gly     | Leu  | Tyr | Gln | Met | Gln  | Ala  | Lys | Ser | Val | Leu  | Phe  | Asp | Asn | Ser | Asn |
| 1300    |      |     |     |     | 1305 |      |     |     |     | 1310 |      |     |     |     |     |
| Leu     | Ser  | Val | Ser | Val | Gly  | Thr  | Ser | Ser | Ile | Lys  | Ala  | Asn | Ala | Ile | Asn |
| 1315    |      |     |     |     | 1320 |      |     |     |     | 1325 |      |     |     |     |     |
| Leu     | Ser  | Gln | Asn | Ala | Ser  | Ile  | Asn | Ala | Ser | Asn  | His  | Ser | Thr | Leu | Glu |
| 1330    |      |     |     |     | 1335 |      |     |     |     | 1340 |      |     |     |     |     |
| Leu     | Gln  | Gly | Asp | Leu | Asn  | Val  | Asn | Asp | Thr | Ser  | Ser  | Leu | Asn | Leu | Asn |
| 345     | 1350 |     |     |     |      | 1355 |     |     |     |      | 1360 |     |     |     |     |
| Gln     | Ser  | Thr | Ile | Asn | Val  | Ser  | Asn | Asn | Ala | Thr  | Ile  | Asn | Asp | Tyr | Ala |
| 1365    |      |     |     |     | 1370 |      |     |     |     | 1375 |      |     |     |     |     |
| Ser     | Leu  | Ile | Ala | Ser | Asn  | Gly  | Ser | His | Leu | Asn  | Phe  | Asn | Gly | Ala | Val |
| 1380    |      |     |     |     | 1385 |      |     |     |     | 1390 |      |     |     |     |     |
| Asn     | Phe  | Asn | Ser | Ala | Asn  | Ile  | Thr | Thr | Ser | Leu  | Asn  | Asn | Ser | Ser | Ile |
| 1395    |      |     |     |     | 1400 |      |     |     |     | 1405 |      |     |     |     |     |
| Val     | Phe  | Lys | Gly | Ala | Val  | Ser  | Leu | Gly | Gly | Gln  | Phe  | Asn | Leu | Ser | Asn |
| 1410    |      |     |     |     | 1415 |      |     |     |     | 1420 |      |     |     |     |     |
| Asn     | Ser  | Ser | Leu | Asp | Phe  | Gln  | Gly | Ser | Ser | Ala  | Ile  | Thr | Ser | Asn | Thr |
| 425     | 1430 |     |     |     |      | 1435 |     |     |     |      | 1440 |     |     |     |     |
| Ala     | Phe  | Asn | Phe | Tyr | Asp  | Asn  | Ala | Phe | Ser | Gln  | Ser  | Pro | Ile | Thr | Phe |
| 1445    |      |     |     |     | 1450 |      |     |     |     | 1455 |      |     |     |     |     |
| His     | Gln  | Ala | Leu | Asp | Ile  | Lys  | Ala | Pro | Leu | Ser  | Leu  | Gly | Gly | Asn | Leu |
| 1460    |      |     |     |     | 1465 |      |     |     |     | 1470 |      |     |     |     |     |
| Leu     | Asn  | Pro | Asn | Asn | Ser  | Ser  | Val | Leu | Asp | Leu  | Lys  | Asn | Ser | Gln | Leu |
| 1475    |      |     |     |     | 1480 |      |     |     |     | 1485 |      |     |     |     |     |
| Val     | Phe  | Gly | Asp | Gln | Gly  | Ser  | Leu | Asn | Ile | Ala  | Asn  | Ile | Asp | Leu | Leu |
| 1490    |      |     |     |     | 1495 |      |     |     |     | 1500 |      |     |     |     |     |
| Ser     | Asp  | Leu | Asn | Asp | Asn  | Lys  | Asn | Arg | Val | Tyr  | Asn  | Ile | Ile | Gln | Ala |
| 505     | 1510 |     |     |     |      | 1515 |     |     |     |      | 1520 |     |     |     |     |
| Asp     | Met  | Asn | Ser | Asn | Trp  | Tyr  | Glu | Arg | Ile | Ser  | Phe  | Phe | Gly | Met | His |
| 1525    |      |     |     |     | 1530 |      |     |     |     | 1535 |      |     |     |     |     |
| Ile     | Asn  | Asp | Gly | Ile | Tyr  | Asp  | Ala | Lys | Asn | Gln  | Thr  | Tyr | Ser | Phe | Thr |
| 1540    |      |     |     |     | 1545 |      |     |     |     | 1550 |      |     |     |     |     |
| Asn     | Pro  | Leu | Asn | Asn | Ala  | Leu  | Lys | Ile | Thr | Glu  | Ser  | Phe | Lys | Asp | Asn |
| 1555    |      |     |     |     | 1560 |      |     |     |     | 1565 |      |     |     |     |     |
| Gln     | Leu  | Ser | Val | Thr | Leu  | Ser  | Gln | Ile | Pro | Gly  | Ile  | Lys | Asn | Thr | Leu |
| 1570    |      |     |     |     | 1575 |      |     |     |     | 1580 |      |     |     |     |     |
| Tyr     | Asn  | Ile | Gly | Ser | Glu  | Ile  | Phe | Asn | Tyr | Gln  | Lys  | Val | Tyr | Asn | Asn |
| 585     | 1590 |     |     |     |      | 1595 |     |     |     |      | 1600 |     |     |     |     |
| Ala     | Asn  | Gly | Val | Tyr | Ser  | Tyr  | Ser | Asp | Asp | Ala  | Gln  | Gly | Val | Phe | Tyr |
| 1605    |      |     |     |     | 1610 |      |     |     |     | 1615 |      |     |     |     |     |
| Leu     | Thr  | Ser | Asn | Val | Lys  | Gly  | Tyr | Tyr | Asn | Pro  | Asn  | Gln | Ser | Tyr | Gln |
| 1620    |      |     |     |     | 1625 |      |     |     |     | 1630 |      |     |     |     |     |
| Ala     | Ser  | Gly | Ser | Asn | Asn  | Thr  | Thr | Lys | Asn | Asn  | Asn  | Leu | Thr | Ser | Glu |
| 1635    |      |     |     |     | 1640 |      |     |     |     | 1645 |      |     |     |     |     |
| Ser     | Ser  | Ile | Ile | Ser | Gln  | Thr  | Tyr | Asn | Ala | Gln  | Gly  | Asn | Pro | Ile | Ser |
| 1650    |      |     |     |     | 1655 |      |     |     |     | 1660 |      |     |     |     |     |
| Ala     | Leu  | His | Ile | Tyr | Asn  | Lys  | Gly | Tyr | Asn | Phe  | Asn  | Asn | Ile | Lys | Ala |
| 665     | 1670 |     |     |     |      | 1675 |     |     |     |      | 1680 |     |     |     |     |
| Leu     | Gly  | Gln | Met | Ala | Leu  | Lys  | Leu | Tyr | Pro | Glu  | Ile  | Lys | Lys | Val | Leu |
| 1685    |      |     |     |     | 1690 |      |     |     |     | 1695 |      |     |     |     |     |
| Gly     | Asn  | Asp | Phe | Ser | Pro  | Ser  | Ser | Leu | Asn | Ala  | Leu  | Asn | Ser | Asn | Ala |

|      |     |     |     |       |      |     |     |     |      |      |     |     |      |     |     |
|------|-----|-----|-----|-------|------|-----|-----|-----|------|------|-----|-----|------|-----|-----|
| 1715 |     |     |     |       | 1720 |     |     |     |      | 1725 |     |     |      |     |     |
| Asn  | Glu | Leu | Ile | Asp   | Asn  | Ala | Asn | Asn | Ser  | Val  | Val | Gln | Asn  | Phe | Asn |
| 1730 |     |     |     |       | 1735 |     |     |     |      | 1740 |     |     |      |     |     |
| Asn  | Gly | Thr | Leu | Ile   | Val  | Gly | Ala | Thr | Gln  | Ile  | Gly | Gln | Thr  | Asp | Thr |
| 745  |     |     |     |       | 1750 |     |     |     | 1755 |      |     |     | 1760 |     |     |
| Asn  | Ser | Ala | Val | Val   | Phe  | Gly | Gly | Leu | Gly  | Tyr  | Gln | Thr | Pro  | Cys | Asp |
| 1765 |     |     |     |       | 1770 |     |     |     |      | 1775 |     |     |      |     |     |
| Tyr  | Thr | Asp | Ile | Val   | Cys  | Gln | Lys | Phe | Arg  | Gly  | Thr | Tyr | Leu  | Gly | Gln |
| 1780 |     |     |     |       | 1785 |     |     |     |      | 1790 |     |     |      |     |     |
| Leu  | Leu | Glu | Ser | Ser   | Ser  | Ala | Asp | Leu | Gly  | Tyr  | Ile | Asp | Thr  | Thr | Phe |
| 1795 |     |     |     |       | 1800 |     |     |     |      | 1805 |     |     |      |     |     |
| Asn  | Ala | Lys | Glu | Ile   | Tyr  | Leu | Thr | Gly | Thr  | Leu  | Gly | Ser | Gly  | Asn | Ala |
| 1810 |     |     |     |       | 1815 |     |     |     |      | 1820 |     |     |      |     |     |
| Trp  | Gly | Thr | Gly | Gly   | Ser  | Ala | Ser | Val | Thr  | Phe  | Asn | Ser | Gln  | Thr | Ser |
| 825  |     |     |     |       | 1830 |     |     |     | 1835 |      |     |     | 1840 |     |     |
| Leu  | Ile | Leu | Asn | Gln   | Ala  | Asn | Ile | Val | Ser  | Ser  | Gln | Thr | Asp  | Gly | Ile |
| 1845 |     |     |     |       | 1850 |     |     |     |      | 1855 |     |     |      |     |     |
| Phe  | Ser | Met | Leu | Gly   | Gln  | Glu | Gly | Ile | Asn  | Lys  | Val | Phe | Asn  | Gln | Ala |
| 1860 |     |     |     |       | 1865 |     |     |     |      | 1870 |     |     |      |     |     |
| Gly  | Leu | Ala | Asn | Ile   | Leu  | Gly | Glu | Val | Ala  | Val  | Gln | Ser | Ile  | Asn | Lys |
| 1875 |     |     |     |       | 1880 |     |     |     |      | 1885 |     |     |      |     |     |
| Ala  | Gly | Gly | Leu | Gly   | Asn  | Leu | Ile | Val | Asn  | Thr  | Leu | Gly | Ser  | Asn | Ser |
| 1890 |     |     |     |       | 1895 |     |     |     |      | 1900 |     |     |      |     |     |
| Val  | Ile | Gly | Gly | Tyr   | Leu  | Thr | Pro | Glu | Gln  | Lys  | Asn | Gln | Thr  | Leu | Ser |
| 905  |     |     |     |       | 1910 |     |     |     | 1915 |      |     |     | 1920 |     |     |
| Gln  | Leu | Leu | Gly | Gln   | Asn  | Asn | Phe | Asp | Asn  | Leu  | Met | Asn | Asp  | Ser | Gly |
| 1925 |     |     |     |       | 1930 |     |     |     |      | 1935 |     |     |      |     |     |
| Leu  | Asn | Thr | Ala | Ile   | Lys  | Asp | Leu | Ile | Arg  | Gln  | Lys | Leu | Gly  | Phe | Trp |
| 1940 |     |     |     |       | 1945 |     |     |     |      | 1950 |     |     |      |     |     |
| Thr  | Gly | Leu | Val | Gly   | Gly  | Leu | Ala | Gly | Leu  | Gly  | Gly | Ile | Asp  | Leu | Gln |
| 1955 |     |     |     |       | 1960 |     |     |     |      | 1965 |     |     |      |     |     |
| Asn  | Pro | Glu | Lys | Leu   | Ile  | Gly | Ser | Met | Ser  | Ile  | Asn | Asp | Leu  | Leu | Ser |
| 1970 |     |     |     |       | 1975 |     |     |     |      | 1980 |     |     |      |     |     |
| Lys  | Lys | Gly | Leu | Phe   | Asn  | Gln | Ile | Thr | Gly  | Phe  | Ile | Ser | Ala  | Asn | Asp |
| 985  |     |     |     |       | 1990 |     |     |     | 1995 |      |     |     | 2000 |     |     |
| Ile  | Gly | Gln | Val | Ile   | Ser  | Val | Met | Leu | Gln  | Asp  | Ile | Val | Lys  | Pro | Ser |
| 2005 |     |     |     |       | 2010 |     |     |     |      | 2015 |     |     |      |     |     |
| Asn  | Ala | Leu | Lys | Asn   | Asp  | Val | Ala | Ala | Leu  | Gly  | Lys | Gln | Met  | Ile | Gly |
| 2020 |     |     |     |       | 2025 |     |     |     |      | 2030 |     |     |      |     |     |
| Glu  | Phe | Leu | Gly | Gln   | Asp  | Thr | Leu | Asn | Ser  | Leu  | Glu | Ser | Leu  | Leu | Gln |
| 2035 |     |     |     |       | 2040 |     |     |     |      | 2045 |     |     |      |     |     |
| Asn  | Gln | Gln | Ile | Lys   | Ser  | Val | Leu | Asp | Lys  | Val  | Leu | Ala | Ala  | Lys | Gly |
| 2050 |     |     |     |       | 2055 |     |     |     |      | 2060 |     |     |      |     |     |
| Leu  | Gly | Pro | Ile | Tyr   | Glu  | Gln | Gly | Leu | Gly  | Asp  | Leu | Ile | Pro  | Asn | Leu |
| 065  |     |     |     |       | 2070 |     |     |     | 2075 |      |     |     | 2080 |     |     |
| Gly  | Lys | Lys | Gly | Leu   | Phe  | Ala | Pro | Tyr | Gly  | Leu  | Ser | Gln | Val  | Trp | Gln |
| 2085 |     |     |     |       | 2090 |     |     |     |      | 2095 |     |     |      |     |     |
| Lys  | Gly | Asp | Phe | Ser   | Phe  | Asn | Ala | Gln | Gly  | Asn  | Val | Phe | Val  | Gln | Asn |
| 2100 |     |     |     |       | 2105 |     |     |     |      | 2110 |     |     |      |     |     |
| Ser  | Thr | Phe | Ser | Asn   | Ala  | Asn | Gly | Gly | Thr  | Leu  | Ser | Phe | Asn  | Ala | Gly |
| 2115 |     |     |     |       | 2120 |     |     |     |      | 2125 |     |     |      |     |     |
| Asn  | Ser | Leu | Ile | Phe   | Ala  | Gly | Asn | Asn | His  | Ile  | Ala | Phe | Thr  | Asn | His |
| 2130 |     |     |     |       | 2135 |     |     |     |      | 2140 |     |     |      |     |     |
| Ala  | Gly | Thr | Leu | Gln   | Leu  | Leu | Ser | Asp | Gln  | Val  | Ser | Asn | Ile  | Asn | Ile |
| 145  |     |     |     |       | 2150 |     |     |     | 2155 |      |     |     | 2160 |     |     |
| Thr  | Thr | Leu | Asn | Ala</ |      |     |     |     |      |      |     |     |      |     |     |

|      |      |     |     |     |     |     |      |      |     |     |     |      |      |     |     |  |
|------|------|-----|-----|-----|-----|-----|------|------|-----|-----|-----|------|------|-----|-----|--|
| 2180 |      |     |     |     |     |     | 2185 |      |     |     |     | 2190 |      |     |     |  |
| Gln  | Gln  | Ser | Asp | Pro | Thr | Thr | Ala  | Asn  | Ile | Ala | Asn | Pro  | Cys  | Ala | Leu |  |
| 2195 |      |     |     |     |     |     | 2200 |      |     |     |     | 2205 |      |     |     |  |
| Ser  | Ala  | Gln | Ser | Thr | Asn | Gly | Ala  | Ser  | Ser | Asn | Asn | Ala  | Ser  | Asn | Asn |  |
| 2210 |      |     |     |     |     |     | 2215 |      |     |     |     | 2220 |      |     |     |  |
| Ala  | Pro  | Ile | Ala | Leu | Ser | Asn | Asn  | Asp  | Glu | Ser | Leu | Met  | Val  | Ala | Ala |  |
| 225  | 2230 |     |     |     |     |     |      | 2235 |     |     |     |      | 2240 |     |     |  |
| Asn  | Asp  | Phe | Asn | Phe | Ser | Gly | Asn  | Ile  | Tyr | Ala | Asn | Gly  | Val  | Val | Asp |  |
| 2245 |      |     |     |     |     |     | 2250 |      |     |     |     | 2255 |      |     |     |  |
| Phe  | Ser  | Lys | Ile | Lys | Gly | Ser | Ala  | Asn  | Ile | Lys | Asn | Leu  | Tyr  | Leu | Tyr |  |
| 2260 |      |     |     |     |     |     | 2265 |      |     |     |     | 2270 |      |     |     |  |
| Asn  | Asn  | Ala | Gln | Phe | Gln | Ala | Asn  | Asn  | Leu | Thr | Ile | Ser  | Asn  | Gln | Ala |  |
| 2275 |      |     |     |     |     |     | 2280 |      |     |     |     | 2285 |      |     |     |  |
| Val  | Leu  | Glu | Lys | Asn | Ala | Ser | Phe  | Val  | Thr | Asn | Asn | Leu  | Asn  | Ile | Gln |  |
| 2290 |      |     |     |     |     |     | 2295 |      |     |     |     | 2300 |      |     |     |  |
| Gly  | Ala  | Phe | Asn | Asn | Asn | Ala | Thr  | Gln  | Lys | Ile | Glu | Val  | Leu  | Gln | Asn |  |
| 305  | 2310 |     |     |     |     |     |      | 2315 |     |     |     |      | 2320 |     |     |  |
| Leu  | Val  | Ile | Ala | Ser | Asn | Ala | Ser  | Leu  | Ser | Thr | Gly | Ile  | Tyr  | Gly | Leu |  |
| 2325 |      |     |     |     |     |     | 2330 |      |     |     |     | 2335 |      |     |     |  |
| Glu  | Val  | Gly | Gly | Ala | Leu | Asn | Asn  | Ser  | Gly | Ala | Ile | His  | Phe  | Asn | Leu |  |
| 2340 |      |     |     |     |     |     | 2345 |      |     |     |     | 2350 |      |     |     |  |
| Glu  | Asn  | Thr | Gln | Thr | Pro | Thr | Pro  | Leu  | Ile | Gln | Ala | Glu  | Gly  | Ile | Ile |  |
| 2355 |      |     |     |     |     |     | 2360 |      |     |     |     | 2365 |      |     |     |  |
| Asn  | Leu  | Asn | Thr | Thr | Gln | Thr | Pro  | Phe  | Met | Asn | Val | Asn  | Asn  | Ser | Met |  |
| 2370 |      |     |     |     |     |     | 2375 |      |     |     |     | 2380 |      |     |     |  |
| Ala  | Asn  | Asn | Thr | Thr | Tyr | Thr | Leu  | Leu  | Lys | Ser | Ser | Arg  | Tyr  | Ile | Asp |  |
| 385  | 2390 |     |     |     |     |     |      | 2395 |     |     |     |      | 2400 |     |     |  |
| Tyr  | Asn  | Ile | Asn | Pro | Asn | Ser | Leu  | Gln  | Ser | Tyr | Leu | Asn  | Leu  | Tyr | Thr |  |
| 2405 |      |     |     |     |     |     | 2410 |      |     |     |     | 2415 |      |     |     |  |
| Leu  | Ile  | Asn | Ile | Asn | Gly | Asn | His  | Ile  | Glu | Glu | Lys | Asn  | Gly  | Ala | Leu |  |
| 2420 |      |     |     |     |     |     | 2425 |      |     |     |     | 2430 |      |     |     |  |
| Thr  | Tyr  | Leu | Gly | Gln | Arg | Val | Leu  | Gln  | Asp | Lys | Gly | Leu  | Leu  | Leu | Leu |  |
| 2435 |      |     |     |     |     |     | 2440 |      |     |     |     | 2445 |      |     |     |  |
| Ser  | Val  | Ala | Leu | Pro | Asn | Ser | Asn  | Asn  | Ala | Ser | Gln | Asn  | Asn  | Ile | Leu |  |
| 2450 |      |     |     |     |     |     | 2455 |      |     |     |     | 2460 |      |     |     |  |
| Ser  | Leu  | Ser | Val | Leu | Tyr | Asn | Gln  | Val  | Lys | Met | Ser | Cys  | Gly  | Asp | Lys |  |
| 465  | 2470 |     |     |     |     |     |      | 2475 |     |     |     |      | 2480 |     |     |  |
| Ala  | Met  | Asp | Phe | Thr | Pro | Pro | Thr  | Leu  | Gln | Asp | Tyr | Ile  | Val  | Gly | Ile |  |
| 2485 |      |     |     |     |     |     | 2490 |      |     |     |     | 2495 |      |     |     |  |
| Gln  | Gly  | Gln | Ser | Ala | Leu | Asn | Gln  | Ile  | Glu | Ala | Val | Gly  | Gly  | Asn | Ala |  |
| 2500 |      |     |     |     |     |     | 2505 |      |     |     |     | 2510 |      |     |     |  |
| Ile  | Lys  | Trp | Leu | Ser | Thr | Leu | Met  | Met  | Glu | Thr | Lys | Glu  | Asn  | Pro | Phe |  |
| 2515 |      |     |     |     |     |     | 2520 |      |     |     |     | 2525 |      |     |     |  |
| Phe  | Ala  | Pro | Ile | Tyr | Leu | Lys | Asn  | His  | Ser | Leu | Asn | Glu  | Ile  | Leu | Gly |  |
| 2530 |      |     |     |     |     |     | 2535 |      |     |     |     | 2540 |      |     |     |  |
| Val  | Thr  | Lys | Asp | Leu | Gln | Asn | Thr  | Ala  | Ser | Leu | Ile | Ser  | Asn  | Pro | Asn |  |
| 545  | 2550 |     |     |     |     |     |      | 2555 |     |     |     |      | 2560 |     |     |  |
| Phe  | Arg  | Asp | Asn | Ala | Thr | Asn | Leu  | Leu  | Glu | Leu | Ala | Ser  | Tyr  | Thr | Gln |  |
| 2565 |      |     |     |     |     |     | 2570 |      |     |     |     | 2575 |      |     |     |  |
| Gln  | Thr  | Ser | Arg | Leu | Thr | Lys | Leu  | Ser  | Asp | Phe | Arg | Ser  | Arg  | Glu | Gly |  |
| 2580 |      |     |     |     |     |     | 2585 |      |     |     |     | 2590 |      |     |     |  |
| Glu  | Ser  | Asp | Phe | Ser | Leu | Leu | Glu  | Leu  | Lys | Asn | Lys | Arg  | Phe  | Ser | Asp |  |
| 2595 |      |     |     |     |     |     | 2600 |      |     |     |     | 2605 |      |     |     |  |
| Pro  | Asn  | Pro | Glu | Val | Phe | Val | Lys  | Tyr  | Ser | Gln | Leu | Ser  | Lys  | His | Pro |  |
| 2610 |      |     |     |     |     |     | 2615 |      |     |     |     | 2620 |      |     |     |  |
| Asn  | Asn  | Leu | Trp | Val | Gln | Gly | Val  | Gly  | Gly |     |     |      |      |     |     |  |



|              |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
|--------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|
| AGA<br>Arg   | CTC<br>Leu | CAC<br>His | ACT<br>Thr | AAG<br>Lys | AAT<br>Asn | GAG<br>Glu | GTG<br>Val | TTG<br>Leu | GAA<br>Glu | AAT<br>Asn | TGT<br>Cys | CGC<br>Arg | AAT<br>Asn | ATC<br>Ile | GCT<br>Ala | 148 |
| 253035       |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| AAG<br>Lys   | GTG<br>Val | ATT<br>Ile | GGT<br>Gly | GGG<br>Gly | GTC<br>Val | AAA<br>Lys | CAG<br>Gln | GGT<br>Gly | TTG<br>Leu | CCT<br>Pro | GGG<br>Gly | TTG<br>Leu | GAT<br>Asp | CTG<br>Leu | ATT<br>Ile | 196 |
| 40455055     |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| ATT<br>Ile   | TTC<br>Phe | CCT<br>Pro | GAA<br>Glu | TAC<br>Tyr | AGC<br>Ser | ACG<br>Thr | CAT<br>His | GGG<br>Gly | ATT<br>Ile | ATG<br>Met | TAT<br>Tyr | GAC<br>Asp | AGA<br>Arg | CAA<br>Gln | GAA<br>Glu | 244 |
| 606570       |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| ATG<br>Met   | TTT<br>Phe | GAT<br>Asp | ACA<br>Thr | GCC<br>Ala | GCA<br>Ala | AGC<br>Ser | GTT<br>Val | CCT<br>Pro | GGA<br>Gly | GAA<br>Glu | GAA<br>Glu | ACC<br>Thr | GCG<br>Ala | ATC<br>Ile | TTT<br>Phe | 292 |
| 758085       |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| GCT<br>Ala   | GAA<br>Glu | GCT<br>Ala | TGT<br>Cys | AAG<br>Lys | AAA<br>Lys | AAC<br>Asn | AAG<br>Lys | GTT<br>Val | TGG<br>Trp | GGA<br>Gly | GTG<br>Val | TTC<br>Phe | TCT<br>Ser | TTG<br>Leu | ACA<br>Thr | 340 |
| 9095100      |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| GGG<br>Gly   | GAA<br>Glu | AAA<br>Lys | CAC<br>His | GAG<br>Glu | CAA<br>Gln | GCC<br>Ala | AAA<br>Lys | AAG<br>Lys | AAT<br>Asn | CCC<br>Pro | TAT<br>Tyr | AAC<br>Asn | ACT<br>Thr | TTG<br>Leu | ATT<br>Ile | 388 |
| 105110115    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| CTT<br>Leu   | GTC<br>Val | AAT<br>Asn | GAT<br>Asp | AAG<br>Lys | GGT<br>Gly | GAG<br>Glu | ATC<br>Ile | GTG<br>Val | CAA<br>Gln | AAA<br>Lys | TAC<br>Tyr | CGC<br>Arg | AAA<br>Lys | ATC<br>Ile | TTG<br>Leu | 436 |
| 120125130135 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| CCT<br>Pro   | TGG<br>Trp | TGC<br>Cys | CCT<br>Pro | ATT<br>Ile | GAA<br>Glu | TGT<br>Cys | TGG<br>Trp | TAT<br>Tyr | CCT<br>Pro | GGG<br>Gly | GAT<br>Asp | AAA<br>Lys | ACT<br>Thr | TAT<br>Tyr | GTG<br>Val | 484 |
| 140145150    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| GTT<br>Val   | GAT<br>Asp | GGG<br>Gly | CCT<br>Pro | AAG<br>Lys | GGC<br>Gly | TTG<br>Leu | AAA<br>Lys | GTT<br>Val | TCT<br>Ser | TTG<br>Leu | ATT<br>Ile | ATT<br>Ile | TGC<br>Cys | GAT<br>Asp | GAT<br>Asp | 532 |
| 155160165    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| GGA<br>Gly   | AAC<br>Asn | TAC<br>Tyr | CCT<br>Pro | GAA<br>Glu | ATT<br>Ile | TGG<br>Trp | CGC<br>Arg | GAT<br>Asp | TGC<br>Cys | GCG<br>Ala | ATG<br>Met | CGT<br>Arg | GGG<br>Gly | GCA<br>Ala | GAA<br>Glu | 580 |
| 170175180    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| CTC<br>Leu   | ATT<br>Ile | GTG<br>Val | CGC<br>Arg | TGT<br>Cys | CAA<br>Gln | GGT<br>Gly | TAC<br>Tyr | ATG<br>Met | TAT<br>Tyr | CCG<br>Pro | GCT<br>Ala | AAG<br>Lys | GAG<br>Glu | CAA<br>Gln | CAA<br>Gln | 628 |
| 185190195    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| ATT<br>Ile   | GCA<br>Ala | ATA<br>Ile | GTA<br>Val | AAA<br>Lys | GCT<br>Ala | ATG<br>Met | GCG<br>Ala | TGG<br>Trp | GCC<br>Ala | AAT<br>Asn | CAA<br>Gln | TGT<br>Cys | TAT<br>Tyr | GTA<br>Val | GCG<br>Ala | 676 |
| 200205210215 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| GTA<br>Val   | GCG<br>Ala | AAT<br>Asn | GCG<br>Ala | ACC<br>Thr | GGT<br>Gly | TTT<br>Phe | GAT<br>Asp | GGG<br>Gly | GTG<br>Val | TAT<br>Tyr | TCC<br>Ser | TAT<br>Tyr | TTT<br>Phe | GGG<br>Gly | CAT<br>His | 724 |
| 220225230235 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| TCT<br>Ser   | AGC<br>Ser | ATT<br>Ile | ATT<br>Ile | GGT<br>Gly | TTT<br>Phe | GAC<br>Asp | GGG<br>Gly | CAT<br>His | ACT<br>Thr | TTG<br>Leu | GGC<br>Gly | GAA<br>Glu | TGC<br>Cys | GGG<br>Gly | GAA<br>Glu | 772 |
| 240245250255 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
| GAA<br>Glu   | GAA<br>Glu | AAT<br>Asn | GGT<br>Gly | CTT<br>Leu | CAA<br>Gln | TAC<br>Tyr | GCT<br>Ala | CAA<br>Gln | CTT<br>Leu | TCT<br>Ser | GTG<br>Val | CAA<br>Gln | CAA<br>Gln | ATC<br>Ile | CGT<br>Arg | 820 |

|                                                                   |     |     |      |
|-------------------------------------------------------------------|-----|-----|------|
| 250                                                               | 255 | 260 |      |
| GAT GCG AGA AAA TAC GAC CAA AGC CAA AAC CAA CTC TTC AAA CTC TTG   |     |     | 868  |
| Asp Ala Arg Lys Tyr Asp Gln Ser Gln Asn Gln Leu Phe Lys Leu Leu   |     |     |      |
| 265                                                               | 270 | 275 |      |
| CAC AGA GGT TAT AGT GGG GTT TTT GCT AGT GGC GAT GGG GAT AAG GGT   |     |     | 916  |
| His Arg Gly Tyr Ser Gly Val Phe Ala Ser Gly Asp Gly Asp Lys Gly   |     |     |      |
| 280                                                               | 285 | 290 | 295  |
| GTG GCG GAA TGC CCT TTT GAG TTC TAT AAA ACT TGG GTG AAT GAC CCC   |     |     | 964  |
| Val Ala Glu Cys Pro Phe Glu Phe Tyr Lys Thr Trp Val Asn Asp Pro   |     |     |      |
| 300                                                               | 305 | 310 |      |
| AAA AAA GCT CAA GAA AAT GTA GAA AAA ATC ACC CGC CCA AGC GTG GGT   |     |     | 1012 |
| Lys Lys Ala Gln Glu Asn Val Glu Lys Ile Thr Arg Pro Ser Val Gly   |     |     |      |
| 315                                                               | 320 | 325 |      |
| GTG GCC GCT TGT CCT GTG GGC GAT TTG CCC ACG AAA TAAAGGGCAA AAGGAG |     |     | 1064 |
| Val Ala Ala Cys Pro Val Gly Asp Leu Pro Thr Lys                   |     |     |      |
| 330                                                               | 335 |     |      |
| GAGGGGGGGG G                                                      |     |     | 1075 |

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | His | Gly | Asp | Ile | Ser | Ser | Ser | Pro | Asp | Thr | Val | Gly | Val | Ala |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Val | Asn | Tyr | Lys | Met | Pro | Arg | Leu | His | Thr | Lys | Asn | Glu | Val | Leu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Glu | Asn | Cys | Arg | Asn | Ile | Ala | Lys | Val | Ile | Gly | Gly | Val | Lys | Gln | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Pro | Gly | Leu | Asp | Leu | Ile | Ile | Phe | Pro | Glu | Tyr | Ser | Thr | His | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ile | Met | Tyr | Asp | Arg | Gln | Glu | Met | Phe | Asp | Thr | Ala | Ala | Ser | Val | Pro |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Glu | Glu | Thr | Ala | Ile | Phe | Ala | Glu | Ala | Cys | Lys | Lys | Asn | Lys | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Trp | Gly | Val | Phe | Ser | Leu | Thr | Gly | Glu | Lys | His | Glu | Gln | Ala | Lys | Lys |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Asn | Pro | Tyr | Asn | Thr | Leu | Ile | Leu | Val | Asn | Asp | Lys | Gly | Glu | Ile | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Lys | Tyr | Arg | Lys | Ile | Leu | Pro | Trp | Cys | Pro | Ile | Glu | Cys | Trp | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Gly | Asp | Lys | Thr | Tyr | Val | Val | Asp | Gly | Pro | Lys | Gly | Leu | Lys | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ser | Leu | Ile | Ile | Cys | Asp | Asp | Gly | Asn | Tyr | Pro | Glu | Ile | Trp | Arg | Asp |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |

```

Cys Ala Met Arg Gly Ala Glu Leu Ile Val Arg Cys Gln Gly Tyr Met
 180 185 190
Tyr Pro Ala Lys Glu Gln Gln Ile Ala Ile Val Lys Ala Met Ala Trp
 195 200 205
Ala Asn Gln Cys Tyr Val Ala Val Ala Asn Ala Thr Gly Phe Asp Gly
 210 215 220
Val Tyr Ser Tyr Phe Gly His Ser Ser Ile Ile Gly Phe Asp Gly His
 225 230 235 240
Thr Leu Gly Glu Cys Gly Glu Glu Glu Asn Gly Leu Gln Tyr Ala Gln
 245 250 255
Leu Ser Val Gln Gln Ile Arg Asp Ala Arg Lys Tyr Asp Gln Ser Gln
 260 265 270
Asn Gln Leu Phe Lys Leu Leu His Arg Gly Tyr Ser Gly Val Phe Ala
 275 280 285
Ser Gly Asp Gly Asp Lys Gly Val Ala Glu Cys Pro Phe Glu Phe Tyr
 290 295 300
Lys Thr Trp Val Asn Asp Pro Lys Lys Ala Gln Glu Asn Val Glu Lys
 305 310 315 320
Ile Thr Arg Pro Ser Val Gly Val Ala Ala Cys Pro Val Gly Asp Leu
 325 330 335
Pro Thr Lys

```

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 40...1686
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

```

ATCTCTATCC TTTATAGAAT TTGTTGTGGA GACTGGCTT ATG AAT AAT GTT TTT 54
 Met Asn Asn Val Phe
 1 5

GTT AAG GGT TTG TTT TTT TTT CTT TTA TTG TTT GGG TTT TTT TTG AAA 102
Val Lys Gly Leu Phe Phe Phe Leu Leu Leu Phe Gly Phe Phe Leu Lys
 10 15 20

GCT TCA GAA AGC CCA AAC GCT ACT CTT AAT CCA TCT AAA GAA AAT GTT 150
Ala Ser Glu Ser Pro Asn Ala Thr Leu Asn Pro Ser Lys Glu Asn Val
 25 30 35

TCT GTT GAA GAG CAA AAG CGT TTT GGA GGC GTT TTA GTT TTT GCA AGA 198
Ser Val Glu Glu Gln Lys Arg Phe Gly Gly Val Leu Val Phe Ala Arg
 40 45 50

GGC GCT GAT GGC TCG AGC ATG GAT CCT GCT TTA GTG ACT GAT GGC GAA 246

```



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ala | Asp | Gly | Ser | Ser | Met | Asp | Pro | Ala | Leu | Val | Thr | Asp | Gly | Glu |     |
| 55  |     |     |     |     |     | 60  |     |     |     |     | 65  |     |     |     |     |     |
| AGC | TAT | GTA | GCA | ACG | GGC | AAT | ATT | TAT | GAC | ACG | CTC | GTG | CAA | TTC | AGA | 294 |
| Ser | Tyr | Val | Ala | Thr | Gly | Asn | Ile | Tyr | Asp | Thr | Leu | Val | Gln | Phe | Arg |     |
| 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |     |     |     | 85  |     |
| TAC | GGC | ACC | ACA | GAA | GTT | GAA | CCC | GCC | TTA | GCG | ACA | AGC | TGG | GAC | ATA | 342 |
| Tyr | Gly | Thr | Thr | Glu | Val | Glu | Pro | Ala | Leu | Ala | Thr | Ser | Trp | Asp | Ile |     |
|     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |     | 100 |     |     |
| TCC | CCA | GAT | GGT | CTT | GTA | TAT | ACC | TTT | CAT | TTA | CGC | AAA | GGG | GTT | TAT | 390 |
| Ser | Pro | Asp | Gly | Leu | Val | Tyr | Thr | Phe | His | Leu | Arg | Lys | Gly | Val | Tyr |     |
|     |     |     | 105 |     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |
| TTC | CAC | CAA | ACG | AAG | TAT | TGG | AAT | AAA | AAA | GTA | GAG | TTT | AGC | GCT | AAA | 438 |
| Phe | His | Gln | Thr | Lys | Tyr | Trp | Asn | Lys | Lys | Val | Glu | Phe | Ser | Ala | Lys |     |
|     |     | 120 |     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     |
| GAT | GTG | CTG | TTT | TCG | TTT | GAA | CGC | CAG | ATG | GAT | AAA | GCT | AAA | CGA | TAT | 486 |
| Asp | Val | Leu | Phe | Ser | Phe | Glu | Arg | Gln | Met | Asp | Lys | Ala | Lys | Arg | Tyr |     |
|     | 135 |     |     |     |     | 140 |     |     |     |     | 145 |     |     |     |     |     |
| TAT | AGC | CCG | GGG | GCT | AAA | AGC | TAT | AAG | TAT | TGG | GAA | GGC | ATG | GGC | ATG | 534 |
| Tyr | Ser | Pro | Gly | Ala | Lys | Ser | Tyr | Lys | Tyr | Trp | Glu | Gly | Met | Gly | Met |     |
| 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |     |     |     | 165 |     |
| TCT | CAT | ATT | ATT | AAG | AGC | ATT | GAA | GCT | TTA | GAT | GAC | TAT | ACC | ATT | AGA | 582 |
| Ser | His | Ile | Ile | Lys | Ser | Ile | Glu | Ala | Leu | Asp | Asp | Tyr | Thr | Ile | Arg |     |
|     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |     | 180 |     |     |
| TTC | ACA | CTT | AAT | GGG | CCA | GAA | GCC | CCG | TTT | TTA | GCG | AAT | TTG | GGC | ATG | 630 |
| Phe | Thr | Leu | Asn | Gly | Pro | Glu | Ala | Pro | Phe | Leu | Ala | Asn | Leu | Gly | Met |     |
|     |     |     | 185 |     |     |     |     | 190 |     |     |     |     | 195 |     |     |     |
| GAC | TTT | TTG | AGC | ATT | TTG | AGT | AAG | GAT | TAC | GCT | GAT | TAC | CTG | GCT | CAA | 678 |
| Asp | Phe | Leu | Ser | Ile | Leu | Ser | Lys | Asp | Tyr | Ala | Asp | Tyr | Leu | Ala | Gln |     |
|     |     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |     |     |     |     |
| AAT | AAT | AAA | AAA | GAC | GAG | TTG | GCT | AAA | AAA | CCT | ATT | GGG | ACA | GGG | CCT | 726 |
| Asn | Asn | Lys | Lys | Asp | Glu | Leu | Ala | Lys | Lys | Pro | Ile | Gly | Thr | Gly | Pro |     |
|     | 215 |     |     |     |     | 220 |     |     |     |     | 225 |     |     |     |     |     |
| TTC | AAA | TTC | TTT | TTG | TGG | AAT | AAA | GAT | GAA | AAA | ATC | ATT | CTT | TTA | AAA | 774 |
| Phe | Lys | Phe | Phe | Leu | Trp | Asn | Lys | Asp | Glu | Lys | Ile | Ile | Leu | Leu | Lys |     |
| 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |     |     |     | 245 |     |
| AAT | CAA | GAT | TAT | TGG | GGG | CCT | AAA | GCG | TAT | TTG | GAT | AAG | GTG | GTG | GTG | 822 |
| Asn | Gln | Asp | Tyr | Trp | Gly | Pro | Lys | Ala | Tyr | Leu | Asp | Lys | Val | Val | Val |     |
|     |     |     |     | 250 |     |     |     |     | 255 |     |     |     |     | 260 |     |     |
| CGC | ACC | ATT | CCT | AAT | TCT | TCC | ACT | CGC | GCT | TTA | GCG | TTG | CGC | ACC | GGC | 870 |
| Arg | Thr | Ile | Pro | Asn | Ser | Ser | Thr | Arg | Ala | Leu | Ala | Leu | Arg | Thr | Gly |     |
|     |     |     | 265 |     |     |     |     | 270 |     |     |     |     | 275 |     |     |     |
| GAA | ATC | ATG | CTC | ATG | ACT | GGG | CCT | AAT | CTC | AAT | GAA | GTG | GAG | CAA | TTA | 918 |
| Glu | Ile | Met | Leu | Met | Thr | Gly | Pro | Asn | Leu | Asn | Glu | Val | Glu | Gln | Leu |     |
|     |     | 280 |     |     |     |     | 285 |     |     |     |     | 290 |     |     |     |     |

|              |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
|--------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| GAA<br>Glu   | AAA<br>Lys | GTC<br>Val | CCT<br>Pro | AAT<br>Asn | ATC<br>Ile | GTG<br>Val | GTG<br>Val | GAC<br>Asp | AAA<br>Lys | AGT<br>Ser | GCT<br>Ala | GGG<br>Gly | TTG<br>Leu | TTG<br>Leu | GCG<br>Ala | 966  |
| 295300305    |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| AGT<br>Ser   | TGG<br>Trp | CTT<br>Leu | TCG<br>Ser | TTG<br>Leu | AAC<br>Asn | ACG<br>Thr | CAA<br>Gln | AAA<br>Lys | AAG<br>Lys | TAT<br>Tyr | TTT<br>Phe | GAC<br>Asp | AAC<br>Asn | CCT<br>Pro | TTG<br>Leu | 1014 |
| 310315320325 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GTG<br>Val   | CGT<br>Arg | TTG<br>Leu | GCT<br>Ala | ATC<br>Ile | AAT<br>Asn | CAT<br>His | GCG<br>Ala | ATC<br>Ile | AAT<br>Asn | GCA<br>Ala | GAT<br>Asp | GAT<br>Asp | TAC<br>Tyr | ATC<br>Ile | AAA<br>Lys | 1062 |
| 330335340345 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GTG<br>Val   | CTT<br>Leu | TAT<br>Tyr | GAA<br>Glu | GGC<br>Gly | TTT<br>Phe | GCT<br>Ala | CAA<br>Gln | AAA<br>Lys | ATG<br>Met | GTC<br>Val | AAT<br>Asn | CCT<br>Pro | TTC<br>Phe | CCG<br>Pro | CCC<br>Pro | 1110 |
| 350355360365 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| ACC<br>Thr   | ATA<br>Ile | TGG<br>Trp | GGT<br>Gly | TAT<br>Tyr | AAC<br>Asn | TAC<br>Tyr | AAT<br>Asn | ATC<br>Ile | AAA<br>Lys | CCC<br>Pro | TAT<br>Tyr | GAA<br>Glu | TAC<br>Tyr | GAT<br>Asp | TTG<br>Leu | 1158 |
| 370375380385 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| AAA<br>Lys   | AAG<br>Lys | GCT<br>Ala | AAG<br>Lys | GAG<br>Glu | TTG<br>Leu | TTG<br>Leu | AAA<br>Lys | CAA<br>Gln | GCG<br>Ala | GGC<br>Gly | TAT<br>Tyr | CCT<br>Pro | AAC<br>Asn | GGC<br>Gly | TTT<br>Phe | 1206 |
| 390400405410 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| AAA<br>Lys   | ACC<br>Thr | ACT<br>Thr | ATT<br>Ile | TTT<br>Phe | ACC<br>Thr | ACT<br>Thr | GCC<br>Ala | ACT<br>Thr | CGT<br>Arg | AAC<br>Asn | CCA<br>Pro | AAA<br>Lys | GGA<br>Gly | GCG<br>Ala | GTG<br>Val | 1254 |
| 415420425430 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| TTC<br>Phe   | ATA<br>Ile | CAG<br>Gln | GCG<br>Ala | AGC<br>Ser | CTG<br>Leu | GCT<br>Ala | AAA<br>Lys | ATT<br>Ile | GGC<br>Gly | ATT<br>Ile | GAT<br>Asp | GTG<br>Val | AAA<br>Lys | ATT<br>Ile | GAA<br>Glu | 1302 |
| 435440445450 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GTG<br>Val   | TAT<br>Tyr | GAG<br>Glu | TGG<br>Trp | GGG<br>Gly | GCT<br>Ala | TAT<br>Tyr | TTG<br>Leu | AAA<br>Lys | AGA<br>Arg | ACG<br>Thr | GGT<br>Gly | CTG<br>Leu | GGC<br>Gly | GAA<br>Glu | CAT<br>His | 1350 |
| 460465470475 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| GAA<br>Glu   | ATG<br>Met | GCG<br>Ala | TTT<br>Phe | TCA<br>Ser | GGC<br>Gly | TGG<br>Trp | ATG<br>Met | GCA<br>Ala | GAC<br>Asp | ATT<br>Ile | GCG<br>Ala | GAT<br>Asp | CCG<br>Pro | GAT<br>Asp | AAT<br>Asn | 1398 |
| 480485490495 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| TTC<br>Phe   | TTA<br>Leu | TAC<br>Tyr | ACC<br>Thr | TTA<br>Leu | TGG<br>Trp | AGC<br>Ser | GAG<br>Glu | CAA<br>Gln | GCC<br>Ala | GCC<br>Ala | TCA<br>Ser | GCT<br>Ala | ATA<br>Ile | CCC<br>Pro | ACT<br>Thr | 1446 |
| 500505510515 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| CAA<br>Gln   | AAC<br>Asn | CAT<br>His | TCC<br>Ser | TTT<br>Phe | TAT<br>Tyr | AAA<br>Lys | AAT<br>Asn | AAG<br>Lys | GAG<br>Glu | TTT<br>Phe | TCC<br>Ser | AAT<br>Asn | CTG<br>Leu | CTC<br>Leu | ATA<br>Ile | 1494 |
| 520525530535 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| AAG<br>Lys   | GCT<br>Ala | AAA<br>Lys | CGC<br>Arg | GTT<br>Val | TCG<br>Ser | GAT<br>Asp | CAA<br>Gln | AAA<br>Lys | GAG<br>Glu | AGG<br>Arg | GAA<br>Glu | GCC<br>Ala | CTT<br>Leu | TAT<br>Tyr | TTA<br>Leu | 1542 |
| 540545550555 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| AAG<br>Lys   | GCA<br>Ala | CAA<br>Gln | GAA<br>Glu | ATT<br>Ile | ATC<br>Ile | CAT<br>His | AAA<br>Lys | GAC<br>Asp | GCG<br>Ala | CCT<br>Pro | TAT<br>Tyr | GTG<br>Val | CCT<br>Pro | TTA<br>Leu | GCC<br>Ala | 1590 |
| 560565570575 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
| TAT<br>Tyr   | CCT<br>Pro | TAT<br>Tyr | TCG<br>Ser | GTG<br>Val | GTG<br>Val | CCG<br>Pro | CAT<br>His | TTG<br>Leu | TCT<br>Ser | AAA<br>Lys | GTT<br>Val | AAG<br>Lys | GGT<br>Gly | TAT<br>Tyr | AAA<br>Lys | 1638 |



Ala Gly Leu Leu Ala Ser Trp Leu Ser Leu Asn Thr Gln Lys Lys Tyr  
 305 310 315 320  
 Phe Asp Asn Pro Leu Val Arg Leu Ala Ile Asn His Ala Ile Asn Ala  
 325 330 335  
 Asp Asp Tyr Ile Lys Val Leu Tyr Glu Gly Phe Ala Gln Lys Met Val  
 340 345 350  
 Asn Pro Phe Pro Pro Thr Ile Trp Gly Tyr Asn Tyr Asn Ile Lys Pro  
 355 360 365  
 Tyr Glu Tyr Asp Leu Lys Lys Ala Lys Glu Leu Leu Lys Gln Ala Gly  
 370 375 380  
 Tyr Pro Asn Gly Phe Lys Thr Thr Ile Phe Thr Thr Ala Thr Arg Asn  
 385 390 395 400  
 Pro Lys Gly Ala Val Phe Ile Gln Ala Ser Leu Ala Lys Ile Gly Ile  
 405 410 415  
 Asp Val Lys Ile Glu Val Tyr Glu Trp Gly Ala Tyr Leu Lys Arg Thr  
 420 425 430  
 Gly Leu Gly Glu His Glu Met Ala Phe Ser Gly Trp Met Ala Asp Ile  
 435 440 445  
 Ala Asp Pro Asp Asn Phe Leu Tyr Thr Leu Trp Ser Glu Gln Ala Ala  
 450 455 460  
 Ser Ala Ile Pro Thr Gln Asn His Ser Phe Tyr Lys Asn Lys Glu Phe  
 465 470 475 480  
 Ser Asn Leu Leu Ile Lys Ala Lys Arg Val Ser Asp Gln Lys Glu Arg  
 485 490 495  
 Glu Ala Leu Tyr Leu Lys Ala Gln Glu Ile Ile His Lys Asp Ala Pro  
 500 505 510  
 Tyr Val Pro Leu Ala Tyr Pro Tyr Ser Val Val Pro His Leu Ser Lys  
 515 520 525  
 Val Lys Gly Tyr Lys Thr Thr Gly Val Ser Val Asn Arg Phe Phe Lys  
 530 535 540  
 Val Tyr Leu Glu Lys  
 545

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...1050
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

GCGTGAATCG CTTCTTTAAG GTGTATTTAG AAAAATAAAA GGGGTTGC ATG CTG AGT 57  
 Met Leu Ser  
 1  
 TTT ATC ATT AAG CGT ATT TTG TGG GCG ATC CCC ACG CTG TTT GGA GTG 105  
 Phe Ile Ile Lys Arg Ile Leu Trp Ala Ile Pro Thr Leu Phe Gly Val  
 5 10 15

|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                  |                   |                   |                   |                   |                   |     |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| AGT<br>Ser<br>20  | ATC<br>Ile        | ATT<br>Ile        | GTG<br>Val        | TTT<br>Phe<br>25  | ATG<br>Met        | ATG<br>Met        | GTG<br>Val        | CAT<br>His        | TTA<br>Leu        | GTG<br>Val<br>30 | CCA<br>Pro        | GGA<br>Gly        | GAT<br>Asp        | CCG<br>Pro        | GCA<br>Ala<br>35  | 153 |
| TTA<br>Leu        | GTG<br>Val        | ATT<br>Ile        | TTA<br>Leu        | GGT<br>Gly<br>40  | GAA<br>Glu        | AAG<br>Lys        | GCC<br>Ala        | AAT<br>Asn        | CAA<br>Gln<br>45  | GCC<br>Ala       | GCT<br>Ala        | ATT<br>Ile        | GAT<br>Asp        | GCT<br>Ala<br>50  | TTA<br>Leu        | 201 |
| AGA<br>Arg        | GAG<br>Glu        | CAA<br>Gln        | TTT<br>Phe<br>55  | GGA<br>Gly        | TTG<br>Leu        | AAT<br>Asn        | AAG<br>Lys        | CCC<br>Pro<br>60  | TTG<br>Leu        | ATA<br>Ile       | GAG<br>Glu        | CAG<br>Gln        | TAT<br>Tyr<br>65  | TTT<br>Phe        | TTC<br>Phe        | 249 |
| TTT<br>Phe        | ATC<br>Ile        | AAT<br>Asn<br>70  | AAT<br>Asn        | GTG<br>Val        | TTG<br>Leu        | CAT<br>His        | GGC<br>Gly<br>75  | AAT<br>Asn        | TTT<br>Phe        | GGC<br>Gly       | ACT<br>Thr<br>80  | TCT<br>Ser        | ATC<br>Ile        | ATG<br>Met        | ACC<br>Thr        | 297 |
| GGT<br>Gly        | GAG<br>Glu<br>85  | CCT<br>Pro        | GTG<br>Val        | ATG<br>Met        | CAT<br>His        | GAG<br>Glu<br>90  | TTT<br>Phe        | TGG<br>Trp        | CAA<br>Gln        | CGC<br>Arg<br>95 | TTC<br>Phe        | CCG<br>Pro        | GCC<br>Ala        | ACG<br>Thr        | GTG<br>Val        | 345 |
| GAA<br>Glu<br>100 | TTA<br>Leu        | GCT<br>Ala        | TTG<br>Leu        | ATC<br>Ile        | GCT<br>Ala<br>105 | CTG<br>Leu        | TTT<br>Phe        | ATG<br>Met        | GCT<br>Ala<br>110 | CTT<br>Leu       | GTT<br>Val        | TTG<br>Leu        | GGT<br>Gly        | ATT<br>Ile<br>115 | AGC<br>Ser<br>115 | 393 |
| GTT<br>Val        | GGC<br>Gly        | GTG<br>Val        | TTA<br>Leu        | GCT<br>Ala<br>120 | GCG<br>Ala        | ATC<br>Ile        | AAA<br>Lys        | CGC<br>Arg        | TAT<br>Tyr<br>125 | AGC<br>Ser       | GTG<br>Val        | TTT<br>Phe        | GAT<br>Asp        | TAT<br>Tyr<br>130 | TCC<br>Ser        | 441 |
| AGC<br>Ser        | ATG<br>Met        | ACT<br>Thr        | TTT<br>Phe<br>135 | GCT<br>Ala        | TTA<br>Leu        | GCC<br>Ala        | GGG<br>Gly        | ATT<br>Ile<br>140 | TCT<br>Ser        | ATG<br>Met       | CCG<br>Pro        | GTG<br>Val        | TTT<br>Phe<br>145 | TGG<br>Trp        | CTA<br>Leu        | 489 |
| GGG<br>Gly        | CTC<br>Leu        | ATG<br>Met<br>150 | CTG<br>Leu        | ATT<br>Ile        | TAT<br>Tyr        | ATC<br>Ile        | TTT<br>Phe<br>155 | AGC<br>Ser        | GTG<br>Val        | CAA<br>Gln       | TTG<br>Leu        | GGG<br>Gly<br>160 | TGG<br>Trp        | TTG<br>Leu        | CCT<br>Pro        | 537 |
| GTT<br>Val        | TTT<br>Phe<br>165 | GGG<br>Gly        | CGT<br>Arg        | TTG<br>Leu        | AGC<br>Ser        | GAT<br>Asp<br>170 | GTG<br>Val        | TAT<br>Tyr        | TAT<br>Tyr        | TTA<br>Leu       | GAT<br>Asp<br>175 | GGC<br>Gly        | CCC<br>Pro        | ACA<br>Thr        | GGT<br>Gly        | 585 |
| CTT<br>Leu<br>180 | TAT<br>Tyr        | TTG<br>Leu        | ATA<br>Ile        | GAC<br>Asp        | AGC<br>Ser<br>185 | CTG<br>Leu        | ATC<br>Ile        | GCA<br>Ala        | AGG<br>Arg<br>190 | GAT<br>Asp       | TAT<br>Tyr        | GGG<br>Gly        | GCG<br>Ala        | TTT<br>Phe        | ATG<br>Met<br>195 | 633 |
| GAT<br>Asp        | ACG<br>Thr        | ATC<br>Ile        | AAG<br>Lys        | CAC<br>His<br>200 | TTG<br>Leu        | ATT<br>Ile        | TTG<br>Leu        | CCT<br>Pro        | AGC<br>Ser<br>205 | ATT<br>Ile       | GTG<br>Val        | TTA<br>Leu        | GCC<br>Ala        | ACG<br>Thr<br>210 | GTT<br>Val        | 681 |
| TCT<br>Ser        | ACC<br>Thr        | GCT<br>Ala        | GTT<br>Val<br>215 | ATT<br>Ile        | GCC<br>Ala        | AGA<br>Arg        | ATG<br>Met        | ACT<br>Thr<br>220 | CGC<br>Arg        | GCG<br>Ala       | AGC<br>Ser        | ATG<br>Met        | GCA<br>Ala<br>225 | GAA<br>Glu        | GTG<br>Val        | 729 |
| TCT<br>Ser        | AAA<br>Lys        | GAA<br>Glu<br>230 | GAT<br>Asp        | TAT<br>Tyr        | GTG<br>Val        | CGT<br>Arg        | ACC<br>Thr<br>235 | GCT<br>Ala        | AAA<br>Lys        | GCT<br>Ala       | AAG<br>Lys        | GGG<br>Gly<br>240 | TGT<br>Cys        | AGC<br>Ser        | TCC<br>Ser        | 777 |
| TTT<br>Phe        | AGG<br>Arg        | GTG<br>Val        | ATT<br>Ile        | TTT<br>Phe        | GTG<br>Val        | CAC<br>His        | ACT<br>Thr        | TTG<br>Leu        | CGT<br>Arg        | AAT<br>Asn       | GCT<br>Ala        | TTA<br>Leu        | ATC<br>Ile        | CCT<br>Pro        | GTA<br>Val        | 825 |

| 245                                                               | 250 | 255 |      |
|-------------------------------------------------------------------|-----|-----|------|
| ACG ACT ATC GCA GGC TTG ATG TTG GCC GGG CTT TTA GGG GGG AGC ATG   |     |     | 873  |
| Thr Thr Ile Ala Gly Leu Met Leu Ala Gly Leu Leu Gly Gly Ser Met   |     |     |      |
| 260                                                               | 265 | 270 | 275  |
| ATA ACT GAA ACG GTT TTC TCA TGG CCT GGG ATT GGT AAG TGG ATT GTT   |     |     | 921  |
| Ile Thr Glu Thr Val Phe Ser Trp Pro Gly Ile Gly Lys Trp Ile Val   |     |     |      |
|                                                                   | 280 | 285 | 290  |
| AAT GCG CTC AAC CAG CGC GAT TTC CCG ATT ATC CAG TCC ATG TCT TTG   |     |     | 969  |
| Asn Ala Leu Asn Gln Arg Asp Phe Pro Ile Ile Gln Ser Met Ser Leu   |     |     |      |
|                                                                   | 295 | 300 | 305  |
| ATT ATT GCC ATG ATG TAT ATT GGG GCT AAT CTC TTA GTG GAT ATT TTA   |     |     | 1017 |
| Ile Ile Ala Met Met Tyr Ile Gly Ala Asn Leu Leu Val Asp Ile Leu   |     |     |      |
|                                                                   | 310 | 315 | 320  |
| TAC GCT TTT ATT GAT CCT AGA ATA AGG TTG TCA TAATGGAGTC TTTTAGAGAG |     |     | 1070 |
| Tyr Ala Phe Ile Asp Pro Arg Ile Arg Leu Ser                       |     |     |      |
|                                                                   | 325 | 330 |      |
| TTTATCCAAC                                                        |     |     | 1080 |

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Ser | Phe | Ile | Ile | Lys | Arg | Ile | Leu | Trp | Ala | Ile | Pro | Thr | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Gly | Val | Ser | Ile | Ile | Val | Phe | Met | Met | Val | His | Leu | Val | Pro | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Asp | Pro | Ala | Leu | Val | Ile | Leu | Gly | Glu | Lys | Ala | Asn | Gln | Ala | Ala | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Asp | Ala | Leu | Arg | Glu | Gln | Phe | Gly | Leu | Asn | Lys | Pro | Leu | Ile | Glu | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Tyr | Phe | Phe | Phe | Ile | Asn | Asn | Val | Leu | His | Gly | Asn | Phe | Gly | Thr | Ser |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Met | Thr | Gly | Glu | Pro | Val | Met | His | Glu | Phe | Trp | Gln | Arg | Phe | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Thr | Val | Glu | Leu | Ala | Leu | Ile | Ala | Leu | Phe | Met | Ala | Leu | Val | Leu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Gly | Ile | Ser | Val | Gly | Val | Leu | Ala | Ala | Ile | Lys | Arg | Tyr | Ser | Val | Phe |
|     | 115 |     |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Asp | Tyr | Ser | Ser | Met | Thr | Phe | Ala | Leu | Ala | Gly | Ile | Ser | Met | Pro | Val |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Phe | Trp | Leu | Gly | Leu | Met | Leu | Ile | Tyr | Ile | Phe | Ser | Val | Gln | Leu | Gly |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Trp | Leu | Pro | Val | Phe | Gly | Arg | Leu | Ser | Asp | Val | Tyr | Tyr | Leu | Asp | Gly |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |

Pro Thr Gly Leu Tyr Leu Ile Asp Ser Leu Ile Ala Arg Asp Tyr Gly  
180 185 190  
Ala Phe Met Asp Thr Ile Lys His Leu Ile Leu Pro Ser Ile Val Leu  
195 200 205  
Ala Thr Val Ser Thr Ala Val Ile Ala Arg Met Thr Arg Ala Ser Met  
210 215 220  
Ala Glu Val Ser Lys Glu Asp Tyr Val Arg Thr Ala Lys Ala Lys Gly  
225 230 235 240  
Cys Ser Ser Phe Arg Val Ile Phe Val His Thr Leu Arg Asn Ala Leu  
245 250 255  
Ile Pro Val Thr Thr Ile Ala Gly Leu Met Leu Ala Gly Leu Leu Gly  
260 265 270  
Gly Ser Met Ile Thr Glu Thr Val Phe Ser Trp Pro Gly Ile Gly Lys  
275 280 285  
Trp Ile Val Asn Ala Leu Asn Gln Arg Asp Phe Pro Ile Ile Gln Ser  
290 295 300  
Met Ser Leu Ile Ile Ala Met Met Tyr Ile Gly Ala Asn Leu Leu Val  
305 310 315 320  
Asp Ile Leu Tyr Ala Phe Ile Asp Pro Arg Ile Arg Leu Ser  
325 330

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 955 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 32...892
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATCCTAAACG CACCTCTTAA AAGGAGCTTG C ATG ATT TTA GAA GTT AAA GAT  | 52  |
| Met Ile Leu Glu Val Lys Asp                                     |     |
| 1 5                                                             |     |
| TTA AAA ACT TAT TTT TTC ACC GAT AAG GGC GTG AAT AAA GCA GTG GAT | 100 |
| Leu Lys Thr Tyr Phe Phe Thr Asp Lys Gly Val Asn Lys Ala Val Asp |     |
| 10 15 20                                                        |     |
| GGT GTG AGT TTT GGT TTG AAA AAG TCT CAA ACG CTC TGC ATT GTA GGG | 148 |
| Gly Val Ser Phe Gly Leu Lys Lys Ser Gln Thr Leu Cys Ile Val Gly |     |
| 25 30 35                                                        |     |
| GAG AGC GGG AGC GGG AAA AGC ATC ACT TCG CTC TCT ATT TTA GGG TTG | 196 |
| Glu Ser Gly Ser Gly Lys Ser Ile Thr Ser Leu Ser Ile Leu Gly Leu |     |
| 40 45 50 55                                                     |     |
| ATT GAA AAA CCG GGT CAA ATT GTG GGA GGG AGC ATT CAA TTT TTA GGG | 244 |
| Ile Glu Lys Pro Gly Gln Ile Val Gly Gly Ser Ile Gln Phe Leu Gly |     |
| 60 65 70                                                        |     |

|                                                                                                                                                       |     |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| CAG GAT TTG TTG CAA CTC AAA GAA AAG CAG ATG CAA AAA GAA ATT AGG<br>Gln Asp Leu Leu Gln Leu Lys Glu Lys Gln Met Gln Lys Glu Ile Arg<br>75 80 85        | 292 |
| GGT AAA AAA ATT GGC ATG ATC TTT CAA GAG CCT ATG ACA AGC CTA AAC<br>Gly Lys Lys Ile Gly Met Ile Phe Gln Glu Pro Met Thr Ser Leu Asn<br>90 95 100       | 340 |
| CCT TCC TAC ACG GTG GGG TTT CAA ATC AAT GAA GTG TTG AAA ATC CAC<br>Pro Ser Tyr Thr Val Gly Phe Gln Ile Asn Glu Val Leu Lys Ile His<br>105 110 115     | 388 |
| CAC CCT AAC CTC AAT AAA AAA GAA CGC TTA GAA AGG GTG GTT TAT GAA<br>His Pro Asn Leu Asn Lys Lys Glu Arg Leu Glu Arg Val Val Tyr Glu<br>120 125 130 135 | 436 |
| TTA GAG CGT GTG GGC ATT CCC CAT GCA GGG GAT AAA TAC CAC GAA TAC<br>Leu Glu Arg Val Gly Ile Pro His Ala Gly Asp Lys Tyr His Glu Tyr<br>140 145 150     | 484 |
| CCT TTC AAT CTC AGC GGG GGG CAG CGC CAA AGG GTG ATG ATC GCT ATG<br>Pro Phe Asn Leu Ser Gly Gly Gln Arg Gln Arg Val Met Ile Ala Met<br>155 160 165     | 532 |
| GCT ATG GTG TGT GAG CCT GAA ATC TTG ATC GCT GAT GAG CCT ACG ACA<br>Ala Met Val Cys Glu Pro Glu Ile Leu Ile Ala Asp Glu Pro Thr Thr<br>170 175 180     | 580 |
| GCC TTA GAT GTA ACC ATT CAA GCG CAA ATT TTA GAA TTG ATG AAA GAA<br>Ala Leu Asp Val Thr Ile Gln Ala Gln Ile Leu Glu Leu Met Lys Glu<br>185 190 195     | 628 |
| TTG CAA CAA AAA AAA GGC ACT TCT ATT TTG TTT ATC ACC CAT GAT TTA<br>Leu Gln Gln Lys Lys Gly Thr Ser Ile Leu Phe Ile Thr His Asp Leu<br>200 205 210 215 | 676 |
| GGC GTG GTG GCG CAA ATC GCT GAT GAA GTG GTG GTG ATG TAT AAA GGG<br>Gly Val Val Ala Gln Ile Ala Asp Glu Val Val Val Met Tyr Lys Gly<br>220 225 230     | 724 |
| CAT GTG GTG GAG CAA GCG AGT GCG AAA GAG CTT TTT GCT GAT CCA AGA<br>His Val Val Glu Gln Ala Ser Ala Lys Glu Leu Phe Ala Asp Pro Arg<br>235 240 245     | 772 |
| CAC CCT TAT ACG AAA GCT CTT TTA AGC GCG ATC CCT AAA CCG GGC AAA<br>His Pro Tyr Thr Lys Ala Leu Leu Ser Ala Ile Pro Lys Pro Gly Lys<br>250 255 260     | 820 |
| GAA TAC CGC AAA AAA CGC TTA GAG ACC GTG GAT GAA AAT GTG GAT TAT<br>Glu Tyr Arg Lys Lys Arg Leu Glu Thr Val Asp Glu Asn Val Asp Tyr<br>265 270 275     | 868 |
| TTG AGT TTT CAA AAG GAG TTG CGA TGAAGCTCTT AGAAATTAAA GAATTGAAAA<br>Leu Ser Phe Gln Lys Glu Leu Arg<br>280 285                                        | 922 |
| AATCCTATGC GATAGACAGG GGGTTATTCA AGC                                                                                                                  | 955 |



(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Leu | Glu | Val | Lys | Asp | Leu | Lys | Thr | Tyr | Phe | Phe | Thr | Asp | Lys | 1   | 5   | 10  | 15  |
| Gly | Val | Asn | Lys | Ala | Val | Asp | Gly | Val | Ser | Phe | Gly | Leu | Lys | Lys | Ser | 20  | 25  | 30  |     |
| Gln | Thr | Leu | Cys | Ile | Val | Gly | Glu | Ser | Gly | Ser | Gly | Lys | Ser | Ile | Thr | 35  | 40  | 45  |     |
| Ser | Leu | Ser | Ile | Leu | Gly | Leu | Ile | Glu | Lys | Pro | Gly | Gln | Ile | Val | Gly | 50  | 55  | 60  |     |
| Gly | Ser | Ile | Gln | Phe | Leu | Gly | Gln | Asp | Leu | Leu | Gln | Leu | Lys | Glu | Lys | 65  | 70  | 75  | 80  |
| Gln | Met | Gln | Lys | Glu | Ile | Arg | Gly | Lys | Lys | Ile | Gly | Met | Ile | Phe | Gln | 85  | 90  | 95  |     |
| Glu | Pro | Met | Thr | Ser | Leu | Asn | Pro | Ser | Tyr | Thr | Val | Gly | Phe | Gln | Ile | 100 | 105 | 110 |     |
| Asn | Glu | Val | Leu | Lys | Ile | His | His | Pro | Asn | Leu | Asn | Lys | Lys | Glu | Arg | 115 | 120 | 125 |     |
| Leu | Glu | Arg | Val | Val | Tyr | Glu | Leu | Glu | Arg | Val | Gly | Ile | Pro | His | Ala | 130 | 135 | 140 |     |
| Gly | Asp | Lys | Tyr | His | Glu | Tyr | Pro | Phe | Asn | Leu | Ser | Gly | Gly | Gln | Arg | 145 | 150 | 155 | 160 |
| Gln | Arg | Val | Met | Ile | Ala | Met | Ala | Met | Val | Cys | Glu | Pro | Glu | Ile | Leu | 165 | 170 | 175 |     |
| Ile | Ala | Asp | Glu | Pro | Thr | Thr | Ala | Leu | Asp | Val | Thr | Ile | Gln | Ala | Gln | 180 | 185 | 190 |     |
| Ile | Leu | Glu | Leu | Met | Lys | Glu | Leu | Gln | Gln | Lys | Lys | Gly | Thr | Ser | Ile | 195 | 200 | 205 |     |
| Leu | Phe | Ile | Thr | His | Asp | Leu | Gly | Val | Val | Ala | Gln | Ile | Ala | Asp | Glu | 210 | 215 | 220 |     |
| Val | Val | Val | Met | Tyr | Lys | Gly | His | Val | Val | Glu | Gln | Ala | Ser | Ala | Lys | 225 | 230 | 235 | 240 |
| Glu | Leu | Phe | Ala | Asp | Pro | Arg | His | Pro | Tyr | Thr | Lys | Ala | Leu | Leu | Ser | 245 | 250 | 255 |     |
| Ala | Ile | Pro | Lys | Pro | Gly | Lys | Glu | Tyr | Arg | Lys | Lys | Arg | Leu | Glu | Thr | 260 | 265 | 270 |     |
| Val | Asp | Glu | Asn | Val | Asp | Tyr | Leu | Ser | Phe | Gln | Lys | Glu | Leu | Arg |     | 275 | 280 | 285 |     |

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 37...840
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

|                                                                 |                         |    |
|-----------------------------------------------------------------|-------------------------|----|
| AAATGTGGAT TATTTGAGTT TTCAAAAGGA GTTGCG                         | ATG AAG CTC TTA GAA ATT | 54 |
|                                                                 | Met Lys Leu Leu Glu Ile |    |
|                                                                 | 1 5                     |    |
| AAA GAA TTG AAA AAA TCC TAT GCG ATA GAC AGG GGG TTA TTC AAG CCT | 102                     |    |
| Lys Glu Leu Lys Lys Ser Tyr Ala Ile Asp Arg Gly Leu Phe Lys Pro |                         |    |
|                                                                 | 10 15 20                |    |
| AAA AGA GTG ATC CAT GCG CTC AAT GGG ATC AGT TTT GAA GTG GAA CAA | 150                     |    |
| Lys Arg Val Ile His Ala Leu Asn Gly Ile Ser Phe Glu Val Glu Gln |                         |    |
|                                                                 | 25 30 35                |    |
| AAT GAA GTT TTG AGC ATT GTG GGG GAG AGC GGT TGC GGG AAA AGC ACG | 198                     |    |
| Asn Glu Val Leu Ser Ile Val Gly Glu Ser Gly Cys Gly Lys Ser Thr |                         |    |
|                                                                 | 40 45 50                |    |
| ACA GCC AAA ATT TTA GCC GGG ATT GAA AGG CAA GAT AGC GGG GCG ATT | 246                     |    |
| Thr Ala Lys Ile Leu Ala Gly Ile Glu Arg Gln Asp Ser Gly Ala Ile |                         |    |
|                                                                 | 55 60 65 70             |    |
| TAT TTC AAT GGT AAG CGC CAT TTG CAT TTT AGC AAA CAG GAT TGG TTT | 294                     |    |
| Tyr Phe Asn Gly Lys Arg His Leu His Phe Ser Lys Gln Asp Trp Phe |                         |    |
|                                                                 | 75 80 85                |    |
| GAT TAC CGC AAA AAG GTG CAA ATG ATT TTT CAA GAC CCT TAT TCT AGC | 342                     |    |
| Asp Tyr Arg Lys Lys Val Gln Met Ile Phe Gln Asp Pro Tyr Ser Ser |                         |    |
|                                                                 | 90 95 100               |    |
| CTA AAC CCT CGG TGG AAA GTG GGC GAG ATC ATC GCT GAA CCC TTG CTT | 390                     |    |
| Leu Asn Pro Arg Trp Lys Val Gly Glu Ile Ile Ala Glu Pro Leu Leu |                         |    |
|                                                                 | 105 110 115             |    |
| TTA AAT TCT CAT TTT TCA AAA AAA GAA ATC AAA ACA AAA GTG CTA GAG | 438                     |    |
| Leu Asn Ser His Phe Ser Lys Lys Glu Ile Lys Thr Lys Val Leu Glu |                         |    |
|                                                                 | 120 125 130             |    |
| ATC ATG CAA AAA GTG GGC TTG AAA TTA GAA TGG ATC GAT CGT TAC CCC | 486                     |    |
| Ile Met Gln Lys Val Gly Leu Lys Leu Glu Trp Ile Asp Arg Tyr Pro |                         |    |
|                                                                 | 135 140 145 150         |    |
| CAC CAA TTT TCA GGC GGT CAA AGG CAA CGA ATC GGC ATT GCT AGG GCG | 534                     |    |
| His Gln Phe Ser Gly Gly Gln Arg Gln Arg Ile Gly Ile Ala Arg Ala |                         |    |
|                                                                 | 155 160 165             |    |
| CTC ATT TTG CAT CCT AGC GTG GTG ATT TGC GAT GAG CCT GTG TCT GCG | 582                     |    |
| Leu Ile Leu His Pro Ser Val Val Ile Cys Asp Glu Pro Val Ser Ala |                         |    |
|                                                                 | 170 175 180             |    |
| CTA GAC GTG TCC ATT CAA GCG CAA GTG TTG AAT TTG CTC TTG GAT TTG | 630                     |    |

Leu Asp Val Ser Ile Gln Ala Gln Val Leu Asn Leu Leu Leu Asp Leu  
 185 190 195  
 CAA AAA GAA ATG GGG CTG ACT TAT ATT TTT ATC AGC CAT GAT TTA GGG 678  
 Gln Lys Glu Met Gly Leu Thr Tyr Ile Phe Ile Ser His Asp Leu Gly  
 200 205 210  
 GTG GTG GAG CAT ATA AGC GAT AAA ATC ATC GTA ATG AAT CAG GGG CAA 726  
 Val Val Glu His Ile Ser Asp Lys Ile Ile Val Met Asn Gln Gly Gln  
 215 220 225 230  
 ATC GTA GAA ACG GGG GAT GTG GAT AGC GTG ATA AGC GCT CCA AAG CAC 774  
 Ile Val Glu Thr Gly Asp Val Asp Ser Val Ile Ser Ala Pro Lys His  
 235 240 245  
 CCT TAT ACG CAG AAA TTA CTC AAT GCG GTG CCG CAT TTG GAA AAA TCC 822  
 Pro Tyr Thr Gln Lys Leu Leu Asn Ala Val Pro His Leu Glu Lys Ser  
 250 255 260  
 ATG CAA AGA TTT GCC AAA TAAAAGAAAG GATTTTAAAG CTGTGTTTGT AGATAGCG 878  
 Met Gln Arg Phe Ala Lys  
 265  
 TGGAAATTAT CATCGC 894

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

Met Lys Leu Leu Glu Ile Lys Glu Leu Lys Lys Ser Tyr Ala Ile Asp  
 1 5 10 15  
 Arg Gly Leu Phe Lys Pro Lys Arg Val Ile His Ala Leu Asn Gly Ile  
 20 25 30  
 Ser Phe Glu Val Glu Gln Asn Glu Val Leu Ser Ile Val Gly Glu Ser  
 35 40 45  
 Gly Cys Gly Lys Ser Thr Thr Ala Lys Ile Leu Ala Gly Ile Glu Arg  
 50 55 60  
 Gln Asp Ser Gly Ala Ile Tyr Phe Asn Gly Lys Arg His Leu His Phe  
 65 70 75 80  
 Ser Lys Gln Asp Trp Phe Asp Tyr Arg Lys Lys Val Gln Met Ile Phe  
 85 90 95  
 Gln Asp Pro Tyr Ser Ser Leu Asn Pro Arg Trp Lys Val Gly Glu Ile  
 100 105 110  
 Ile Ala Glu Pro Leu Leu Leu Asn Ser His Phe Ser Lys Lys Glu Ile  
 115 120 125  
 Lys Thr Lys Val Leu Glu Ile Met Gln Lys Val Gly Leu Lys Leu Glu  
 130 135 140  
 Trp Ile Asp Arg Tyr Pro His Gln Phe Ser Gly Gly Gln Arg Gln Arg  
 145 150 155 160  
 Ile Gly Ile Ala Arg Ala Leu Ile Leu His Pro Ser Val Val Ile Cys

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |
| Asp | Glu | Pro | Val | Ser | Ala | Leu | Asp | Val | Ser | Ile | Gln | Ala | Gln | Val | Leu |
|     |     |     | 180 |     |     |     |     |     | 185 |     |     |     | 190 |     |     |
| Asn | Leu | Leu | Leu | Asp | Leu | Gln | Lys | Glu | Met | Gly | Leu | Thr | Tyr | Ile | Phe |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Ser | His | Asp | Leu | Gly | Val | Val | Glu | His | Ile | Ser | Asp | Lys | Ile | Ile |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Met | Asn | Gln | Gly | Gln | Ile | Val | Glu | Thr | Gly | Asp | Val | Asp | Ser | Val |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ile | Ser | Ala | Pro | Lys | His | Pro | Tyr | Thr | Gln | Lys | Leu | Leu | Asn | Ala | Val |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Pro | His | Leu | Glu | Lys | Ser | Met | Gln | Arg | Phe | Ala | Lys |     |     |     |     |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1141 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 62...1087
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| TTAAGCTGTG TTTGTAGATA GCGTGGAAAT TATCATCGCT TCGGGTAAGG GGGGGCCTGG | 60  |
| A ATG GTG AGT TTT AGG CGA GAA AAA TTT GTC ATC AAA GGA GGC CCT GAT | 109 |
| Met Val Ser Phe Arg Arg Glu Lys Phe Val Ile Lys Gly Gly Pro Asp   |     |
| 1 5 10 15                                                         |     |
| GGG GGC GAT GGA GGC GAT GGA GGC GAT GTG TAT TTT GAA GTG GAT AAC   | 157 |
| Gly Gly Asp Gly Gly Asp Gly Gly Asp Val Tyr Phe Glu Val Asp Asn   |     |
| 20 25 30                                                          |     |
| AAT ACC GAC ACT CTA GCG AGT TTT AGA GGC ACC AAA CAC CAT AAG GCT   | 205 |
| Asn Thr Asp Thr Leu Ala Ser Phe Arg Gly Thr Lys His His Lys Ala   |     |
| 35 40 45                                                          |     |
| AAA AAT GGG GCT CCA GGA GGT ACA CGA AAT TGC GCG GGC AAA AAG GGC   | 253 |
| Lys Asn Gly Ala Pro Gly Gly Thr Arg Asn Cys Ala Gly Lys Lys Gly   |     |
| 50 55 60                                                          |     |
| GAA GAC AAG ATC ATT GTC GTG CCA CCA GGA ACG CAG GTT TTT GTA GGT   | 301 |
| Glu Asp Lys Ile Ile Val Val Pro Pro Gly Thr Gln Val Phe Val Gly   |     |
| 65 70 75 80                                                       |     |
| GAT GAG TTG TGG CTT GAT TTA GTG GAA CCT AAA GAA AGG GTG TTA GCC   | 349 |
| Asp Glu Leu Trp Leu Asp Leu Val Glu Pro Lys Glu Arg Val Leu Ala   |     |
| 85 90 95                                                          |     |
| TTA AAA GGG GGC AAG GGG GGG TTA GGG AAT GCA CAT TTT AAA AGC GCG   | 397 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Leu | Lys | Gly | Gly | Lys | Gly | Gly | Leu | Gly | Asn | Ala | His | Phe | Lys | Ser | Ala |      |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |      |  |
| ACT | AAA | CAA | CAA | CCC | ACT | TAC | GCG | CAA | AAA | GGC | TTA | GAG | GGG | GTT | GAA | 445  |  |
| Thr | Lys | Gln | Gln | Pro | Thr | Tyr | Ala | Gln | Lys | Gly | Leu | Glu | Gly | Val | Glu |      |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |      |  |
| AAA | TGC | GTG | CGT | TTG | GAA | TTA | AAA | CTC | ATC | GCT | GAT | ATA | GGG | TTA | GTG | 493  |  |
| Lys | Cys | Val | Arg | Leu | Glu | Leu | Lys | Leu | Ile | Ala | Asp | Ile | Gly | Leu | Val |      |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |      |  |
| GGC | TTC | CCT | AAT | GCG | GGT | AAA | TCC | ACG | CTC | ATT | TCC | ACC | ATC | TCT | AAC | 541  |  |
| Gly | Phe | Pro | Asn | Ala | Gly | Lys | Ser | Thr | Leu | Ile | Ser | Thr | Ile | Ser | Asn |      |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |      |  |
| GCT | AAG | CCT | AAA | ATC | GCT | AAC | TAT | GAA | TTT | ACG | ACT | CTA | GTG | CCT | AAT | 589  |  |
| Ala | Lys | Pro | Lys | Ile | Ala | Asn | Tyr | Glu | Phe | Thr | Thr | Leu | Val | Pro | Asn |      |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |      |  |
| TTA | GGG | GTT | GTG | AGC | GTG | GAT | GAA | AAA | AGC | GGA | TTT | CTA | ATG | GCG | GAT | 637  |  |
| Leu | Gly | Val | Val | Ser | Val | Asp | Glu | Lys | Ser | Gly | Phe | Leu | Met | Ala | Asp |      |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |      |  |
| ATT | CCT | GGC | ATT | ATT | GAA | GGG | GCT | AGC | GAG | GGA | AAG | GGC | TTA | GGG | ATT | 685  |  |
| Ile | Pro | Gly | Ile | Ile | Glu | Gly | Ala | Ser | Glu | Gly | Lys | Gly | Leu | Gly | Ile |      |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |      |  |
| AGC | TTT | TTA | AAG | CAT | ATT | GAA | CGC | ACC | AAA | GTT | CTA | GCT | TTT | GTT | TTA | 733  |  |
| Ser | Phe | Leu | Lys | His | Ile | Glu | Arg | Thr | Lys | Val | Leu | Ala | Phe | Val | Leu |      |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |      |  |
| GAC | GCT | TCC | AGG | CTG | GAT | TTA | GGC | ATT | AAA | GAG | CAA | TAC | CAA | CGC | TTG | 781  |  |
| Asp | Ala | Ser | Arg | Leu | Asp | Leu | Gly | Ile | Lys | Glu | Gln | Tyr | Gln | Arg | Leu |      |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |      |  |
| AGG | TTG | GAG | TTG | GAA | AAA | TTT | TCA | TCC | GCT | TTG | GCC | AAT | AAG | CCT | TTT | 829  |  |
| Arg | Leu | Glu | Leu | Glu | Lys | Phe | Ser | Ser | Ala | Leu | Ala | Asn | Lys | Pro | Phe |      |  |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     | 255 |     |     |      |  |
| GGG | GTG | TTG | CTC | AAT | AAA | TGC | GAT | GTT | GTA | GAA | AAC | ATT | GAT | GAG | ATG | 877  |  |
| Gly | Val | Leu | Leu | Asn | Lys | Cys | Asp | Val | Val | Glu | Asn | Ile | Asp | Glu | Met |      |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |      |  |
| ACT | AAG | GAT | TTT | TGT | GCC | TTT | TTA | AAT | TTG | GGA | GCG | CAG | AAA | TTA | AAC | 925  |  |
| Thr | Lys | Asp | Phe | Cys | Ala | Phe | Leu | Asn | Leu | Gly | Ala | Gln | Lys | Leu | Asn |      |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |      |  |
| GAG | TTT | GGT | TTA | GAG | CCG | TAT | TTA | GGG | TTT | TTG | CAC | CCC | CAT | TTA | ACC | 973  |  |
| Glu | Phe | Gly | Leu | Glu | Pro | Tyr | Leu | Gly | Phe | Leu | His | Pro | His | Leu | Thr |      |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |      |  |
| AAT | GAT | TTT | GAA | AAT | AAC | CCT | AAT | GAG | CAA | TCA | GCG | CTC | TTT | GTC | TTG | 1021 |  |
| Asn | Asp | Phe | Glu | Asn | Asn | Pro | Asn | Glu | Gln | Ser | Ala | Leu | Phe | Val | Leu |      |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |      |  |
| CCC | CTT | TCA | GCG | GTT | AGC | GCT | CTT | AAT | GTG | CAT | GCA | CTC | AAA | TTT | GTG | 1069 |  |
| Pro | Leu | Ser | Ala | Val | Ser | Ala | Leu | Asn | Val | His | Ala | Leu | Lys | Phe | Val |      |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |      |  |

TTG TTG GAA GCG TTA CCC TAAAACGCTA TTTTAAAAT AATCCATTAA AATAAAGG 1125  
Leu Leu Glu Ala Leu Pro  
340

CGAGGAATGA AAAGAT 1141

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ser | Phe | Arg | Arg | Glu | Lys | Phe | Val | Ile | Lys | Gly | Gly | Pro | Asp | 1   | 5   | 10  | 15  |
| Gly | Gly | Asp | Gly | Gly | Asp | Gly | Gly | Asp | Val | Tyr | Phe | Glu | Val | Asp | Asn | 20  | 25  | 30  |     |
| Asn | Thr | Asp | Thr | Leu | Ala | Ser | Phe | Arg | Gly | Thr | Lys | His | His | Lys | Ala | 35  | 40  | 45  |     |
| Lys | Asn | Gly | Ala | Pro | Gly | Gly | Thr | Arg | Asn | Cys | Ala | Gly | Lys | Lys | Gly | 50  | 55  | 60  |     |
| Glu | Asp | Lys | Ile | Ile | Val | Val | Pro | Pro | Gly | Thr | Gln | Val | Phe | Val | Gly | 65  | 70  | 75  | 80  |
| Asp | Glu | Leu | Trp | Leu | Asp | Leu | Val | Glu | Pro | Lys | Glu | Arg | Val | Leu | Ala | 85  | 90  | 95  |     |
| Leu | Lys | Gly | Gly | Lys | Gly | Gly | Leu | Gly | Asn | Ala | His | Phe | Lys | Ser | Ala | 100 | 105 | 110 |     |
| Thr | Lys | Gln | Gln | Pro | Thr | Tyr | Ala | Gln | Lys | Gly | Leu | Glu | Gly | Val | Glu | 115 | 120 | 125 |     |
| Lys | Cys | Val | Arg | Leu | Glu | Leu | Lys | Leu | Ile | Ala | Asp | Ile | Gly | Leu | Val | 130 | 135 | 140 |     |
| Gly | Phe | Pro | Asn | Ala | Gly | Lys | Ser | Thr | Leu | Ile | Ser | Thr | Ile | Ser | Asn | 145 | 150 | 155 | 160 |
| Ala | Lys | Pro | Lys | Ile | Ala | Asn | Tyr | Glu | Phe | Thr | Thr | Leu | Val | Pro | Asn | 165 | 170 | 175 |     |
| Leu | Gly | Val | Val | Ser | Val | Asp | Glu | Lys | Ser | Gly | Phe | Leu | Met | Ala | Asp | 180 | 185 | 190 |     |
| Ile | Pro | Gly | Ile | Ile | Glu | Gly | Ala | Ser | Glu | Gly | Lys | Gly | Leu | Gly | Ile | 195 | 200 | 205 |     |
| Ser | Phe | Leu | Lys | His | Ile | Glu | Arg | Thr | Lys | Val | Leu | Ala | Phe | Val | Leu | 210 | 215 | 220 |     |
| Asp | Ala | Ser | Arg | Leu | Asp | Leu | Gly | Ile | Lys | Glu | Gln | Tyr | Gln | Arg | Leu | 225 | 230 | 235 | 240 |
| Arg | Leu | Glu | Leu | Glu | Lys | Phe | Ser | Ser | Ala | Leu | Ala | Asn | Lys | Pro | Phe | 245 | 250 | 255 |     |
| Gly | Val | Leu | Leu | Asn | Lys | Cys | Asp | Val | Val | Glu | Asn | Ile | Asp | Glu | Met | 260 | 265 | 270 |     |
| Thr | Lys | Asp | Phe | Cys | Ala | Phe | Leu | Asn | Leu | Gly | Ala | Gln | Lys | Leu | Asn | 275 | 280 | 285 |     |
| Glu | Phe | Gly | Leu | Glu | Pro | Tyr | Leu | Gly | Phe | Leu | His | Pro | His | Leu | Thr | 290 | 295 | 300 |     |
| Asn | Asp | Phe | Glu | Asn | Asn | Pro | Asn | Glu | Gln | Ser | Ala | Leu | Phe | Val | Leu | 305 | 310 | 315 | 320 |
| Pro | Leu | Ser | Ala | Val | Ser | Ala | Leu | Asn | Val | His | Ala | Leu | Lys | Phe | Val | 325 | 330 | 335 |     |
| Leu | Leu | Glu | Ala | Leu | Pro |     |     |     |     |     |     |     |     |     |     | 340 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...567
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| ATTAAAGGAT AATGA ATG AAA AAA ATG GTT TTG GTA TCG GTT TTA CTA GCA | 51  |
| Met Lys Lys Met Val Leu Val Ser Val Leu Leu Ala                  |     |
| 1 5 10                                                           |     |
| GGG TTT TTG CAA GCG GTG AAT TTG GAT TTA TCT TCG GCT AAG CTA ACA  | 99  |
| Gly Phe Leu Gln Ala Val Asn Leu Asp Leu Ser Ser Ala Lys Leu Thr  |     |
| 15 20 25                                                         |     |
| TGG ACA GCC TTT AAA ACT AAG GCT AAA ACA CCA GTA AAT GGG AGT TTT  | 147 |
| Trp Thr Ala Phe Lys Thr Lys Ala Lys Thr Pro Val Asn Gly Ser Phe  |     |
| 30 35 40                                                         |     |
| GAA AGC ATC ACC TAT AAA TTG GGT AAA TCT CAA GAT AGT TTA AAA ACC  | 195 |
| Glu Ser Ile Thr Tyr Lys Leu Gly Lys Ser Gln Asp Ser Leu Lys Thr  |     |
| 45 50 55 60                                                      |     |
| CTT TTA GAG GGA GCG AGC GCG AGC ATG GAT AGC TTG AAA GTC AAT TTA  | 243 |
| Leu Leu Glu Gly Ala Ser Ala Ser Met Asp Ser Leu Lys Val Asn Leu  |     |
| 65 70 75                                                         |     |
| GGC GAT GAA TTG AAA AAC AAA AAT GTG AAA GAA GCT TTT TTC GCT CTT  | 291 |
| Gly Asp Glu Leu Lys Asn Lys Asn Val Lys Glu Ala Phe Phe Ala Leu  |     |
| 80 85 90                                                         |     |
| TTT AAA AAC ACT AAC ATC AAA GTA ACT TTC AGG AAT GTG ATA GAA GGC  | 339 |
| Phe Lys Asn Thr Asn Ile Lys Val Thr Phe Arg Asn Val Ile Glu Gly  |     |
| 95 100 105                                                       |     |
| GAT CAT GCA GGT TCT CTT ACG GCT TAT GTG AGA ATG AAT GAA AAG CTG  | 387 |
| Asp His Ala Gly Ser Leu Thr Ala Tyr Val Arg Met Asn Glu Lys Leu  |     |
| 110 115 120                                                      |     |
| GTG AAA GTG CCT ATG CAA TAC ACG ATT GCT GAG GAT AAG ATC GTG GTT  | 435 |
| Val Lys Val Pro Met Gln Tyr Thr Ile Ala Glu Asp Lys Ile Val Val  |     |
| 125 130 135 140                                                  |     |
| AAA GGG GTT TTG GAT TTA TTG AAT TTT GGC TTG AAA AAC GAA TTA GCG  | 483 |
| Lys Gly Val Leu Asp Leu Leu Asn Phe Gly Leu Lys Asn Glu Leu Ala  |     |
| 145 150 155                                                      |     |
| AGC TTG GCC AAA CGA TGC GAA AGC TTT CAT GAG GGC TTG ACT TGG TCG  | 531 |
| Ser Leu Ala Lys Arg Cys Glu Ser Phe His Glu Gly Leu Thr Trp Ser  |     |



160 165 170

CAA GTG GAA ATC CAA TTT GAA AGC ATG ATC AAG GGA TAATGTAAAA TCATGG 583  
 Gln Val Glu Ile Gln Phe Glu Ser Met Ile Lys Gly  
 175 180

AGTTGTTGCA CAGCATTAAT GATTTCATG AAGCTAAG 621

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

Met Lys Lys Met Val Leu Val Ser Val Leu Leu Ala Gly Phe Leu Gln  
 1 5 10 15  
 Ala Val Asn Leu Asp Leu Ser Ser Ala Lys Leu Thr Trp Thr Ala Phe  
 20 25 30  
 Lys Thr Lys Ala Lys Thr Pro Val Asn Gly Ser Phe Glu Ser Ile Thr  
 35 40 45  
 Tyr Lys Leu Gly Lys Ser Gln Asp Ser Leu Lys Thr Leu Leu Glu Gly  
 50 55 60  
 Ala Ser Ala Ser Met Asp Ser Leu Lys Val Asn Leu Gly Asp Glu Leu  
 65 70 75 80  
 Lys Asn Lys Asn Val Lys Glu Ala Phe Phe Ala Leu Phe Lys Asn Thr  
 85 90 95  
 Asn Ile Lys Val Thr Phe Arg Asn Val Ile Glu Gly Asp His Ala Gly  
 100 105 110  
 Ser Leu Thr Ala Tyr Val Arg Met Asn Glu Lys Leu Val Lys Val Pro  
 115 120 125  
 Met Gln Tyr Thr Ile Ala Glu Asp Lys Ile Val Val Lys Gly Val Leu  
 130 135 140  
 Asp Leu Leu Asn Phe Gly Leu Lys Asn Glu Leu Ala Ser Leu Ala Lys  
 145 150 155 160  
 Arg Cys Glu Ser Phe His Glu Gly Leu Thr Trp Ser Gln Val Glu Ile  
 165 170 175  
 Gln Phe Glu Ser Met Ile Lys Gly  
 180

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...1338

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

|            |            |            |            |          |     |     |     |     |
|------------|------------|------------|------------|----------|-----|-----|-----|-----|
| CAAGTGGAAA | TCCAATTTGA | AAGCATGATC | AAGGGATAAT | GTAAAATC | ATG | GAG | TTG | 57  |
|            |            |            |            |          | Met | Glu | Leu |     |
|            |            |            |            |          | 1   |     |     |     |
| TTG        | CAC        | AGC        | ATT        | AAT      | GAT | TTC | AAT | 105 |
| Leu        | His        | Ser        | Ile        | Asn      | Asp | Phe | Asn |     |
| 5          |            |            |            |          |     | 10  |     |     |
|            |            |            |            |          |     |     |     |     |
| GGG        | GTC        | AAT        | TCA        | CCT      | GTT | AGG | GCG | 153 |
| Gly        | Val        | Asn        | Ser        | Pro      | Val | Arg | Ala |     |
| 20         |            |            |            |          | 25  |     |     |     |
|            |            |            |            |          |     |     |     |     |
| CCC        | TTT        | ATT        | TTA        | AAA      | GGC | AAG | GGG | 201 |
| Pro        | Phe        | Ile        | Leu        | Lys      | Gly | Lys | Gly |     |
|            |            |            |            | 40       |     |     | 45  |     |
|            |            |            |            |          |     |     |     |     |
| AAC        | CAT        | TAT        | ATA        | GAT      | TTT | GTG | CAA | 249 |
| Asn        | His        | Tyr        | Ile        | Asp      | Phe | Val | Gln |     |
|            |            |            |            |          |     |     | 60  |     |
|            |            |            |            |          |     |     |     |     |
| CAT        | GCT        | GAT        | GAA        | GAG      | ATT | GAA | GAA | 297 |
| His        | Ala        | Asp        | Glu        | Glu      | Ile | Glu | Glu |     |
|            |            |            |            |          |     |     | 75  |     |
|            |            |            |            |          |     |     |     |     |
| GGC        | ACT        | TCT        | TTT        | GGC      | GCT | CCC | ACA | 345 |
| Gly        | Thr        | Ser        | Phe        | Gly      | Ala | Pro | Thr |     |
| 85         |            |            |            |          |     | 90  |     |     |
|            |            |            |            |          |     |     |     |     |
| GAA        | ATC        | ATT        | TCT        | TGT      | TAT | GAA | GGC | 393 |
| Glu        | Ile        | Ile        | Ser        | Cys      | Tyr | Glu | Gly |     |
| 100        |            |            |            |          |     | 105 |     |     |
|            |            |            |            |          |     |     |     |     |
| AGC        | GGC        | ACA        | GAA        | GCG      | ACC | ATG | AGC | 441 |
| Ser        | Gly        | Thr        | Glu        | Ala      | Thr | Met | Ser |     |
|            |            |            |            |          |     |     |     |     |
|            |            |            |            |          |     |     |     |     |
| AGC        | CAA        | AAA        | GAT        | GAT      | TTG | ATC | AAG | 489 |
| Ser        | Gln        | Lys        | Asp        | Asp      | Leu | Ile | Lys |     |
|            |            |            |            |          |     |     |     |     |
|            |            |            |            |          |     |     |     |     |
| AGC        | GAC        | TCC        | TTA        | TTG      | GTG | AAA | GCG | 537 |
| Ser        | Asp        | Ser        | Leu        | Leu      | Val | Lys | Ala |     |
|            |            |            |            |          |     |     |     |     |
|            |            |            |            |          |     |     |     |     |
| TCG        | CCT        | TCT        | TCT        | TTA      | GGC | GTG | CCG | 585 |
| Ser        | Pro        | Ser        | Ser        | Leu      | Gly | Val | Pro |     |
| 165        |            |            |            |          |     |     |     |     |
|            |            |            |            |          |     |     |     |     |
| GTG        | GCT        | CGT        | TAT        | AAC      | GAT | TTA | AAC | 633 |
| Val        | Ala        | Arg        | Tyr        | Asn      | Asp | Leu | Asn |     |
| 180        |            |            |            |          |     | 185 |     |     |
|            |            |            |            |          |     |     |     |     |
| GGC        | AAT        | GTG        | GGT        | TGC      | GTC | ATC | ATT | 681 |
|            |            |            |            |          |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |         |            |     |      |      |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---------|------------|-----|------|------|-----|
| Gly | Asn | Val | Gly | Cys | Val | Ile | Ile | Glu | Pro | Ile | Ala | Gly     | Asn        | Met | Gly  |      |     |
|     |     |     |     | 200 |     |     |     |     | 205 |     |     |         |            | 210 |      |      |     |
| TTA | GTG | CCG | GCT | CAA | AAA | GAG | TTT | TTA | TTG | GGC | TTA | AAG     | GCC        | TTG | TGT  | 729  |     |
| Leu | Val | Pro | Ala | Gln | Lys | Glu | Phe | Leu | Leu | Gly | Leu | Lys     | Ala        | Leu | Cys  |      |     |
|     |     |     |     | 215 |     |     |     |     | 220 |     |     |         |            | 225 |      |      |     |
| GAA | AAA | TAC | CAA | GCG | GTG | CTG | ATT | TTA | GAT | GAA | GTG | ATG     | AGC        | GGT | TTT  | 777  |     |
| Glu | Lys | Tyr | Gln | Ala | Val | Leu | Ile | Leu | Asp | Glu | Val | Met     | Ser        | Gly | Phe  |      |     |
|     |     |     |     | 230 |     |     |     |     | 235 |     |     |         |            | 240 |      |      |     |
| AGA | GCG | AGC | TTG | AGC | GGT | TCG | CAA | GAA | TTT | TAT | GGC | GTG     | GTG        | CCG | GAT  | 825  |     |
| Arg | Ala | Ser | Leu | Ser | Gly | Ser | Gln | Glu | Phe | Tyr | Gly | Val     | Val        | Pro | Asp  |      |     |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |         |            | 255 |      |      |     |
| TTG | GTA | ACC | TTT | GGT | AAG | GTG | ATA | GGT | GCT | GGG | CTT | CCT     | TTG        | GCG | TGT  | 873  |     |
| Leu | Val | Thr | Phe | Gly | Lys | Val | Ile | Gly | Ala | Gly | Leu | Pro     | Leu        | Ala | Cys  |      |     |
|     |     |     |     | 260 |     |     |     |     | 265 |     |     |         |            | 270 |      |      | 275 |
| TTT | GGA | GGG | CGT | GCA | GAA | ATT | ATG | GAC | TTG | CTT | TCG | CCC     | ATT        | GGA | AGC  | 921  |     |
| Phe | Gly | Gly | Arg | Ala | Glu | Ile | Met | Asp | Leu | Leu | Ser | Pro     | Ile        | Gly | Ser  |      |     |
|     |     |     |     | 280 |     |     |     |     | 285 |     |     |         |            | 290 |      |      |     |
| GTG | TAT | CAA | GCA | GGC | ACT | TTG | AGC | GGT | AAC | CCC | CTA | GCG     | GTG        | TGC | GCG  | 969  |     |
| Val | Tyr | Gln | Ala | Gly | Thr | Leu | Ser | Gly | Asn | Pro | Leu | Ala     | Val        | Cys | Ala  |      |     |
|     |     |     |     | 295 |     |     |     |     | 300 |     |     |         |            | 305 |      |      |     |
| GGG | TTG | AGT | GCG | CTT | TAT | AAA | ATC | AAA | AGA | GAC | AAA | ACC     | CTT        | TAT | ACT  | 1017 |     |
| Gly | Leu | Ser | Ala | Leu | Tyr | Lys | Ile | Lys | Arg | Asp | Lys | Thr     | Leu        | Tyr | Thr  |      |     |
|     |     |     |     | 310 |     |     |     |     | 315 |     |     |         |            | 320 |      |      |     |
| CGC | TTA | GAC | GCT | TTA | GCT | ATT | CGT | TTG | ACT | CAA | GGC | TTA     | CAA        | AAG | AGC  | 1065 |     |
| Arg | Leu | Asp | Ala | Leu | Ala | Ile | Arg | Leu | Thr | Gln | Gly | Leu     | Gln        | Lys | Ser  |      |     |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |         |            | 335 |      |      |     |
| GCT | CAA | AAC | TAT | AAC | ATC | GCT | TTA | GAG | ACG | CTT | AAC | ATG     | GGG        | AGC | ATG  | 1113 |     |
| Ala | Gln | Asn | Tyr | Asn | Ile | Ala | Leu | Glu | Thr | Leu | Asn | Met     | Gly        | Ser | Met  |      |     |
|     |     |     |     | 340 |     |     |     |     | 345 |     |     |         |            | 350 |      |      | 355 |
| TTT | GGC | TTT | TTC | TTT | AAC | GAA | AAT | GCG | GTG | CAC | GAT | TTT     | GAT        | GAC | GCT  | 1161 |     |
| Phe | Gly | Phe | Phe | Phe | Asn | Glu | Asn | Ala | Val | His | Asp | Phe     | Asp        | Asp | Ala  |      |     |
|     |     |     |     | 360 |     |     |     |     | 365 |     |     |         |            | 370 |      |      |     |
| TTA | AAA | AGC | GAT | ACG | GAG | ATG | TTT | GCA | AAA | TTC | CAC | CAA     | AAA        | ATG | CTC  | 1209 |     |
| Leu | Lys | Ser | Asp | Thr | Glu | Met | Phe | Ala | Lys | Phe | His | Gln     | Lys        | Met | Leu  |      |     |
|     |     |     |     | 375 |     |     |     |     | 380 |     |     |         |            | 385 |      |      |     |
| TTT | AAG | GGC | GTG | TAT | TTG | GCG | TGC | TCA | AGC | TTT | GAA | ACC     | GGC        | TTT | ATT  | 1257 |     |
| Phe | Lys | Gly | Val | Tyr | Leu | Ala | Cys | Ser | Ser | Phe | Glu | Thr     | Gly        | Phe | Ile  |      |     |
|     |     |     |     | 390 |     |     |     |     | 395 |     |     |         |            | 400 |      |      |     |
| TGT | GAG | CCT | ATG | ACT | GAA | GAG | ATG | ATT | GAT | TTA | ACG | ATC     | GCA        | AAA | GCC  | 1305 |     |
| Cys | Glu | Pro | Met | Thr | Glu | Glu | Met | Ile | Asp | Leu | Thr | Ile     | Ala        | Lys | Ala  |      |     |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |         |            | 415 |      |      |     |
| GAT | GAA | AGT | TTT | GAT | GAA | ATC | ATA | AAA | GGT | GTG | TGA | ATTTTTT | GAAAAAGCCA |     | 1358 |      |     |
| Asp | Glu | Ser | Phe | Asp | Glu | Ile | Ile | Lys | Gly | Val |     |         |            |     |      |      |     |
|     |     |     |     | 420 |     |     |     |     | 425 |     |     |         |            | 430 |      |      |     |

## (2) INFORMATION FOR SEQ ID NO:538:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | Leu | His | Ser | Ile | Asn | Asp | Phe | Asn | Glu | Ala | Lys | Gln | Val | 1   | 5   | 10  | 15  |
| Ile | Ala | Gly | Gly | Val | Asn | Ser | Pro | Val | Arg | Ala | Phe | Lys | Ser | Val | Lys | 20  | 25  | 30  |     |
| Gly | Thr | Pro | Pro | Phe | Ile | Leu | Lys | Gly | Lys | Gly | Ala | Tyr | Leu | Tyr | Asp | 35  | 40  | 45  |     |
| Val | Asp | Asn | Asn | His | Tyr | Ile | Asp | Phe | Val | Gln | Ser | Trp | Gly | Pro | Leu | 50  | 55  | 60  |     |
| Ile | Phe | Gly | His | Ala | Asp | Glu | Glu | Ile | Glu | Glu | Asn | Ile | Ile | Asn | Ala | 65  | 70  | 75  | 80  |
| Leu | Lys | Lys | Gly | Thr | Ser | Phe | Gly | Ala | Pro | Thr | Glu | Leu | Glu | Thr | Thr | 85  | 90  | 95  |     |
| Leu | Ala | Lys | Glu | Ile | Ile | Ser | Cys | Tyr | Glu | Gly | Leu | Asp | Lys | Val | Arg | 100 | 105 | 110 |     |
| Leu | Val | Ser | Ser | Gly | Thr | Glu | Ala | Thr | Met | Ser | Ala | Ile | Arg | Leu | Ala | 115 | 120 | 125 |     |
| Arg | Ala | Tyr | Ser | Gln | Lys | Asp | Leu | Ile | Lys | Phe | Glu | Gly | Cys | Tyr |     | 130 | 135 | 140 |     |
| His | Gly | His | Ser | Asp | Ser | Leu | Leu | Val | Lys | Ala | Gly | Ser | Gly | Cys | Ala | 145 | 150 | 155 | 160 |
| Thr | Phe | Gly | Ser | Pro | Ser | Ser | Leu | Gly | Val | Pro | Asn | Asp | Phe | Ser | Lys | 165 | 170 | 175 |     |
| His | Thr | Leu | Val | Ala | Arg | Tyr | Asn | Asp | Leu | Asn | Ser | Thr | Glu | Glu | Cys | 180 | 185 | 190 |     |
| Phe | Lys | Lys | Gly | Asn | Val | Gly | Cys | Val | Ile | Ile | Glu | Pro | Ile | Ala | Gly | 195 | 200 | 205 |     |
| Asn | Met | Gly | Leu | Val | Pro | Ala | Gln | Lys | Glu | Phe | Leu | Leu | Gly | Leu | Lys | 210 | 215 | 220 |     |
| Ala | Leu | Cys | Glu | Lys | Tyr | Gln | Ala | Val | Leu | Ile | Leu | Asp | Glu | Val | Met | 225 | 230 | 235 | 240 |
| Ser | Gly | Phe | Arg | Ala | Ser | Leu | Ser | Gly | Ser | Gln | Glu | Phe | Tyr | Gly | Val | 245 | 250 | 255 |     |
| Val | Pro | Asp | Leu | Val | Thr | Phe | Gly | Lys | Val | Ile | Gly | Ala | Gly | Leu | Pro | 260 | 265 | 270 |     |
| Leu | Ala | Cys | Phe | Gly | Gly | Arg | Ala | Glu | Ile | Met | Asp | Leu | Leu | Ser | Pro | 275 | 280 | 285 |     |
| Ile | Gly | Ser | Val | Tyr | Gln | Ala | Gly | Thr | Leu | Ser | Gly | Asn | Pro | Leu | Ala | 290 | 295 | 300 |     |
| Val | Cys | Ala | Gly | Leu | Ser | Ala | Leu | Tyr | Lys | Ile | Lys | Arg | Asp | Lys | Thr | 305 | 310 | 315 | 320 |
| Leu | Tyr | Thr | Arg | Leu | Asp | Ala | Leu | Ala | Ile | Arg | Leu | Thr | Gln | Gly | Leu | 325 | 330 | 335 |     |
| Gln | Lys | Ser | Ala | Gln | Asn | Tyr | Asn | Ile | Ala | Leu | Glu | Thr | Leu | Asn | Met | 340 | 345 | 350 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ser | Met | Phe | Gly | Phe | Phe | Phe | Asn | Glu | Asn | Ala | Val | His | Asp | Phe |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Asp | Asp | Ala | Leu | Lys | Ser | Asp | Thr | Glu | Met | Phe | Ala | Lys | Phe | His | Gln |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Lys | Met | Leu | Phe | Lys | Gly | Val | Tyr | Leu | Ala | Cys | Ser | Ser | Phe | Glu | Thr |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Gly | Phe | Ile | Cys | Glu | Pro | Met | Thr | Glu | Glu | Met | Ile | Asp | Leu | Thr | Ile |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Ala | Lys | Ala | Asp | Glu | Ser | Phe | Asp | Glu | Ile | Ile | Lys | Gly | Val |     |     |
|     |     | 420 |     |     |     |     |     | 425 |     |     |     |     | 430 |     |     |

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 90...1052
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

|             |             |             |             |             |                 |     |
|-------------|-------------|-------------|-------------|-------------|-----------------|-----|
| AAGGCGCAAA  | ACTTAGCCAA  | AAAAGAGATG  | GACGCACTAG  | ATTCTCATCT  | GTTAGCGTTT      | 60  |
| TTAAATCAAA  | ATGCAAATGC  | CATTCAGTG   | ATG CCC AAA | ATC CCT ATC | ACG CTC         | 113 |
|             |             | Met         | Pro Lys     | Ile         | Pro Ile Thr Leu |     |
|             |             | 1           |             | 5           |                 |     |
| ATC ACC GGT | TTT TTA GGC | AGC GGT AAA | ACG AGT TTT | TTG AGC GAA | TAT             | 161 |
| Ile Thr Gly | Phe Leu Gly | Ser Gly Lys | Thr Ser Phe | Leu Ser Glu | Tyr             |     |
| 10          |             | 15          |             | 20          |                 |     |
| TTA AAC CAA | ACA GAT CAC | CAA GGC GTC | GCT CTT ATC | ATC AAT GAA | ATC             | 209 |
| Leu Asn Gln | Thr Asp His | Gln Gly Val | Ala Leu Ile | Ile Asn Glu | Ile             |     |
| 25          |             | 30          |             | 35          | 40              |     |
| GGT CAA GCC | GCT TTG GAT | CAG CGC ATC | TTA AGC GTT | CAA TAT TGC | GGT             | 257 |
| Gly Gln Ala | Ala Leu Asp | Gln Arg Ile | Leu Ser Val | Gln Tyr Cys | Gly             |     |
|             | 45          |             | 50          |             | 55              |     |
| GAA AAA ATG | CTC TAT CTT | AAC GCA GGG | TGC GTG TGT | TGC AAC AAA | CGC             | 305 |
| Glu Lys Met | Leu Tyr Leu | Asn Ala Gly | Cys Val Cys | Cys Asn Lys | Arg             |     |
|             | 60          |             | 65          |             | 70              |     |
| TTG GAT TTA | GTG GAG TCT | CTA AAA GCC | ACG CTC AAC | AAC TAT GAA | TGG             | 353 |
| Leu Asp Leu | Val Glu Ser | Leu Lys Ala | Thr Leu Asn | Asn Tyr Glu | Trp             |     |
|             | 75          |             | 80          |             | 85              |     |
| CAC GGC GAA | ATT CTA AGG | CGC ATC ATC | ATT GAA ACT | ACC GGT TTA | GCC             | 401 |
| His Gly Glu | Ile Leu Arg | Arg Ile Ile | Ile Glu Thr | Thr Gly Leu | Ala             |     |
|             | 90          |             | 95          |             | 100             |     |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| AAC CCG GCA CCG ATT TTA TGG ACG ATT TTG AGC GAC ACT TTT TTA GGA<br>Asn Pro Ala Pro Ile Leu Trp Thr Ile Leu Ser Asp Thr Phe Leu Gly<br>105 110 115 120 | 449  |
| GTG CAT TTT GAG ATT CAA AGC GTG GTG GCT TGC GTG GAT GCA TTG AAT<br>Val His Phe Glu Ile Gln Ser Val Val Ala Cys Val Asp Ala Leu Asn<br>125 130 135     | 497  |
| GCT AGA GAG CAT TTA ACC AAC AAT GAA GCT AAA GAG CAA ATC GTT TTT<br>Ala Arg Glu His Leu Thr Asn Asn Glu Ala Lys Glu Gln Ile Val Phe<br>140 145 150     | 545  |
| GCT GAT AGC GTT TTA TTG ACC AAA ACG GAT TTA CAA AAC GAT AGC GCG<br>Ala Asp Ser Val Leu Leu Thr Lys Thr Asp Leu Gln Asn Asp Ser Ala<br>155 160 165     | 593  |
| GCT TTA ACA AAA CTA AAA GAG AGG ATA CAA GCC CTT AAC CCT AGT GCA<br>Ala Leu Thr Lys Leu Lys Glu Arg Ile Gln Ala Leu Asn Pro Ser Ala<br>170 175 180     | 641  |
| GAA ATT TTT GAC AAG AGG GCG ATA GAC TAT GAG AGC CTC TTT TCA CGC<br>Glu Ile Phe Asp Lys Arg Ala Ile Asp Tyr Glu Ser Leu Phe Ser Arg<br>185 190 195 200 | 689  |
| AAA AAT AGG GCG CGA AAT TTT ATG CCA AGA ATG CCA AAA GAT TCG CAC<br>Lys Asn Arg Ala Arg Asn Phe Met Pro Arg Met Pro Lys Asp Ser His<br>205 210 215     | 737  |
| TCG CAA GGC TTT GAG ACT TTA AGC ATT AAT TTT GAA GGC ACG ATG GAG<br>Ser Gln Gly Phe Glu Thr Leu Ser Ile Asn Phe Glu Gly Thr Met Glu<br>220 225 230     | 785  |
| TGG AGC GCG TTT GGG ATT TGG CTG AGT TTG TTA TTG CAT CAA TAC GGC<br>Trp Ser Ala Phe Gly Ile Trp Leu Ser Leu Leu Leu His Gln Tyr Gly<br>235 240 245     | 833  |
| ACA CAG ATT TTA CGC ATC AAG GGG ATT ATT GAC ATT GGA AGC GGC TTT<br>Thr Gln Ile Leu Arg Ile Lys Gly Ile Ile Asp Ile Gly Ser Gly Phe<br>250 255 260     | 881  |
| TTG GTG AGT ATT AAC GGC GTG ATG CAT GTC ATT TAC CCG CCT AAG CAT<br>Leu Val Ser Ile Asn Gly Val Met His Val Ile Tyr Pro Pro Lys His<br>265 270 275 280 | 929  |
| ATT TTA AAG GAT CAA AAC GGC TCT AAC CTC GTT TTT ATC ATG CGC CAT<br>Ile Leu Lys Asp Gln Asn Gly Ser Asn Leu Val Phe Ile Met Arg His<br>285 290 295     | 977  |
| TTA GAG CGT GAA AAA ATC TTA AAT TCC TTA AAG GGT TTT AAG GAT TTT<br>Leu Glu Arg Glu Lys Ile Leu Asn Ser Leu Lys Gly Phe Lys Asp Phe<br>300 305 310     | 1025 |
| CTC GGC ATC AAG GGT TTT GAA ACC CAA TAATTTTCT ATTTATGGAT AGCTGTT<br>Leu Gly Ile Lys Gly Phe Glu Thr Gln<br>315 320                                    | 1079 |
| TGCATTTTGA TGGGGAAAAAG A                                                                                                                              | 1100 |

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Lys | Ile | Pro | Ile | Thr | Leu | Ile | Thr | Gly | Phe | Leu | Gly | Ser | Gly | 1   | 5   | 10  | 15  |
| Lys | Thr | Ser | Phe | Leu | Ser | Glu | Tyr | Leu | Asn | Gln | Thr | Asp | His | Gln | Gly | 20  | 25  | 30  |     |
| Val | Ala | Leu | Ile | Ile | Asn | Glu | Ile | Gly | Gln | Ala | Ala | Leu | Asp | Gln | Arg | 35  | 40  | 45  |     |
| Ile | Leu | Ser | Val | Gln | Tyr | Cys | Gly | Glu | Lys | Met | Leu | Tyr | Leu | Asn | Ala | 50  | 55  | 60  |     |
| Gly | Cys | Val | Cys | Cys | Asn | Lys | Arg | Leu | Asp | Leu | Val | Glu | Ser | Leu | Lys | 65  | 70  | 75  | 80  |
| Ala | Thr | Leu | Asn | Asn | Tyr | Glu | Trp | His | Gly | Glu | Ile | Leu | Arg | Arg | Ile | 85  | 90  | 95  |     |
| Ile | Ile | Glu | Thr | Thr | Gly | Leu | Ala | Asn | Pro | Ala | Pro | Ile | Leu | Trp | Thr | 100 | 105 | 110 |     |
| Ile | Leu | Ser | Asp | Thr | Phe | Leu | Gly | Val | His | Phe | Glu | Ile | Gln | Ser | Val | 115 | 120 | 125 |     |
| Val | Ala | Cys | Val | Asp | Ala | Leu | Asn | Ala | Arg | Glu | His | Leu | Thr | Asn | Asn | 130 | 135 | 140 |     |
| Glu | Ala | Lys | Glu | Gln | Ile | Val | Phe | Ala | Asp | Ser | Val | Leu | Leu | Thr | Lys | 145 | 150 | 155 | 160 |
| Thr | Asp | Leu | Gln | Asn | Asp | Ser | Ala | Ala | Leu | Thr | Lys | Leu | Lys | Glu | Arg | 165 | 170 | 175 |     |
| Ile | Gln | Ala | Leu | Asn | Pro | Ser | Ala | Glu | Ile | Phe | Asp | Lys | Arg | Ala | Ile | 180 | 185 | 190 |     |
| Asp | Tyr | Glu | Ser | Leu | Phe | Ser | Arg | Lys | Asn | Arg | Ala | Arg | Asn | Phe | Met | 195 | 200 | 205 |     |
| Pro | Arg | Met | Pro | Lys | Asp | Ser | His | Ser | Gln | Gly | Phe | Glu | Thr | Leu | Ser | 210 | 215 | 220 |     |
| Ile | Asn | Phe | Glu | Gly | Thr | Met | Glu | Trp | Ser | Ala | Phe | Gly | Ile | Trp | Leu | 225 | 230 | 235 | 240 |
| Ser | Leu | Leu | Leu | His | Gln | Tyr | Gly | Thr | Gln | Ile | Leu | Arg | Ile | Lys | Gly | 245 | 250 | 255 |     |
| Ile | Ile | Asp | Ile | Gly | Ser | Gly | Phe | Leu | Val | Ser | Ile | Asn | Gly | Val | Met | 260 | 265 | 270 |     |
| His | Val | Ile | Tyr | Pro | Pro | Lys | His | Ile | Leu | Lys | Asp | Gln | Asn | Gly | Ser | 275 | 280 | 285 |     |
| Asn | Leu | Val | Phe | Ile | Met | Arg | His | Leu | Glu | Arg | Glu | Lys | Ile | Leu | Asn | 290 | 295 | 300 |     |
| Ser | Leu | Lys | Gly | Phe | Lys | Asp | Phe | Leu | Gly | Ile | Lys | Gly | Phe | Glu | Thr | 305 | 310 | 315 | 320 |
| Gln |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1713 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA  
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 26...1648  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

|                 |                 |             |         |         |         |     |     |     |     |     |     |    |
|-----------------|-----------------|-------------|---------|---------|---------|-----|-----|-----|-----|-----|-----|----|
| TTAAAAGCAA      | ACAAGAAAGT      | TAAGC       | ATG     | CAC     | ACT     | CTC | ATT | AAG | GGC | ATT | TTA | 52 |
|                 |                 |             | Met     | His     | Thr     | Leu | Ile | Lys | Gly | Ile | Leu |    |
|                 |                 |             | 1       |         |         |     | 5   |     |     |     |     |    |
| GAA GAG ATT TTA | GAA GAA GAA GTC | ATT GTT     | GAA TAC | CCT AAA | GAC AGA | 100 |     |     |     |     |     |    |
| Glu Glu Ile Leu | Glu Glu Glu Val | Ile Val     | Glu Tyr | Pro Lys | Asp Arg |     |     |     |     |     |     |    |
| 10              | 15              |             | 20      |         | 25      |     |     |     |     |     |     |    |
| GAG CAT GGG CAT | TAC GCT ACG CCC | ATT GCT TTC | AAT CTC | GCC AAA | GTT     | 148 |     |     |     |     |     |    |
| Glu His Gly His | Tyr Ala Thr Pro | Ile Ala Phe | Asn Leu | Ala Lys | Val     |     |     |     |     |     |     |    |
|                 | 30              |             | 35      |         | 40      |     |     |     |     |     |     |    |
| TTT AAA AAA TCG | CCC TTA GCC ATC | GCT GAA GAG | TTA GCC | CTT AAA | ATC     | 196 |     |     |     |     |     |    |
| Phe Lys Lys Ser | Pro Leu Ala Ile | Ala Glu Glu | Leu Ala | Leu Lys | Ile     |     |     |     |     |     |     |    |
|                 | 45              |             | 50      |         | 55      |     |     |     |     |     |     |    |
| AGC ACG CAT GAA | AAA ACT CAA GGG | CTT TTT GAC | AGC GTA | GTG GCT | TGT     | 244 |     |     |     |     |     |    |
| Ser Thr His Glu | Lys Thr Gln Gly | Leu Phe Asp | Ser Val | Val Ala | Cys     |     |     |     |     |     |     |    |
|                 | 60              |             | 65      |         | 70      |     |     |     |     |     |     |    |
| AAG GGC TAT ATC | AAT TTC ACG CTT | TCT TTA GAT | TTT TTG | GAG CGT | TTC     | 292 |     |     |     |     |     |    |
| Lys Gly Tyr Ile | Asn Phe Thr Leu | Ser Leu Asp | Phe Leu | Glu Arg | Phe     |     |     |     |     |     |     |    |
|                 | 75              |             | 80      |         | 85      |     |     |     |     |     |     |    |
| ACC CAA AAA GCT | TTG GAA TTG AAA | GAA AAA TTT | GGC TCT | CAA GTT | AAA     | 340 |     |     |     |     |     |    |
| Thr Gln Lys Ala | Leu Glu Leu Lys | Glu Lys Phe | Gly Ser | Gln Val | Lys     |     |     |     |     |     |     |    |
|                 | 90              |             | 95      |         | 100     |     |     |     |     |     |     |    |
| AGC GAA CGT TCT | CAA AAA ATC TTT | TTA GAA TTT | GTG AGC | GCT AAC | CCC     | 388 |     |     |     |     |     |    |
| Ser Glu Arg Ser | Gln Lys Ile Phe | Leu Glu Phe | Val Ser | Ala Asn | Pro     |     |     |     |     |     |     |    |
|                 | 110             |             | 115     |         | 120     |     |     |     |     |     |     |    |
| ACA GGG CCT TTA | CAC ATA GGG CAT | GCT AGA GGG | GCG GTG | TTT GGC | GAT     | 436 |     |     |     |     |     |    |
| Thr Gly Pro Leu | His Ile Gly His | Ala Arg Gly | Ala Val | Phe Gly | Asp     |     |     |     |     |     |     |    |
|                 | 125             |             | 130     |         | 135     |     |     |     |     |     |     |    |
| AGT TTG GCT AAA | ATC GCT CGC TTT | TTA GGG CAT | GAA GTT | TTA TGC | GAG     | 484 |     |     |     |     |     |    |
| Ser Leu Ala Lys | Ile Ala Arg Phe | Leu Gly His | Glu Val | Leu Cys | Glu     |     |     |     |     |     |     |    |
|                 | 140             |             | 145     |         | 150     |     |     |     |     |     |     |    |
| TAT TAT GTC AAT | GAC ATG GGA TCT | CAA ATC CGC | TTG TTA | GGG CTT | TCT     | 532 |     |     |     |     |     |    |
| Tyr Tyr Val Asn | Asp Met Gly Ser | Gln Ile Arg | Leu Leu | Gly Leu | Ser     |     |     |     |     |     |     |    |
|                 | 155             |             | 160     |         | 165     |     |     |     |     |     |     |    |



|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| GTA<br>Val<br>170 | TGG<br>Trp        | CTC<br>Leu        | GCT<br>Ala        | TAC<br>Tyr        | AGA<br>Arg<br>175 | GAA<br>Glu        | CAT<br>His        | GTT<br>Val        | TTA<br>Leu        | AAA<br>Lys<br>180 | GAA<br>Glu        | AGC<br>Ser        | GTA<br>Val        | ACT<br>Thr        | TAC<br>Tyr<br>185 | 580  |
| CCA<br>Pro        | GAA<br>Glu        | GTC<br>Val        | TTT<br>Phe        | TAC<br>Tyr<br>190 | AAA<br>Lys        | GGC<br>Gly        | GAA<br>Glu        | TAC<br>Tyr        | ATC<br>Ile<br>195 | ATT<br>Ile        | GAA<br>Glu        | ATC<br>Ile        | GCT<br>Ala        | AAA<br>Lys<br>200 | AAG<br>Lys        | 628  |
| GCG<br>Ala        | AAC<br>Asn        | AAC<br>Asn        | GAT<br>Asp<br>205 | TTA<br>Leu        | GAA<br>Glu        | CCA<br>Pro        | AGC<br>Ser        | CTT<br>Leu<br>210 | TTA<br>Leu        | AAA<br>Lys        | GAA<br>Glu        | AAC<br>Asn        | GAA<br>Glu<br>215 | GAA<br>Glu        | ACG<br>Thr        | 676  |
| ATT<br>Ile        | ATT<br>Ile        | GAA<br>Glu<br>220 | GTT<br>Val        | TTA<br>Leu        | AGC<br>Ser        | GGC<br>Gly        | TAT<br>Tyr<br>225 | GCT<br>Ala        | AGG<br>Arg        | GAT<br>Asp        | CTA<br>Leu<br>230 | ATG<br>Met        | CTT<br>Leu        | TTA<br>Leu        | GAA<br>Glu        | 724  |
| ATT<br>Ile        | AAA<br>Lys<br>235 | GAT<br>Asp        | AAT<br>Asn        | TTA<br>Leu        | GAC<br>Asp<br>240 | GCT<br>Ala        | TTA<br>Leu        | GGC<br>Gly        | ATT<br>Ile        | CAT<br>His        | TTT<br>Phe<br>245 | GAT<br>Asp        | TCC<br>Ser        | TAT<br>Tyr        | GCG<br>Ala        | 772  |
| AGC<br>Ser<br>250 | GAA<br>Glu        | AAA<br>Lys        | GAA<br>Glu        | GTT<br>Val        | TTT<br>Phe<br>255 | AAA<br>Lys        | CAT<br>His        | AAA<br>Lys        | GAT<br>Asp        | GCG<br>Ala<br>260 | GTG<br>Val        | TTT<br>Phe        | GAA<br>Glu        | CAA<br>Gln        | TTA<br>Leu<br>265 | 820  |
| GAA<br>Glu        | AAA<br>Lys        | GCG<br>Ala        | AAC<br>Asn        | GCC<br>Ala<br>270 | CTT<br>Leu        | TAT<br>Tyr        | GAA<br>Glu        | AAG<br>Lys        | GAT<br>Asp<br>275 | TCT<br>Ser        | AAA<br>Lys        | ATC<br>Ile        | TGG<br>Trp        | CTC<br>Leu<br>280 | AAA<br>Lys        | 868  |
| TCT<br>Ser        | TCA<br>Ser        | CTC<br>Leu        | TAC<br>Tyr<br>285 | CAG<br>Gln        | GAT<br>Asp        | GAA<br>Glu        | AGC<br>Ser        | GAT<br>Asp<br>290 | CGG<br>Arg        | GTG<br>Val        | CTC<br>Leu        | ATT<br>Ile        | AAA<br>Lys<br>295 | GAA<br>Glu        | GAT<br>Asp        | 916  |
| AAA<br>Lys        | AGC<br>Ser        | TAC<br>Tyr<br>300 | ACT<br>Thr        | TAT<br>Tyr        | TTA<br>Leu        | GCG<br>Ala        | GGC<br>Gly<br>305 | GAT<br>Asp        | ATT<br>Ile        | GTC<br>Val        | TAT<br>Tyr        | CAT<br>His<br>310 | GAT<br>Asp        | GAA<br>Glu        | AAA<br>Lys        | 964  |
| TTC<br>Phe        | AAG<br>Lys<br>315 | CAA<br>Gln        | GAT<br>Asp        | TAT<br>Tyr        | ACC<br>Thr        | AAA<br>Lys<br>320 | TAC<br>Tyr        | ATC<br>Ile        | AAC<br>Asn        | ATT<br>Ile        | TGG<br>Trp<br>325 | GGG<br>Gly        | GCA<br>Ala        | GAC<br>Asp        | CAC<br>His        | 1012 |
| CAC<br>His<br>330 | GGC<br>Gly        | TAT<br>Tyr        | ATC<br>Ile        | GCT<br>Ala        | AGA<br>Arg<br>335 | GTG<br>Val        | AAA<br>Lys        | GCC<br>Ala        | AGC<br>Ser        | CTT<br>Leu<br>340 | GAG<br>Glu        | TTT<br>Phe        | TTG<br>Leu        | GGC<br>Gly        | TAT<br>Tyr<br>345 | 1060 |
| GAT<br>Asp        | TCC<br>Ser        | AAC<br>Asn        | AAG<br>Lys        | CTT<br>Leu<br>350 | GAA<br>Glu        | GTC<br>Val        | TTG<br>Leu        | CTC<br>Leu        | GCT<br>Ala<br>355 | CAA<br>Gln        | ATG<br>Met        | GTG<br>Val        | CGC<br>Arg        | TTG<br>Leu<br>360 | CTC<br>Leu        | 1108 |
| AAA<br>Lys        | GAT<br>Asp        | AAC<br>Asn        | GAG<br>Glu<br>365 | CCT<br>Pro        | TAC<br>Tyr        | AAG<br>Lys        | ATG<br>Met        | AGT<br>Ser<br>370 | AAA<br>Lys        | AGA<br>Arg        | GCG<br>Ala        | GGT<br>Gly        | AAT<br>Asn<br>375 | TTT<br>Phe        | ATT<br>Ile        | 1156 |
| TTG<br>Leu        | ATT<br>Ile        | AAA<br>Lys<br>380 | GAT<br>Asp        | GTG<br>Val        | GTT<br>Val        | GAT<br>Asp        | GAT<br>Asp<br>385 | GTG<br>Val        | GGT<br>Gly        | AAG<br>Lys        | GAC<br>Asp        | GCT<br>Ala<br>390 | TTG<br>Leu        | AGG<br>Arg        | TTT<br>Phe        | 1204 |
| ATT<br>Ile        | TTT<br>Phe        | TTG<br>Leu        | AGC<br>Ser        | AAA<br>Lys        | CGG<br>Arg        | CTT<br>Leu        | GAC<br>Asp        | ACT<br>Thr        | CAT<br>His        | TTA<br>Leu        | GAA<br>Glu        | TTT<br>Phe        | GAT<br>Asp        | GTC<br>Val        | AAT<br>Asn        | 1252 |

[illegible]

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Thr | Leu | Ile | Lys | Gly | Ile | Leu | Glu | Glu | Ile | Leu | Glu | Glu | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ile | Val | Glu | Tyr | Pro | Lys | Asp | Arg | Glu | His | Gly | His | Tyr | Ala | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ile | Ala | Phe | Asn | Leu | Ala | Lys | Val | Phe | Lys | Lys | Ser | Pro | Leu | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|         |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile 50  | Ala | Glu | Glu | Leu | Ala | Leu | Lys | Ile | Ser | Thr | His | Glu | Lys | Thr | Gln |
| Gly 65  | Leu | Phe | Asp | Ser | Val | Val | Ala | Cys | Lys | Gly | Tyr | Ile | Asn | Phe | Thr |
| Leu     | Ser | Leu | Asp | Phe | Leu | Glu | Arg | Phe | Thr | Gln | Lys | Ala | Leu | Glu | Leu |
| Lys     | Glu | Lys | Phe | Gly | Ser | Gln | Val | Lys | Ser | Glu | Arg | Ser | Gln | Lys | Ile |
| Phe     | Leu | Glu | Phe | Val | Ser | Ala | Asn | Pro | Thr | Gly | Pro | Leu | His | Ile | Gly |
| His     | Ala | Arg | Gly | Ala | Val | Phe | Gly | Asp | Ser | Leu | Ala | Lys | Ile | Ala | Arg |
| Phe 145 | Leu | Gly | His | Glu | Val | Leu | Cys | Glu | Tyr | Tyr | Val | Asn | Asp | Met | Gly |
| Ser     | Gln | Ile | Arg | Leu | Leu | Gly | Leu | Ser | Val | Trp | Leu | Ala | Tyr | Arg | Glu |
| His     | Val | Leu | Lys | Glu | Ser | Val | Thr | Tyr | Pro | Glu | Val | Phe | Tyr | Lys | Gly |
| Glu     | Tyr | Ile | Ile | Glu | Ile | Ala | Lys | Lys | Ala | Asn | Asn | Asp | Leu | Glu | Pro |
| Ser     | Leu | Leu | Lys | Glu | Asn | Glu | Glu | Thr | Ile | Ile | Glu | Val | Leu | Ser | Gly |
| Tyr 225 | Ala | Arg | Asp | Leu | Met | Leu | Leu | Glu | Ile | Lys | Asp | Asn | Leu | Asp | Ala |
| Leu     | Gly | Ile | His | Phe | Asp | Ser | Tyr | Ala | Ser | Glu | Lys | Glu | Val | Phe | Lys |
| His     | Lys | Asp | Ala | Val | Phe | Glu | Gln | Leu | Glu | Lys | Ala | Asn | Ala | Leu | Tyr |
| Glu     | Lys | Asp | Ser | Lys | Ile | Trp | Leu | Lys | Ser | Ser | Leu | Tyr | Gln | Asp | Glu |
| Ser     | Asp | Arg | Val | Leu | Ile | Lys | Glu | Asp | Lys | Ser | Tyr | Thr | Tyr | Leu | Ala |
| Gly 305 | Asp | Ile | Val | Tyr | His | Asp | Glu | Lys | Phe | Lys | Gln | Asp | Tyr | Thr | Lys |
| Tyr     | Ile | Asn | Ile | Trp | Gly | Ala | Asp | His | His | Gly | Tyr | Ile | Ala | Arg | Val |
| Lys     | Ala | Ser | Leu | Glu | Phe | Leu | Gly | Tyr | Asp | Ser | Asn | Lys | Leu | Glu | Val |
| Leu     | Leu | Ala | Gln | Met | Val | Arg | Leu | Lys | Asp | Asn | Glu | Pro | Tyr | Lys |     |
| Met     | Ser | Lys | Arg | Ala | Gly | Asn | Phe | Ile | Leu | Ile | Lys | Asp | Val | Val | Asp |
| Asp 385 | Val | Gly | Lys | Asp | Ala | Leu | Arg | Phe | Ile | Phe | Leu | Ser | Lys | Arg | Leu |
| Asp     | Thr | His | Leu | Glu | Phe | Asp | Val | Asn | Thr | Leu | Lys | Lys | Gln | Asp | Ser |
| Ser     | Asn | Pro | Ile | Tyr | Tyr | Ile | His | Tyr | Ala | Asn | Ser | Arg | Ile | His | Thr |
| Met     | Leu | Glu | Lys | Ser | Pro | Phe | Ser | Lys | Glu | Glu | Val | Leu | Gln | Thr | Pro |
| Leu     | Thr | Asn | Leu | Asn | Ala | Glu | Glu | Lys | Tyr | Leu | Leu | Phe | Ser | Ala | Leu |
| Ser 465 | Leu | Pro | Lys | Ala | Ile | Glu | Ser | Ser | Phe | Glu | Glu | Tyr | Gly | Leu | Gln |
| Lys     | Met | Cys | Glu | Tyr | Ala | Lys | Thr | Leu | Ala | Ser | Glu | Phe | His | Arg | Phe |
| Tyr     | Asn | Ala | Gly | Lys | Ile | Leu | Asp | Thr | Pro | Lys | Ala | Lys | Glu | Leu | Leu |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ile | Cys | Leu | Ile | Val | Ser | Leu | Ser | Leu | Ser | Asn | Ala | Phe | Lys | Leu |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Leu | Gly | Ile | Glu | Ile | Lys | Thr | Lys | Ile | Ser | Ala | Arg | Asp |     |     |     |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 896 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 38...835
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| AAGTAGAGAT TATATTACCT AGATAGTGAA TCAACGA ATG AAA AGC CAC TTC CAA | 55  |
| Met Lys Ser His Phe Gln                                          |     |
| 1 5                                                              |     |
| TAC AGC ACG CTA GAA AAT ATC CCT AAA GCC TTT GAC ATT CTC AAA GAC  | 103 |
| Tyr Ser Thr Leu Glu Asn Ile Pro Lys Ala Phe Asp Ile Leu Lys Asp  |     |
| 10 15 20                                                         |     |
| CCC CCT AAA AAA CTC TAT TGT GTG GGC GAT ACC AAG CTT TTG GAC ACG  | 151 |
| Pro Pro Lys Lys Leu Tyr Cys Val Gly Asp Thr Lys Leu Leu Asp Thr  |     |
| 25 30 35                                                         |     |
| CCT TTA AAA GTG GCG ATC ATA GGC ACA AGA AGA CCC ACC CCT TAC AGC  | 199 |
| Pro Leu Lys Val Ala Ile Ile Gly Thr Arg Arg Pro Thr Pro Tyr Ser  |     |
| 40 45 50                                                         |     |
| AAG CAA CAC ACG ATC ACT CTA GCT AGA GAG CTT GCT AAA AAT GGC GCG  | 247 |
| Lys Gln His Thr Ile Thr Leu Ala Arg Glu Leu Ala Lys Asn Gly Ala  |     |
| 55 60 65 70                                                      |     |
| GTT ATT GTG AGT GGG GGA GCG TTA GGC GTG GAT ATT ATC GCT CAA GAA  | 295 |
| Val Ile Val Ser Gly Gly Ala Leu Gly Val Asp Ile Ile Ala Gln Glu  |     |
| 75 80 85                                                         |     |
| AAC GCC TTG CCA AAA ACG ATC ATG CTT TCG CCT TGC AGT TTG GAT TTC  | 343 |
| Asn Ala Leu Pro Lys Thr Ile Met Leu Ser Pro Cys Ser Leu Asp Phe  |     |
| 90 95 100                                                        |     |
| ATC TAT CCT ACG AAC AAT CAT AAA GTG ATC CAA GAA ATC GCG CAA AAC  | 391 |
| Ile Tyr Pro Thr Asn Asn His Lys Val Ile Gln Glu Ile Ala Gln Asn  |     |
| 105 110 115                                                      |     |
| GGC TTG ATT TTA AGC GAA TAT GAA AAG GAT TTC ATG CCC ATT AAA GGC  | 439 |
| Gly Leu Ile Leu Ser Glu Tyr Glu Lys Asp Phe Met Pro Ile Lys Gly  |     |
| 120 125 130                                                      |     |

|           |        |     |     |           |            |            |            |       |     |     |     |     |     |     |     |     |
|-----------|--------|-----|-----|-----------|------------|------------|------------|-------|-----|-----|-----|-----|-----|-----|-----|-----|
| TCT       | TTT    | TTG | GCG | AGA       | AAC        | CGC        | CTG        | GTG   | ATC | GCT | TTA | AGC | GAT | GTG | GTG | 487 |
| Ser       | Phe    | Leu | Ala | Arg       | Asn        | Arg        | Leu        | Val   | Ile | Ala | Leu | Ser | Asp | Val | Val |     |
| 135       |        |     |     |           | 140        |            |            |       |     | 145 |     |     |     |     | 150 |     |
|           |        |     |     |           |            |            |            |       |     |     |     |     |     |     |     |     |
| ATT       | ATC    | CCC | CAA | GCG       | GAT        | TTA        | AAA        | AGC   | GGC | TCT | ATG | AGC | AGC | GCG | AGA | 535 |
| Ile       | Ile    | Pro | Gln | Ala       | Asp        | Leu        | Lys        | Ser   | Gly | Ser | Met | Ser | Ser | Ala | Arg |     |
|           |        |     | 155 |           |            |            |            |       | 160 |     |     |     |     | 165 |     |     |
|           |        |     |     |           |            |            |            |       |     |     |     |     |     |     |     |     |
| TTA       | GCC    | CAG | AAA | TAC       | CAA        | AAG        | CCT        | TTA   | TTT | GTT | TTA | CCC | CAA | CGC | CTG | 583 |
| Leu       | Ala    | Gln | Lys | Tyr       | Gln        | Lys        | Pro        | Leu   | Phe | Val | Leu | Pro | Gln | Arg | Leu |     |
|           |        |     | 170 |           |            |            |            | 175   |     |     |     |     | 180 |     |     |     |
|           |        |     |     |           |            |            |            |       |     |     |     |     |     |     |     |     |
| AAT       | GAG    | AGC | GAT | GGC       | ACT        | AAT        | GAG        | CTT   | TTA | GAA | AAA | GGG | CAG | GCT | CAA | 631 |
| Asn       | Glu    | Ser | Asp | Gly       | Thr        | Asn        | Glu        | Leu   | Leu | Glu | Lys | Gly | Gln | Ala | Gln |     |
|           |        | 185 |     |           |            |            | 190        |       |     |     |     | 195 |     |     |     |     |
|           |        |     |     |           |            |            |            |       |     |     |     |     |     |     |     |     |
| GGG       | ATA    | TTT | AAT | ATT       | CAA        | AAT        | TTT        | ATA   | AAC | ACC | CTT | TTA | AAA | GAC | TAC | 679 |
| Gly       | Ile    | Phe | Asn | Ile       | Gln        | Asn        | Phe        | Ile   | Asn | Thr | Leu | Leu | Lys | Asp | Tyr |     |
|           | 200    |     |     |           |            | 205        |            |       |     |     | 210 |     |     |     |     |     |
|           |        |     |     |           |            |            |            |       |     |     |     |     |     |     |     |     |
| CAT       | TTA    | AAA | GAA | ATG       | CCT        | GAA        | ATG        | GAA   | GAT | GAA | TTT | TTA | GAA | TAT | TGT | 727 |
| His       | Leu    | Lys | Glu | Met       | Pro        | Glu        | Met        | Glu   | Asp | Glu | Phe | Leu | Glu | Tyr | Cys |     |
| 215       |        |     |     |           | 220        |            |            |       | 225 |     |     |     |     |     | 230 |     |
|           |        |     |     |           |            |            |            |       |     |     |     |     |     |     |     |     |
| GCC       | AAA    | AAC | CCG | AGC       | TAT        | GAA        | GAA        | GCG   | TAT | CTC | AAA | TTT | GGG | GAT | AAG | 775 |
| Ala       | Lys    | Asn | Pro | Ser       | Tyr        | Glu        | Glu        | Ala   | Tyr | Leu | Lys | Phe | Gly | Asp | Lys |     |
|           |        |     |     | 235       |            |            |            |       | 240 |     |     |     |     | 245 |     |     |
|           |        |     |     |           |            |            |            |       |     |     |     |     |     |     |     |     |
| CTT       | TTA    | GAA | TAC | GAG       | CTG        | TTG        | GGT        | AAG   | ATC | AAG | CGC | ATC | AAT | CAC | ATT | 823 |
| Leu       | Leu    | Glu | Tyr | Glu       | Leu        | Leu        | Gly        | Lys   | Ile | Lys | Arg | Ile | Asn | His | Ile |     |
|           |        |     | 250 |           |            |            |            | 255   |     |     |     |     | 260 |     |     |     |
|           |        |     |     |           |            |            |            |       |     |     |     |     |     |     |     |     |
| GTG       | GTG    | TTA | GCG | TTGTTTGGC | ATGCGATGTG | GGGTAAAAAC | GCATTGGCAT | CGCTG |     |     |     |     |     |     |     | 880 |
| Val       | Val    | Leu | Ala |           |            |            |            |       |     |     |     |     |     |     |     |     |
|           |        |     | 265 |           |            |            |            |       |     |     |     |     |     |     |     |     |
|           |        |     |     |           |            |            |            |       |     |     |     |     |     |     |     |     |
| CGCTTTTAA | TGGCGT |     |     |           |            |            |            |       |     |     |     |     |     |     |     | 896 |

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Lys | Ser | His | Phe | Gln | Tyr | Ser | Thr | Leu | Glu | Asn | Ile | Pro | Lys | Ala |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Phe | Asp | Ile | Leu | Lys | Asp | Pro | Pro | Lys | Lys | Leu | Tyr | Cys | Val | Gly | Asp |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Thr | Lys | Leu | Leu | Asp | Thr | Pro | Leu | Lys | Val | Ala | Ile | Ile | Gly | Thr | Arg |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg | Pro | Thr | Pro | Tyr | Ser | Lys | Gln | His | Thr | Ile | Thr | Leu | Ala | Arg | Glu |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |



|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ATC TTA AAG CCT GAG TTT AAA TAC GGC GTT TCG CTC ATT TAC TTG ATA    | 255 |
| Ile Leu Lys Pro Glu Phe Lys Tyr Gly Val Ser Leu Ile Tyr Leu Ile    |     |
| 45 50 55                                                           |     |
|                                                                    |     |
| GAG AGC ACA ATC CTT TAC TTT GTC AGC AAA GAT CTT TCT TGG ATA GTA    | 303 |
| Glu Ser Thr Ile Leu Tyr Phe Val Ser Lys Asp Leu Ser Trp Ile Val    |     |
| 60 65 70                                                           |     |
|                                                                    |     |
| GCG CTA ACG ATA TTC TCA CTA TCT TTG ATA CTG GTA GCG TTT AAG ATC    | 351 |
| Ala Leu Thr Ile Phe Ser Leu Ser Leu Ile Leu Val Ala Phe Lys Ile    |     |
| 75 80 85 90                                                        |     |
|                                                                    |     |
| TTC CTC CTT AAA GAC AAC CCT AAC AAA CGC TTC AAA AAC AAC AAG AGG    | 399 |
| Phe Leu Leu Lys Asp Asn Pro Asn Lys Arg Phe Lys Asn Asn Lys Arg    |     |
| 95 100 105                                                         |     |
|                                                                    |     |
| GAT AAA AAA TAATGTCTTA TTTTTTTTAAA ATCATTCTGG GCACAAGCGT GATCGTGGG | 457 |
| Asp Lys Lys                                                        |     |
|                                                                    |     |
| GG                                                                 | 459 |

(2) INFORMATION FOR SEQ ID NO:546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Val | Asp | Lys | Asn | Ser | Ala | Asp | Gln | Lys | Met | Trp | Arg | Ile | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Lys | Ala | Leu | Trp | Val | Leu | Ser | Leu | Leu | Gly | Gly | Ser | Val | Gly | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Val | Ala | Met | Val | Val | Ser | His | His | Lys | Ile | Leu | Lys | Pro | Glu | Phe |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Tyr | Gly | Val | Ser | Leu | Ile | Tyr | Leu | Ile | Glu | Ser | Thr | Ile | Leu | Tyr |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Val | Ser | Lys | Asp | Leu | Ser | Trp | Ile | Val | Ala | Leu | Thr | Ile | Phe | Ser |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Ser | Leu | Ile | Leu | Val | Ala | Phe | Lys | Ile | Phe | Leu | Leu | Lys | Asp | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Asn | Lys | Arg | Phe | Lys | Asn | Asn | Lys | Arg | Asp | Lys | Lys |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 47...379
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AGCGCTCAAA TCATTTATTG GTTATCAAAA TATTTTAGGA GTGAGT ATG GAA AAT    | 55  |
| Met Glu Asn                                                       |     |
| 1                                                                 |     |
| <br>                                                              |     |
| GAT GTT AAA GAA GAT CTA GAG CAA GCA AGA CCA AAG TTA GAG CCA GAA   | 103 |
| Asp Val Lys Glu Asp Leu Glu Gln Ala Arg Pro Lys Leu Glu Pro Glu   |     |
| 5 10 15                                                           |     |
| <br>                                                              |     |
| AAG CAA AAG CAA GAG CCA GAG GAA CAG AAA CAA GAA AAA CAA GAC AAA   | 151 |
| Lys Gln Lys Gln Glu Pro Glu Glu Gln Lys Gln Glu Lys Gln Asp Lys   |     |
| 20 25 30 35                                                       |     |
| <br>                                                              |     |
| CAA GAG CAG AAG CCA AAG CAA GAA AAA GAA GAG TCA AAG AGC AAG GAA   | 199 |
| Gln Glu Gln Lys Pro Lys Gln Glu Lys Glu Glu Ser Lys Ser Lys Glu   |     |
| 40 45 50                                                          |     |
| <br>                                                              |     |
| CAA GAA GAA AAC AAA AAA CAA AAG AGA TCT AGC TAT ATT TTT TGG GGA   | 247 |
| Gln Glu Glu Asn Lys Lys Gln Lys Arg Ser Ser Tyr Ile Phe Trp Gly   |     |
| 55 60 65                                                          |     |
| <br>                                                              |     |
| TGT ATT ATT GGT TTG TGT ATA GTT GTT ATT ATT GCC AAA ATT ATT GCG   | 295 |
| Cys Ile Ile Gly Leu Cys Ile Val Val Ile Ile Ala Lys Ile Ile Ala   |     |
| 70 75 80                                                          |     |
| <br>                                                              |     |
| TTT GGC GGA TCT AGT GAG GAG GCA AAA GCA GAC AAA CCA AAA AAC TCT   | 343 |
| Phe Gly Gly Ser Ser Glu Glu Ala Lys Ala Asp Lys Pro Lys Asn Ser   |     |
| 85 90 95                                                          |     |
| <br>                                                              |     |
| TTA AGT ATG CTG AAA AAC TTT TAC CTA CCG ATA TTA TAAAAGATAA TCTTAA | 395 |
| Leu Ser Met Leu Lys Asn Phe Tyr Leu Pro Ile Leu                   |     |
| 100 105 110                                                       |     |
| <br>                                                              |     |
| TAAC                                                              | 399 |

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Glu Asn Asp Val Lys Glu Asp Leu Glu Gln Ala Arg Pro Lys Leu |  |
| 1 5 10 15                                                       |  |
| Glu Pro Glu Lys Gln Lys Gln Glu Pro Glu Glu Gln Lys Gln Glu Lys |  |





|                |                |                |                |                |                |                |                |                |                |                |                |                |                |                |                |      |
|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|------|
| ACG Thr        | GTG Val        | GAT Asp        | AAC Asn<br>110 | GGG Gly        | ATT Ile        | AAC Asn        | GCC Ala        | TTT Phe<br>115 | GAA Glu        | GCC Ala        | GCG Ala        | CGA Arg        | TTT Phe<br>120 | TGT Cys        | AAA Lys        | 386  |
| GAA Glu        | AAA Lys        | AAT Asn<br>125 | TAC Tyr        | ACC Thr        | CTT Leu        | ATC Ile        | ATC Ile<br>130 | ACA Thr        | GAT Asp        | CAC His        | CAT His        | TGC Cys<br>135 | TTA Leu        | CAC His        | CAT His        | 434  |
| GAT Asp        | GAA Glu        | GTC Val        | CCA Pro        | GAC Asp        | GCT Ala        | TAT Tyr<br>145 | GCG Ala        | GTG Val        | ATC Ile        | AAC Asn        | CCC Pro<br>150 | AAG Lys        | CAA Gln        | CCG Pro        | GAT Asp        | 482  |
| TGT Cys<br>155 | GAT Asp        | TTT Phe        | ATC Ile        | CAA Gln        | AAG Lys<br>160 | GAA Glu        | GTG Val        | TGC Cys        | GGG Gly<br>165 | GCG Ala        | TTG Leu        | GTA Val        | GCG Ala        | TTT Phe        | TAT Tyr<br>170 | 530  |
| TTG Leu        | TGC Cys        | TAT Tyr        | GGG Gly        | ATC Ile<br>175 | CAT His        | CAG Gln        | CTT Leu        | TTA Leu        | GGA Gly<br>180 | AAA Lys        | GAA Glu        | AAA Lys        | AGC Ser        | CAT His<br>185 | TCT Ser        | 578  |
| AGT Ser        | GAG Glu        | TTA Leu        | TTA Leu<br>190 | TGT Cys        | TTA Leu        | GCG Ala        | GGC Gly        | GTG Val<br>195 | GCG Ala        | ACT Thr        | ATT Ile        | GCT Ala        | GAC Asp<br>200 | ATG Met        | ATG Met        | 626  |
| CCT Pro        | TTG Leu        | ACT Thr<br>205 | TTT Phe        | TTT Phe        | AAC Asn        | CGC Arg        | TTT Phe<br>210 | TTA Leu        | GTT Val        | TCT Ser        | AAA Lys        | GCC Ala<br>215 | TTG Leu        | TAT Tyr        | TTT Phe        | 674  |
| TTG Leu        | CAA Gln<br>220 | AAA Lys        | GAA Glu        | TCC Ser        | TTA Leu        | GGG Gly<br>225 | GCG Ala        | ATG Met        | GGT Gly        | TTT Phe        | TTG Leu<br>230 | CGC Arg        | CAA Gln        | AGA Arg        | GAA Glu        | 722  |
| GTT Val<br>235 | TTT Phe        | AGA Arg        | AAA Lys        | CGC Arg        | TCT Ser<br>240 | TTA Leu        | AAA Lys        | GCG Ala        | AGT Ser        | GAT Asp<br>245 | ATT Ile        | TCT Ser        | TTT Phe        | AAT Asn        | ATC Ile<br>250 | 770  |
| GCC Ala        | CCC Pro        | TTA Leu        | ATC Ile        | AAC Asn<br>255 | TCC Ser        | GCA Ala        | GGG Gly        | CGC Arg        | ATG Met<br>260 | CAA Gln        | GAT Asp        | GCG Ala        | AAA Lys        | ATG Met<br>265 | GCT Ala        | 818  |
| TTA Leu        | GAT Asp        | TTT Phe        | TTA Leu<br>270 | AGC Ser        | GCG Ala        | AAT Asn        | AAT Asn        | TCT Ser<br>275 | CAA Gln        | GAT Asp        | GGC Gly        | TAT Tyr        | TCT Ser<br>280 | TTG Leu        | TAT Tyr        | 866  |
| GAA Glu        | CGC Arg        | TTG Leu<br>285 | AAA Lys        | GCA Ala        | TGC Cys        | AAT Asn        | TTG Leu<br>290 | AAG Lys        | CGT Arg        | AAA Lys        | ATG Met        | ATC Ile<br>295 | CAA Gln        | CAG Gln        | CAG Gln        | 914  |
| GTT Val        | TTT Phe<br>300 | GAA Glu        | GAA Glu        | GCT Ala        | TTT Phe        | AAG Lys<br>305 | CAT His        | GCG Ala        | ATG Met        | GTT Val        | GGA Gly<br>310 | GAA Glu        | AAA Lys        | ATT Ile        | ATC Ile        | 962  |
| GTC Val<br>315 | GCT Ala        | TTT Phe        | AAG Lys        | GAC Asp        | AAT Asn<br>320 | TGG Trp        | CAT His        | GAG Glu        | GGA Gly        | GTG Val<br>325 | CTG Leu        | GGG Gly        | ATT Ile        | GTG Val        | GCT Ala<br>330 | 1010 |
| TCA Ser        | AAA Lys        | TTA Leu        | GTG Val        | GAA Glu        | GCC Ala        | ACT Thr        | CAA Gln        | AAG Lys        | CCA Pro        | AGC Ser        | CTG Leu        | GTT Val        | TTT Phe        | ACC Thr        | TTT Phe        | 1058 |

|                                         |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |      |
|-----------------------------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|------|
| 335                                     |            |            |            |            | 340        |            |            |            |            | 345        |            |            |            |            |            |      |      |
| AAA<br>Lys                              | GAA<br>Glu | GGG<br>Gly | GTG<br>Val | TAT<br>Tyr | AAA<br>Lys | GGG<br>Gly | AGC<br>Ser | GCT<br>Ala | CGT<br>Arg | AGC<br>Ser | TCT<br>Ser | TCA<br>Ser | AAC<br>Asn | ATT<br>Ile | GAC<br>Asp | 1106 |      |
| 350                                     |            |            |            |            | 355        |            |            |            |            | 360        |            |            |            |            |            |      |      |
| TTG<br>Leu                              | ATT<br>Ile | GAC<br>Asp | GCT<br>Ala | TTG<br>Leu | AAT<br>Asn | GGG<br>Gly | GTT<br>Val | TCT<br>Ser | TCT<br>Ser | TTA<br>Leu | TTG<br>Leu | CTC<br>Leu | GGC<br>Gly | TAT<br>Tyr | GGA<br>Gly | 1154 |      |
| 365                                     |            |            |            |            | 370        |            |            |            |            | 375        |            |            |            |            |            |      |      |
| GGG<br>Gly                              | CAT<br>His | AGG<br>Arg | CAA<br>Gln | GCT<br>Ala | TGC<br>Cys | GGG<br>Gly | TTG<br>Leu | AGC<br>Ser | GTT<br>Val | GAA<br>Glu | AAA<br>Lys | AAC<br>Asn | AAT<br>Asn | ATC<br>Ile | ATC<br>Ile | 1202 |      |
| 380                                     |            |            |            |            | 385        |            |            |            |            | 390        |            |            |            |            |            |      |      |
| TCG<br>Ser                              | CTC<br>Leu | TTT<br>Phe | GAA<br>Glu | ACT<br>Thr | TTA<br>Leu | GAA<br>Glu | AAT<br>Asn | TTT<br>Phe | GAT<br>Asp | TTT<br>Phe | AAA<br>Lys | GTT<br>Val | TTA<br>Leu | CCT<br>Pro | TTT<br>Phe | 1250 |      |
| 395                                     |            |            |            |            | 400        |            |            |            |            | 405        |            |            |            |            | 410        |      |      |
| TGT<br>Cys                              | AAA<br>Lys | ACA<br>Thr | GAG<br>Glu | CCC<br>Pro | CCT<br>Pro | TTA<br>Leu | ACG<br>Thr | CTC<br>Leu | AAA<br>Lys | TTA<br>Leu | AAA<br>Lys | GAC<br>Asp | ATT<br>Ile | GAC<br>Asp | AGA<br>Arg | 1298 |      |
| 415                                     |            |            |            |            | 420        |            |            |            |            | 425        |            |            |            |            |            |      |      |
| GAG<br>Glu                              | CTT<br>Leu | TTA<br>Leu | GAG<br>Glu | ATT<br>Ile | ATA<br>Ile | GAA<br>Glu | ATG<br>Met | GGC<br>Gly | GAA<br>Glu | CCT<br>Pro | TAT<br>Tyr | GGG<br>Gly | CAA<br>Gln | GAA<br>Glu | AAC<br>Asn | 1346 |      |
| 430                                     |            |            |            |            | 435        |            |            |            |            | 440        |            |            |            |            |            |      |      |
| CCT<br>Pro                              | GAA<br>Glu | CCC<br>Pro | CTA<br>Leu | TTC<br>Phe | CAA<br>Gln | GCA<br>Ala | AAA<br>Lys | AAT<br>Asn | TTA<br>Leu | GAA<br>Glu | GTC<br>Val | ATA<br>Ile | GAA<br>Glu | GAA<br>Glu | AAA<br>Lys | 1394 |      |
| 445                                     |            |            |            |            | 450        |            |            |            |            | 455        |            |            |            |            |            |      |      |
| ATC<br>Ile                              | ATT<br>Ile | AAA<br>Lys | GAA<br>Glu | AGC<br>Ser | CAC<br>His | CAG<br>Gln | GTT<br>Val | TTG<br>Leu | CGT<br>Arg | TTT<br>Phe | AAG<br>Lys | GAT<br>Asp | AAA<br>Lys | GAA<br>Glu | TGC<br>Cys | 1442 |      |
| 460                                     |            |            |            |            | 465        |            |            |            |            | 470        |            |            |            |            |            |      |      |
| GTC<br>Val                              | AAA<br>Lys | GAG<br>Glu | GCT<br>Ala | ATT<br>Ile | TAT<br>Tyr | TTT<br>Phe | AGC<br>Ser | GCT<br>Ala | GAG<br>Glu | CGG<br>Arg | TTT<br>Phe | TTG<br>Leu | AAA<br>Lys | GCG<br>Ala | GGC<br>Gly | 1490 |      |
| 475                                     |            |            |            |            | 480        |            |            |            |            | 485        |            |            |            |            | 490        |      |      |
| GAA<br>Glu                              | AAG<br>Lys | GTG<br>Val | AGC<br>Ser | GTG<br>Val | CTT<br>Leu | TTT<br>Phe | AGC<br>Ser | GTG<br>Val | GAA<br>Glu | TTA<br>Leu | GAT<br>Asp | GAG<br>Glu | TGT<br>Cys | TCT<br>Ser | AAT<br>Asn | 1538 |      |
| 495                                     |            |            |            |            | 500        |            |            |            |            | 505        |            |            |            |            |            |      |      |
| GAG<br>Glu                              | CCT<br>Pro | AAA<br>Lys | ATG<br>Met | TTT<br>Phe | GTT<br>Val | AAA<br>Lys | AGT<br>Ser | TTG<br>Leu | TTG<br>Leu | TAGTGCCTTT |            |            |            |            | TGTTGAAGAA | GAA  | 1591 |
| 510                                     |            |            |            |            | 515        |            |            |            |            |            |            |            |            |            |            |      |      |
| TTTGAAATTT TAAAACCCAC CAAAGCCTTG TTTTTT |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            | 1627 |      |

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:

- ```
(A) LENGTH: 516 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
```

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

Met	Lys	Gln	Lys	Leu	Lys	Ala	Gln	Ile	Lys	Glu	Arg	Met	Ala	Ser	Ile	1	5	10	15
Ala	Tyr	Asn	Glu	Lys	Gly	Phe	Pro	Ser	Pro	Phe	Leu	Phe	Lys	Asp	Leu	20	25	30	
Lys	Lys	Ala	Ala	Leu	Lys	Ile	Ile	Glu	Ala	Met	Arg	Thr	Asn	Thr	Glu	35	40	45	
Ile	Leu	Val	Val	Gly	Asp	Tyr	Asp	Ala	Asp	Gly	Val	Ile	Ser	Ser	Ala	50	55	60	
Ile	Met	Ala	Lys	Phe	Phe	Glu	Ser	Leu	Asn	Tyr	Lys	His	Val	Arg	Ile	65	70	75	80
Ala	Ile	Pro	Asn	Arg	Phe	Met	Asp	Gly	Tyr	Gly	Ile	Ser	Lys	Lys	Phe	85	90	95	
Leu	Glu	Lys	His	His	Ala	Pro	Leu	Ile	Ile	Thr	Val	Asp	Asn	Gly	Ile	100	105	110	
Asn	Ala	Phe	Glu	Ala	Ala	Arg	Phe	Cys	Lys	Glu	Lys	Asn	Tyr	Thr	Leu	115	120	125	
Ile	Ile	Thr	Asp	His	His	Cys	Leu	His	His	Asp	Glu	Val	Pro	Asp	Ala	130	135	140	
Tyr	Ala	Val	Ile	Asn	Pro	Lys	Gln	Pro	Asp	Cys	Asp	Phe	Ile	Gln	Lys	145	150	155	160
Glu	Val	Cys	Gly	Ala	Leu	Val	Ala	Phe	Tyr	Leu	Cys	Tyr	Gly	Ile	His	165	170	175	
Gln	Leu	Leu	Gly	Lys	Glu	Lys	Ser	His	Ser	Ser	Glu	Leu	Leu	Cys	Leu	180	185	190	
Ala	Gly	Val	Ala	Thr	Ile	Ala	Asp	Met	Met	Pro	Leu	Thr	Phe	Phe	Asn	195	200	205	
Arg	Phe	Leu	Val	Ser	Lys	Ala	Leu	Tyr	Phe	Leu	Gln	Lys	Glu	Ser	Leu	210	215	220	
Gly	Ala	Met	Gly	Phe	Leu	Arg	Gln	Arg	Glu	Val	Phe	Arg	Lys	Arg	Ser	225	230	235	240
Leu	Lys	Ala	Ser	Asp	Ile	Ser	Phe	Asn	Ile	Ala	Pro	Leu	Ile	Asn	Ser	245	250	255	
Ala	Gly	Arg	Met	Gln	Asp	Ala	Lys	Met	Ala	Leu	Asp	Phe	Leu	Ser	Ala	260	265	270	
Asn	Asn	Ser	Gln	Asp	Gly	Tyr	Ser	Leu	Tyr	Glu	Arg	Leu	Lys	Ala	Cys	275	280	285	
Asn	Leu	Lys	Arg	Lys	Met	Ile	Gln	Gln	Gln	Val	Phe	Glu	Glu	Ala	Phe	290	295	300	
Lys	His	Ala	Met	Val	Gly	Glu	Lys	Ile	Ile	Val	Ala	Phe	Lys	Asp	Asn	305	310	315	320
Trp	His	Glu	Gly	Val	Leu	Gly	Ile	Val	Ala	Ser	Lys	Leu	Val	Glu	Ala	325	330	335	
Thr	Gln	Lys	Pro	Ser	Leu	Val	Phe	Thr	Phe	Lys	Glu	Gly	Val	Tyr	Lys	340	345	350	
Gly	Ser	Ala	Arg	Ser	Ser	Ser	Asn	Ile	Asp	Leu	Ile	Asp	Ala	Leu	Asn	355	360	365	
Gly	Val	Ser	Ser	Leu	Leu	Leu	Gly	Tyr	Gly	Gly	His	Arg	Gln	Ala	Cys	370	375	380	
Gly	Leu	Ser	Val	Glu	Lys	Asn	Asn	Ile	Ile	Ser	Leu	Phe	Glu	Thr	Leu	385	390	395	400
Glu	Asn	Phe	Asp	Phe	Lys	Val	Leu	Pro	Phe	Cys	Lys	Thr	Glu	Pro	Pro	405	410	415	
Leu	Thr	Leu	Lys	Leu	Lys	Asp	Ile	Asp	Arg	Glu	Leu	Leu	Glu	Ile	Ile	420	425	430	
Glu	Met	Gly	Glu	Pro	Tyr	Gly	Gln	Glu	Asn	Pro	Glu	Pro	Leu	Phe	Gln	435	440	445	

Ala	Lys	Asn	Leu	Glu	Val	Ile	Glu	Glu	Lys	Ile	Ile	Lys	Glu	Ser	His
450						455					460				
Gln	Val	Leu	Arg	Phe	Lys	Asp	Lys	Glu	Cys	Val	Lys	Glu	Ala	Ile	Tyr
465					470				475						480
Phe	Ser	Ala	Glu	Arg	Phe	Leu	Lys	Ala	Gly	Glu	Lys	Val	Ser	Val	Leu
				485					490						495
Phe	Ser	Val	Glu	Leu	Asp	Glu	Cys	Ser	Asn	Glu	Pro	Lys	Met	Phe	Val
			500					505					510		
Lys	Ser	Leu	Leu												
			515												

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 961 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...908
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

ATCGTAATGA	AATAATCACC	ACCCCTATAA	GCTTTGTAGC	GACGGCTAAC	ATG CTT	56
					Met Leu	
					1	
TTA GAA AGC GGT TAT ACA CCC GTA TTT GCT GGA ATT AAA AAC GAT GGC	104					
Leu Glu Ser Gly Tyr Thr Pro Val Phe Ala Gly Ile Lys Asn Asp Gly						
5 10 15						
AAT ATA GAT GAA TTA GCC CTA GAA AAG CTC ATT AAC GAA AGA ACC AAA	152					
Asn Ile Asp Glu Leu Ala Leu Glu Lys Leu Ile Asn Glu Arg Thr Lys						
20 25 30						
GCC ATA GTG AGC GTG GAT TAT GCC GGT AAA AGC GTG GAA GTA GAA AGC	200					
Ala Ile Val Ser Val Asp Tyr Ala Gly Lys Ser Val Glu Val Glu Ser						
35 40 45 50						
GTT CAA AAG CTT TGC AAA AAG CAT TCT TTG AGC TTT CTT TCT GAC AGC	248					
Val Gln Lys Leu Cys Lys Lys His Ser Leu Ser Phe Leu Ser Asp Ser						
55 60 65						
TCG CAT GCT CTA GGA AGC GAG TAT CAA AAC AAA AAA GTA GGA GGC TTT	296					
Ser His Ala Leu Gly Ser Glu Tyr Gln Asn Lys Lys Val Gly Gly Phe						
70 75 80						
GCG TTA GCG AGC GTG TTT AGT TTC CAT GCC ATT AAG CCC ATC ACT ACG	344					
Ala Leu Ala Ser Val Phe Ser Phe His Ala Ile Lys Pro Ile Thr Thr						
85 90 95						
GCT GAA GGG GGA GCG GTC GTT ACT AAC GAT AGC GAA TTG CAT GAA AAA	392					

Ala	Glu	Gly	Gly	Ala	Val	Val	Thr	Asn	Asp	Ser	Glu	Leu	His	Glu	Lys		
100						105					110						
ATG	AAA	TTG	TTT	CGC	TCT	CAT	GGC	ATG	CTC	AAA	AAA	GAT	TTT	TTT	GAA	440	
Met	Lys	Leu	Phe	Arg	Ser	His	Gly	Met	Leu	Lys	Lys	Asp	Phe	Phe	Glu		
115					120					125					130		
GGC	GAA	GTC	AAA	AGC	ATA	GGG	CAT	AAC	TTC	CGC	TTG	AAT	GAA	ATC	CAA	488	
Gly	Glu	Val	Lys	Ser	Ile	Gly	His	Asn	Phe	Arg	Leu	Asn	Glu	Ile	Gln		
				135					140					145			
AGC	GCT	TTG	GGT	TTG	AGC	CAG	CTT	AAA	AAA	GCC	CCC	TTT	TTA	ATG	CAA	536	
Ser	Ala	Leu	Gly	Leu	Ser	Gln	Leu	Lys	Lys	Ala	Pro	Phe	Leu	Met	Gln		
			150					155					160				
AAA	AGA	GAA	GAA	GCC	GCT	CTA	ACC	TAT	GAC	AGG	ATT	TTT	AAA	GAT	AAC	584	
Lys	Arg	Glu	Glu	Ala	Ala	Leu	Thr	Tyr	Asp	Arg	Ile	Phe	Lys	Asp	Asn		
		165					170					175					
CCT	TAT	TTC	ACC	CCT	TTA	CAC	CCC	TTG	TTA	AAA	GAT	AAA	AGC	TCT	AAC	632	
Pro	Tyr	Phe	Thr	Pro	Leu	His	Pro	Leu	Leu	Lys	Asp	Lys	Ser	Ser	Asn		
						185					190						
CAC	CTT	TAT	CCT	ATT	TTA	ATG	CAC	CAA	AAA	TTT	TTT	ACA	TGC	AAA	AAA	680	
His	Leu	Tyr	Pro	Ile	Leu	Met	His	Gln	Lys	Phe	Phe	Thr	Cys	Lys	Lys		
195					200					205					210		
CTC	ATT	TTA	GAA	AGT	TTG	CAC	AAG	CGT	GGC	ATT	TTA	GCC	CAA	GTG	CAT	728	
Leu	Ile	Leu	Glu	Ser	Leu	His	Lys	Arg	Gly	Ile	Leu	Ala	Gln	Val	His		
				215					220					225			
TAC	AAG	CCC	ATT	TAT	CAA	TAC	CAA	TTG	TAC	CAA	CAG	CTC	TTC	AAT	ACA	776	
Tyr	Lys	Pro	Ile	Tyr	Gln	Tyr	Gln	Leu	Tyr	Gln	Gln	Leu	Phe	Asn	Thr		
			230					235					240				
GCC	CCA	TTA	AAA	AGC	GCA	GAG	GAT	TTC	TAT	CAC	GCT	GAA	ATT	TCC	TTG	824	
Ala	Pro	Leu	Lys	Ser	Ala	Glu	Asp	Phe	Tyr	His	Ala	Glu	Ile	Ser	Leu		
		245					250					255					
CCT	TGT	CAT	GCG	AAT	TTA	AAT	TTA	GAG	AGC	GTT	CAA	AAC	ATC	GCT	CAT	872	
Pro	Cys	His	Ala	Asn	Leu	Asn	Leu	Glu	Ser	Val	Gln	Asn	Ile	Ala	His		
		260				265					270						
AGC	GTT	TTA	AAA	ACT	TTT	GAG	AGT	TTT	AAA	ATA	GAA	TGAGTTTCAT	TTAGGG			924	
Ser	Val	Leu	Lys	Thr	Phe	Glu	Ser	Phe	Lys	Ile	Glu						
275					280					285							
CTTCAAATCT	TAATCATTA	GAATGGTGCG	GAAGAAA													961	

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

Met	Leu	Leu	Glu	Ser	Gly	Tyr	Thr	Pro	Val	Phe	Ala	Gly	Ile	Lys	Asn	1	5	10	15
Asp	Gly	Asn	Ile	Asp	Glu	Leu	Ala	Leu	Glu	Lys	Leu	Ile	Asn	Glu	Arg	20	25	30	
Thr	Lys	Ala	Ile	Val	Ser	Val	Asp	Tyr	Ala	Gly	Lys	Ser	Val	Glu	Val	35	40	45	
Glu	Ser	Val	Gln	Lys	Leu	Cys	Lys	Lys	His	Ser	Leu	Ser	Phe	Leu	Ser	50	55	60	
Asp	Ser	Ser	His	Ala	Leu	Gly	Ser	Glu	Tyr	Gln	Asn	Lys	Lys	Val	Gly	65	70	75	80
Gly	Phe	Ala	Leu	Ala	Ser	Val	Phe	Ser	Phe	His	Ala	Ile	Lys	Pro	Ile	85	90	95	
Thr	Thr	Ala	Glu	Gly	Gly	Ala	Val	Val	Thr	Asn	Asp	Ser	Glu	Leu	His	100	105	110	
Glu	Lys	Met	Lys	Leu	Phe	Arg	Ser	His	Gly	Met	Leu	Lys	Lys	Asp	Phe	115	120	125	
Phe	Glu	Gly	Glu	Val	Lys	Ser	Ile	Gly	His	Asn	Phe	Arg	Leu	Asn	Glu	130	135	140	
Ile	Gln	Ser	Ala	Leu	Gly	Leu	Ser	Gln	Leu	Lys	Lys	Ala	Pro	Phe	Leu	145	150	155	160
Met	Gln	Lys	Arg	Glu	Glu	Ala	Ala	Leu	Thr	Tyr	Asp	Arg	Ile	Phe	Lys	165	170	175	
Asp	Asn	Pro	Tyr	Phe	Thr	Pro	Leu	His	Pro	Leu	Leu	Lys	Asp	Lys	Ser	180	185	190	
Ser	Asn	His	Leu	Tyr	Pro	Ile	Leu	Met	His	Gln	Lys	Phe	Phe	Thr	Cys	195	200	205	
Lys	Lys	Leu	Ile	Leu	Glu	Ser	Leu	His	Lys	Arg	Gly	Ile	Leu	Ala	Gln	210	215	220	
Val	His	Tyr	Lys	Pro	Ile	Tyr	Gln	Tyr	Gln	Leu	Tyr	Gln	Gln	Leu	Phe	225	230	235	240
Asn	Thr	Ala	Pro	Leu	Lys	Ser	Ala	Glu	Asp	Phe	Tyr	His	Ala	Glu	Ile	245	250	255	
Ser	Leu	Pro	Cys	His	Ala	Asn	Leu	Asn	Leu	Glu	Ser	Val	Gln	Asn	Ile	260	265	270	
Ala	His	Ser	Val	Leu	Lys	Thr	Phe	Glu	Ser	Phe	Lys	Ile	Glu			275	280	285	

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 728 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 15...692
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

TAATGGGCCT	TTGA	ATG	CGT	TTT	GTC	TAT	CAC	CCT	TTA	GCC	AAA	GAG	CCT			50
		Met	Arg	Phe	Val	Tyr	His	Pro	Leu	Ala	Lys	Glu	Pro			
		1				5					10					
GTT	TTA	AAA	ATA	GAA	GGC	GAG	AGT	TAT	ACG	CAT	TTA	TAC	CGA	TCA	AGG	98
Val	Leu	Lys	Ile	Glu	Gly	Glu	Ser	Tyr	Thr	His	Leu	Tyr	Arg	Ser	Arg	
		15				20						25				
CGT	GTC	AAA	AGT	GCG	AGT	CGT	TTG	GAT	TTG	AGA	AAT	TTA	AAA	GAC	GGC	146
Arg	Val	Lys	Ser	Ala	Ser	Arg	Leu	Asp	Leu	Arg	Asn	Leu	Lys	Asp	Gly	
	30					35					40					
TTT	TTA	TAC	ACC	TAT	GAG	CAT	GCA	GAA	ATC	ACT	AAA	AAA	CAC	GCC	CTT	194
Phe	Leu	Tyr	Thr	Tyr	Glu	His	Ala	Glu	Ile	Thr	Lys	Lys	His	Ala	Leu	
45				50					55						60	
TTA	AAG	CTA	GTG	GGC	GCG	CGA	TTA	TTA	GAG	GTT	ATG	GCC	AGT	AAA	AAA	242
Leu	Lys	Leu	Val	Gly	Ala	Arg	Leu	Leu	Glu	Val	Met	Ala	Ser	Lys	Lys	
			65						70				75			
ACG	CAT	TTG	ATT	TTA	AGC	GTG	ATT	GAA	ATC	AAA	AAC	ATT	GAA	AAA	ATC	290
Thr	His	Leu	Ile	Leu	Ser	Val	Ile	Glu	Ile	Lys	Asn	Ile	Glu	Lys	Ile	
			80					85					90			
CTA	CCC	TTT	TTA	AAT	CAG	TTA	GGC	GTG	AGC	AAG	TTG	AGT	TTA	TTC	TAT	338
Leu	Pro	Phe	Leu	Asn	Gln	Leu	Gly	Val	Ser	Lys	Leu	Ser	Leu	Phe	Tyr	
		95					100					105				
GCG	GAT	TTT	AGC	CAA	CGC	AAT	GAA	AAA	ATA	GAC	ATC	GCT	AAA	TTA	GAG	386
Ala	Asp	Phe	Ser	Gln	Arg	Asn	Glu	Lys	Ile	Asp	Ile	Ala	Lys	Leu	Glu	
	110					115					120					
CGC	TTT	CAA	AAG	ATT	TTG	ATC	CAT	TCT	TGC	GAG	CAG	TGT	GGT	AGG	AGT	434
Arg	Phe	Gln	Lys	Ile	Leu	Ile	His	Ser	Cys	Glu	Gln	Cys	Gly	Arg	Ser	
125				130					135						140	
GCT	TTA	ATG	GAA	TTG	GAA	GTG	TTT	TCA	AAC	ACT	AAA	GAG	GCG	CTA	AAA	482
Ala	Leu	Met	Glu	Leu	Glu	Val	Phe	Ser	Asn	Thr	Lys	Glu	Ala	Leu	Lys	
			145					150						155		
GCC	TAT	CCT	AAG	GCG	AGC	GTT	TTG	GAT	TTT	AAG	GGC	GAA	ACC	TTA	NCC	530
Ala	Tyr	Pro	Lys	Ala	Ser	Val	Leu	Asp	Phe	Lys	Gly	Glu	Thr	Leu	Xaa	
			160				165						170			
GCA	AGC	GCG	GAT	TTT	GAA	AAG	GGC	GTT	ATC	ATA	GGG	CCT	GAG	GGG	GGC	578
Ala	Ser	Ala	Asp	Phe	Glu	Lys	Gly	Val	Ile	Ile	Gly	Pro	Glu	Gly	Gly	
		175					180					185				
TTT	AGC	GAA	CCA	GAA	AGA	GGG	TAT	TTT	AAA	GAG	CGT	GAA	ATT	TAT	CGC	626
Phe	Ser	Glu	Pro	Glu	Arg	Gly	Tyr	Phe	Lys	Glu	Arg	Glu	Ile	Tyr	Arg	
	190					195					200					
ATC	CCG	TTA	GAT	ATG	GTG	CTA	AAG	TCT	GAG	AGT	GCA	TGC	GTG	TTT	GTA	674
Ile	Pro	Leu	Asp	Met	Val	Leu	Lys	Ser	Glu	Ser	Ala	Cys	Val	Phe	Val	
205				210					215						220	
GCG	AGT	ATC	GCA	CAA	GTT	TAGGGGGTTA TTGGGGATTT TAAATCCTAA AAAATC										728
Ala	Ser	Ile	Ala	Gln	Val											

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

```

Met Arg Phe Val Tyr His Pro Leu Ala Lys Glu Pro Val Leu Lys Ile
 1           5           10           15
Glu Gly Glu Ser Tyr Thr His Leu Tyr Arg Ser Arg Arg Val Lys Ser
          20           25           30
Ala Ser Arg Leu Asp Leu Arg Asn Leu Lys Asp Gly Phe Leu Tyr Thr
      35           40           45
Tyr Glu His Ala Glu Ile Thr Lys Lys His Ala Leu Lys Leu Val
 50           55           60
Gly Ala Arg Leu Leu Glu Val Met Ala Ser Lys Lys Thr His Leu Ile
65           70           75           80
Leu Ser Val Ile Glu Ile Lys Asn Ile Glu Lys Ile Leu Pro Phe Leu
          85           90           95
Asn Gln Leu Gly Val Ser Lys Leu Ser Leu Phe Tyr Ala Asp Phe Ser
      100           105           110
Gln Arg Asn Glu Lys Ile Asp Ile Ala Lys Leu Glu Arg Phe Gln Lys
      115           120           125
Ile Leu Ile His Ser Cys Glu Gln Cys Gly Arg Ser Ala Leu Met Glu
      130           135           140
Leu Glu Val Phe Ser Asn Thr Lys Glu Ala Leu Lys Ala Tyr Pro Lys
      145           150           155           160
Ala Ser Val Leu Asp Phe Lys Gly Glu Thr Leu Xaa Ala Ser Ala Asp
          165           170           175
Phe Glu Lys Gly Val Ile Ile Gly Pro Glu Gly Gly Phe Ser Glu Pro
      180           185           190
Glu Arg Gly Tyr Phe Lys Glu Arg Glu Ile Tyr Arg Ile Pro Leu Asp
      195           200           205
Met Val Leu Lys Ser Glu Ser Ala Cys Val Phe Val Ala Ser Ile Ala
      210           215           220
Gln Val
225

```

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence

CTT TTT GGG GGG GTT AAA GGC GAT GAG ATC TTA AAA GAA ATC GTT TTT	675
Leu Phe Gly Gly Val Lys Gly Asp Glu Ile Leu Lys Glu Ile Val Phe	
210 215 220	
TTA GCC GCT AAA TTA AAA ATC CCT TTT TTG GTT TGT GAA ATG GGG TAT	723
Leu Ala Ala Lys Leu Lys Ile Pro Phe Leu Val Cys Glu Met Gly Tyr	
225 230 235	
GAC CAG TTG AAA AGC TTG AAA GAA TGC TTG GAA TTT TGC GGT TAT GAT	771
Asp Gln Leu Lys Ser Leu Lys Glu Cys Leu Glu Phe Cys Gly Tyr Asp	
240 245 250	
GCA GAG TTT TAC AAG GAT TTG AGC GGC TTT GAT AGA GGG TTT GTG GGC	819
Ala Glu Phe Tyr Lys Asp Leu Ser Gly Phe Asp Arg Gly Phe Val Gly	
255 260 265	
GTT TTA AAA AGT TTT TTA AGA TAAATTAAAA CTTAATTACC CTTTTAGTGT TACA	874
Val Leu Lys Ser Phe Leu Arg	
270 275	
ATAAAAAACAC TTAA	888

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

Met Thr Leu Ser Gln Ala Leu Asn Lys Ala Lys Lys Gly Leu Ser Gln	
1 5 10 15	
Lys Gly Phe Arg Gly Gly Leu Glu Ser Glu Ile Leu Leu Gly Phe Val	
20 25 30	
Leu Gln Lys Glu Arg Val Phe Leu His Thr His Ala Tyr Leu Glu Leu	
35 40 45	
Asn His Glu Glu Glu Val Arg Phe Phe Glu Leu Val Glu Lys Arg Leu	
50 55 60	
Asn Asn Cys Pro Ile Glu Tyr Leu Leu Glu Ser Cys Asp Phe Tyr Gly	
65 70 75 80	
Arg Ser Phe Phe Val Asn Glu His Val Leu Ile Pro Arg Pro Glu Thr	
85 90 95	
Glu Ile Leu Val Gln Lys Ala Leu Asp Ile Ile Ser Gln Tyr His Leu	
100 105 110	
Lys Glu Ile Gly Glu Ile Gly Ile Gly Ser Gly Cys Val Ser Val Ser	
115 120 125	
Leu Ala Leu Glu Asn Pro Asn Leu Ser Ile Tyr Ala Ser Asp Ile Ser	
130 135 140	
Pro Asn Ala Leu Glu Val Ala Ser Lys Asn Ile Glu His Phe Cys Leu	
145 150 155 160	
Lys Glu Arg Val Phe Leu Lys Gln Thr Arg Leu Trp Asp His Met Pro	
165 170 175	
Met Ile Glu Met Leu Val Ser Asn Pro Pro Tyr Ile Ala Arg Asn Tyr	
180 185 190	

Pro	Leu	Glu	Lys	Ser	Val	Leu	Lys	Glu	Pro	His	Glu	Ala	Leu	Phe	Gly
	195						200					205			
Gly	Val	Lys	Gly	Asp	Glu	Ile	Leu	Lys	Glu	Ile	Val	Phe	Leu	Ala	Ala
	210					215					220				
Lys	Leu	Lys	Ile	Pro	Phe	Leu	Val	Cys	Glu	Met	Gly	Tyr	Asp	Gln	Leu
	225				230					235					240
Lys	Ser	Leu	Lys	Glu	Cys	Leu	Glu	Phe	Cys	Gly	Tyr	Asp	Ala	Glu	Phe
			245						250					255	
Tyr	Lys	Asp	Leu	Ser	Gly	Phe	Asp	Arg	Gly	Phe	Val	Gly	Val	Leu	Lys
			260					265					270		
Ser	Phe	Leu	Arg												
			275												

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 28...960
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

CCATCTCAAA ATAAGGACGC CTAAATC ATG GCA GAA AAA ACA GCT AAC GAT TTA	54
Met Ala Glu Lys Thr Ala Asn Asp Leu	
1 5	
AAA CTA AGT GAG ATA GAA CTC GTG GAT TTT CGT ATT TAT GGC ATG CAA	102
Lys Leu Ser Glu Ile Glu Leu Val Asp Phe Arg Ile Tyr Gly Met Gln	
10 15 20 25	
GAG GGC GTC CCT TAT GAG GGG ATT TAT GGT ATC AAT GTG GCT AAA GTC	150
Glu Gly Val Pro Tyr Glu Gly Ile Tyr Gly Ile Asn Val Ala Lys Val	
30 35 40	
CAA GAA ATC ATC CCC ATG CCC ACC CTT TTT GAA TAC CCC ACG AAT TTG	198
Gln Glu Ile Ile Pro Met Pro Thr Leu Phe Glu Tyr Pro Thr Asn Leu	
45 50 55	
GAT TAC ATT ATC GGC GTG TTT GAT TTG CGC TCC ATA ATC ATT CCG CTT	246
Asp Tyr Ile Ile Gly Val Phe Asp Leu Arg Ser Ile Ile Ile Pro Leu	
60 65 70	
ATA GAC TTG GCT AAA TGG ATA GGG ATT ATC CCA GAT AAA AGC AAG GAA	294
Ile Asp Leu Ala Lys Trp Ile Gly Ile Ile Pro Asp Lys Ser Lys Glu	
75 80 85	
AAC GAA AAA ATC GTC ATT ATC ACT GAA TTT AAC AAC GTT AAA ATG GGT	342
Asn Glu Lys Ile Val Ile Ile Thr Glu Phe Asn Asn Val Lys Met Gly	
90 95 100 105	

TTT TTA GTC CAT TCG GCT AGG CGT ATC AGG CGC ATT AGC TGG AAA GAT	390
Phe Leu Val His Ser Ala Arg Arg Ile Arg Arg Ile Ser Trp Lys Asp	
110 115 120	
GTG GAG CCT GCA TCC TTT AGC GCC TCT AAT AGC ATC AAT AAA GAA AAT	438
Val Glu Pro Ala Ser Phe Ser Ala Ser Asn Ser Ile Asn Lys Glu Asn	
125 130 135	
ATT ACC GGC ACG ACA CGC ATT GAA AAC GAC AAA ACC CTG CTC ATT TTG	486
Ile Thr Gly Thr Thr Arg Ile Glu Asn Asp Lys Thr Leu Leu Ile Leu	
140 145 150	
GAT TTA GAA AGC ATT TTA GAC GAT TTA AAG CTT AAT GAA GAC GCT AAA	534
Asp Leu Glu Ser Ile Leu Asp Asp Leu Lys Leu Asn Glu Asp Ala Lys	
155 160 165	
AAC GCT AAA GAT ACC CAT AAA GAG CGT TTT GAA GGC GAA GTG TTG TTT	582
Asn Ala Lys Asp Thr His Lys Glu Arg Phe Glu Gly Glu Val Leu Phe	
170 175 180 185	
TTA GAC GAT AGC AAG ACC GCA AGA AAA ACC TTA AAA AAC CAT TTG AGC	630
Leu Asp Asp Ser Lys Thr Ala Arg Lys Thr Leu Lys Asn His Leu Ser	
190 195 200	
AAA TTA GGT TTT AGC ATC ACT GAA GCT GTG GAT GGG GAA GAC GGG TTG	678
Lys Leu Gly Phe Ser Ile Thr Glu Ala Val Asp Gly Glu Asp Gly Leu	
205 210 215	
AAC AAA TTA GAA ATG TTA TTC AAA AAA TAC GGG GAC GAT TTG AGA AAG	726
Asn Lys Leu Glu Met Leu Phe Lys Lys Tyr Gly Asp Asp Leu Arg Lys	
220 225 230	
CAT TTG AAA TTC ATT ATT TCA GAT GTT GAA ATG CCT AAA ATG GAT GGC	774
His Leu Lys Phe Ile Ile Ser Asp Val Glu Met Pro Lys Met Asp Gly	
235 240 245	
TAT CAT TTC TTA TTC AAG CTC CAA AAA GAC CCT AGG TTT GCT TAT ATT	822
Tyr His Phe Leu Phe Lys Leu Gln Lys Asp Pro Arg Phe Ala Tyr Ile	
250 255 260 265	
CCT GTG ATT TTT AAT TCT TCT ATT TGC GAT AAT TAC AGC GCT GAA AGG	870
Pro Val Ile Phe Asn Ser Ser Ile Cys Asp Asn Tyr Ser Ala Glu Arg	
270 275 280	
GCT AAA GAA ATG GGG GCT GTA GCG TAT TTA GTC AAG TTT GAC GCA GAA	918
Ala Lys Glu Met Gly Ala Val Ala Tyr Leu Val Lys Phe Asp Ala Glu	
285 290 295	
AAA TTC ACC GAA GAA ATT TCT AAG ATT TTA GAC AAG AAT GCG TAATTCTTT	969
Lys Phe Thr Glu Glu Ile Ser Lys Ile Leu Asp Lys Asn Ala	
300 305 310	
TTATAAAATT GTAAAATACT CTTATCTCAA ACGCTAAAAA GGGGTTTTAA ATGGATG	1026

(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 311 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

```

Met Ala Glu Lys Thr Ala Asn Asp Leu Lys Leu Ser Glu Ile Glu Leu
 1      5      10      15
Val Asp Phe Arg Ile Tyr Gly Met Gln Glu Gly Val Pro Tyr Glu Gly
      20      25      30
Ile Tyr Gly Ile Asn Val Ala Lys Val Gln Glu Ile Ile Pro Met Pro
      35      40      45
Thr Leu Phe Glu Tyr Pro Thr Asn Leu Asp Tyr Ile Ile Gly Val Phe
      50      55      60
Asp Leu Arg Ser Ile Ile Ile Pro Leu Ile Asp Leu Ala Lys Trp Ile
      65      70      75      80
Gly Ile Ile Pro Asp Lys Ser Lys Glu Asn Glu Lys Ile Val Ile Ile
      85      90      95
Thr Glu Phe Asn Asn Val Lys Met Gly Phe Leu Val His Ser Ala Arg
      100     105     110
Arg Ile Arg Arg Ile Ser Trp Lys Asp Val Glu Pro Ala Ser Phe Ser
      115     120     125
Ala Ser Asn Ser Ile Asn Lys Glu Asn Ile Thr Gly Thr Thr Arg Ile
      130     135     140
Glu Asn Asp Lys Thr Leu Leu Ile Leu Asp Leu Glu Ser Ile Leu Asp
      145     150     155     160
Asp Leu Lys Leu Asn Glu Asp Ala Lys Asn Ala Lys Asp Thr His Lys
      165     170     175
Glu Arg Phe Glu Gly Glu Val Leu Phe Leu Asp Asp Ser Lys Thr Ala
      180     185     190
Arg Lys Thr Leu Lys Asn His Leu Ser Lys Leu Gly Phe Ser Ile Thr
      195     200     205
Glu Ala Val Asp Gly Glu Asp Gly Leu Asn Lys Leu Glu Met Leu Phe
      210     215     220
Lys Lys Tyr Gly Asp Asp Leu Arg Lys His Leu Lys Phe Ile Ile Ser
      225     230     235     240
Asp Val Glu Met Pro Lys Met Asp Gly Tyr His Phe Leu Phe Lys Leu
      245     250     255
Gln Lys Asp Pro Arg Phe Ala Tyr Ile Pro Val Ile Phe Asn Ser Ser
      260     265     270
Ile Cys Asp Asn Tyr Ser Ala Glu Arg Ala Lys Glu Met Gly Ala Val
      275     280     285
Ala Tyr Leu Val Lys Phe Asp Ala Glu Lys Phe Thr Glu Glu Ile Ser
      290     295     300
Lys Ile Leu Asp Lys Asn Ala
      305     310

```

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 32...697
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

GATCTATAAA GAATAGCCAT AAAGAAGAAT T ATG TTA GAT TAT CGC CAA AAA	52
Met Leu Asp Tyr Arg Gln Lys	
1 5	
ATT GAT GCT CTC ATC ACC AAA ATA GAA AAG GCT CGC ACC GCC TAT TCA	100
Ile Asp Ala Leu Ile Thr Lys Ile Glu Lys Ala Arg Thr Ala Tyr Ser	
10 15 20	
AGG CAC CAC ATT GTC AAA ATC GTG GCT GTT TCA AAA AAC GCT TCC CCA	148
Arg His His Ile Val Lys Ile Val Ala Val Ser Lys Asn Ala Ser Pro	
25 30 35	
GAA GCT ATC CAA CAT TAT TAT AAC TGC TCT CAA AGG GCT TTT GGA GAA	196
Glu Ala Ile Gln His Tyr Tyr Asn Cys Ser Gln Arg Ala Phe Gly Glu	
40 45 50 55	
AAT AAA GTT CAA GAT TTA AAA ACT AAA ATG CAT TCT TTA GAG CAT TTG	244
Asn Lys Val Gln Asp Leu Lys Thr Lys Met His Ser Leu Glu His Leu	
60 65 70	
CCC CTT GAA TGG CAC ATG ATA GGC TCT TTA CAA GAA AAT AAA ATC AAT	292
Pro Leu Glu Trp His Met Ile Gly Ser Leu Gln Glu Asn Lys Ile Asn	
75 80 85	
GCG CTT TTG AGT TTA AAG CCC GCT CTT TTG CAT TCT TTA GAC TCT TTA	340
Ala Leu Leu Ser Leu Lys Pro Ala Leu Leu His Ser Leu Asp Ser Leu	
90 95 100	
AAA CTC GCT TTG AAA ATA GAA AAG CGT TGC GAA ATA TTG GGC GTC AAT	388
Lys Leu Ala Leu Lys Ile Glu Lys Arg Cys Glu Ile Leu Gly Val Asn	
105 110 115	
TTA AAC GCT CTT TTA CAG GTT AAT AGC GCG TAT GAG GAA AGT AAA AGC	436
Leu Asn Ala Leu Leu Gln Val Asn Ser Ala Tyr Glu Glu Ser Lys Ser	
120 125 130 135	
GGG GTG GTG CCT GAA GAA GCG CTA GAA ATT TAT TCT CAA ATC AGT GAA	484
Gly Val Val Pro Glu Glu Ala Leu Glu Ile Tyr Ser Gln Ile Ser Glu	
140 145 150	
ACT TGC AAG CAC CTC AAG CTT AAG GGG CTT ATG TGT ATA GGG GCA CAC	532
Thr Cys Lys His Leu Lys Leu Lys Gly Leu Met Cys Ile Gly Ala His	
155 160 165	
ACA GAT GAT GAA AAG GAA ATT GAA AAA TCC TTT ATC ACC ACC AAA AAG	580
Thr Asp Asp Glu Lys Glu Ile Glu Lys Ser Phe Ile Thr Thr Lys Lys	
170 175 180	
CTT TTT GAC CAA ATA AAG AAT GCG AGC GTT CTT TCA ATG GGC ATG AGT	628

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 22...1593
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

TTTTAAATTC AAAGGATAAA A ATG TAT CAA GTA GCC ATT TGC GAC CCC ATC	51
Met Tyr Gln Val Ala Ile Cys Asp Pro Ile	
1 5 10	
CAT GCT AAA GGC ATT CAA ATT TTA GAA GCT CAA AAA GAC ATT GTC TTG	99
His Ala Lys Gly Ile Gln Ile Leu Glu Ala Gln Lys Asp Ile Val Leu	
15 20 25	
CAT GAT TAT TCC AAA TGC CCT AAA AAG GAG CTT TTA GAA AAA CTC ACT	147
His Asp Tyr Ser Lys Cys Pro Lys Lys Glu Leu Leu Glu Lys Leu Thr	
30 35 40	
CCC ATG GAT GCG CTC ATC ACT CGC AGC ATG ACC CCT ATC ACA AGC GAT	195
Pro Met Asp Ala Leu Ile Thr Arg Ser Met Thr Pro Ile Thr Ser Asp	
45 50 55	
TTT TTA AAG CCC TTA ACC CAC TTA AAA TCC ATC GTG AGA GCG GGC GTG	243
Phe Leu Lys Pro Leu Thr His Leu Lys Ser Ile Val Arg Ala Gly Val	
60 65 70	
GGA GTG GAT AAT ATT GAT TTA GAA AGC TGC TCT CAA AAA GGG ATT GTA	291
Gly Val Asp Asn Ile Asp Leu Glu Ser Cys Ser Gln Lys Gly Ile Val	
75 80 85 90	
GTG ATG AAT ATC CCT ACC GCT AAC ACG ATT GCC GCT GTG GAA TTG ACC	339
Val Met Asn Ile Pro Thr Ala Asn Thr Ile Ala Ala Val Glu Leu Thr	
95 100 105	
ATG GCG CAT TTG ATC AAT GCA GTG CGT TCG TTC CCT TGT GCA AAC GAT	387
Met Ala His Leu Ile Asn Ala Val Arg Ser Phe Pro Cys Ala Asn Asp	
110 115 120	
CAA ATC AAA CAC CAA AGG TTA TGG AAA AGA GAA GAT TGG TAT GGC ACG	435
Gln Ile Lys His Gln Arg Leu Trp Lys Arg Glu Asp Trp Tyr Gly Thr	
125 130 135	
GAA TTG AAA AAT AAA AAG CTG GGC ATC ATT GGT TTT GGG AAT ATT GGC	483
Glu Leu Lys Asn Lys Lys Leu Gly Ile Ile Gly Phe Gly Asn Ile Gly	
140 145 150	
TCT AGG GTG GGC ATT AGA GCA AAA GCC TTT GAA ATG GAA GTT CTA GCC	531
Ser Arg Val Gly Ile Arg Ala Lys Ala Phe Glu Met Glu Val Leu Ala	
155 160 165 170	

TAT Tyr	GAT Asp	CCT Pro	TAT Tyr	ATC Ile 175	CCT Pro	TCT Ser	TCA Ser	AAA Lys	GCC Ala 180	ACT Thr	GAT Asp	TTA Leu	GGA Gly	GTC Val 185	ATT Ile	579
TAC Tyr	ACG Thr	AAA Lys	AAT Asn 190	TTT Phe	GAA Glu	GAC Asp	ATT Ile	TTG Leu 195	CAA Gln	TGC Cys	GAT Asp	ATG Met	ATC Ile 200	ACT Thr	ATC Ile	627
CAC His	ACC Thr	CCT Pro 205	AAA Lys	AAT Asn	AAA Lys	GAA Glu	ACG Thr 210	ATT Ile	AAC Asn	ATG Met	ATA Ile	GGT Gly 215	GCT Ala	AAA Lys	GAG Glu	675
ATT Ile	GAG Glu 220	CGC Arg	ATG Met	AAA Lys	AAA Lys	GGG Gly 225	GTT Val	ATT Ile	TTG Leu	CTC Leu	AAT Asn 230	TGC Cys	GCT Ala	AGG Arg	GGT Gly	723
GGG Gly 235	CTT Leu	TAT Tyr	AAT Asn	GAA Glu 240	GAC Asp	GCT Ala	CTT Leu	TAT Tyr	GAG Glu	GCT Ala 245	TTA Leu	GAA Glu	ACC Thr	AAA Lys 250	AAA Lys	771
GTG Val	CGT Arg	TGG Trp	CTT Leu 255	GGC Gly	ATT Ile	GAT Asp	GTC Val	TTT Phe 260	TCT Ser	AAA Lys	GAG Glu	CCT Pro	GGC Gly 265	ATT Ile 265	CAC His	819
AAC Asn	AAG Lys	CTT Leu 270	TTA Leu	GAC Asp	TTG Leu	CCC Pro	AAT Asn 275	GTT Val	TAT Tyr	GCG Ala	ACC Thr	CCC Pro 280	CAT His	ATT Ile	GGC Gly	867
GCA Ala	AAC Asn 285	ACT Thr	TTA Leu	GAA Glu	TCC Ser	CAA Gln	GAA Glu 290	GAA Glu	ATT Ile	TCC Ser	AAA Lys	CAA Gln 295	GCC Ala	GCT Ala	CAA Gln	915
GGG Gly 300	GTT Val	ATG Met	GAA Glu	TCT Ser	TTA Leu	AGG Arg 305	GGT Gly	TCA Ser	AGC Ser	CAC His 310	CCG Pro	CAT His	GCT Ala	TTG Leu	AAT Asn	963
TTA Leu 315	CCC Pro	ATG Met	CAA Gln	GCT Ala 320	TTT Phe	GAC Asp	GCG Ala	AGC Ser	GCA Ala	AAA Lys 325	GCC Ala	TAC Tyr	TTG Leu	AAT Asn 330	TTA Leu	1011
GCG Ala	CAA Gln	AAA Lys	TTG Leu 335	GGT Gly	TAT Tyr	TTT Phe	TCC Ser	AGT Ser 340	CAA Gln	ATC Ile	CAT His	AAG Lys	GGC Gly 345	GTG Val	TGC Cys	1059
CAA Gln	AAA Lys	ATT Ile 350	GAG Glu	CTC Leu	AGT Ser	CTT Leu	TGT Cys 355	GGG Gly	GAG Glu	ATC Ile	AAC Asn	CAA Gln 360	TTT Phe 360	AAA Lys	GAC Asp	1107
GCT Ala	CTT Leu 365	GTA Val	GCC Ala	TTT Phe	ATG Met	TTA Leu 370	GTG Val	GGG Gly	GTG Val	TTA Leu	AAA Lys	CCT Pro 375	GTT Val	GTA Val	GGG Gly	1155
GAT Asp 380	AAA Lys	ATC Ile	AAT Asn	TAC Tyr	ATT Ile 385	AAC Asn	GCC Ala	CCC Pro	TTT Phe	GTG Val 390	GCC Ala	AAA Lys	GAA Glu	AGA Arg	GGT Gly	1203
ATT Ile	GAG Glu	ATT Ile	AAG Lys	GTT Val	AGC Ser	CTT Leu	AAA Lys	GAA Glu	AGC Ser	GCT Ala	TCG Ser	CCC Pro	TAT Tyr	AAG Lys	AAC Asn	1251

															85																90																95		
Ala	Asn	Thr			Ile	Ala	Ala	Val	Glu	Leu	Thr	Met	Ala	His	Leu	Ile	Asn																																
																	100																105																110
Ala	Val	Arg	Ser	Phe	Pro	Cys	Ala	Asn	Asp	Gln	Ile	Lys	His	Gln	Arg																																		
																	115																120																125
Leu	Trp	Lys	Arg	Glu	Asp	Trp	Tyr	Gly	Thr	Glu	Leu	Lys	Asn	Lys	Lys																																		
																	130																135																140
Leu	Gly	Ile	Ile	Gly	Phe	Gly	Asn	Ile	Gly	Ser	Arg	Val	Gly	Ile	Arg																																		
																	145																150																155
Ala	Lys	Ala	Phe	Glu	Met	Glu	Val	Leu	Ala	Tyr	Asp	Pro	Tyr	Ile	Pro																																		
																	165																170																175
Ser	Ser	Lys	Ala	Thr	Asp	Leu	Gly	Val	Ile	Tyr	Thr	Lys	Asn	Phe	Glu																																		
																	180																185																190
Asp	Ile	Leu	Gln	Cys	Asp	Met	Ile	Thr	Ile	His	Thr	Pro	Lys	Asn	Lys																																		
																	195																200																205
Glu	Thr	Ile	Asn	Met	Ile	Gly	Ala	Lys	Glu	Ile	Glu	Arg	Met	Lys	Lys																																		
																	210																215																220
Gly	Val	Ile	Leu	Leu	Asn	Cys	Ala	Arg	Gly	Gly	Leu	Tyr	Asn	Glu	Asp																																		
																	225																230																240
Ala	Leu	Tyr	Glu	Ala	Leu	Glu	Thr	Lys	Lys	Val	Arg	Trp	Leu	Gly	Ile																																		
																	245																250																255
Asp	Val	Phe	Ser	Lys	Glu	Pro	Gly	Ile	His	Asn	Lys	Leu	Leu	Asp	Leu																																		
																	260																265																270
Pro	Asn	Val	Tyr	Ala	Thr	Pro	His	Ile	Gly	Ala	Asn	Thr	Leu	Glu	Ser																																		
																	275																280																285
Gln	Glu	Glu	Ile	Ser	Lys	Gln	Ala	Ala	Gln	Gly	Val	Met	Glu	Ser	Leu																																		
																	290																295																300
Arg	Gly	Ser	Ser	His	Pro	His	Ala	Leu	Asn	Leu	Pro	Met	Gln	Ala	Phe																																		
																	305																310																315
Asp	Ala	Ser	Ala	Lys	Ala	Tyr	Leu	Asn	Leu	Ala	Gln	Lys	Leu	Gly	Tyr																																		
																	325																330																335
Phe	Ser	Ser	Gln	Ile	His	Lys	Gly	Val	Cys	Gln	Lys	Ile	Glu	Leu	Ser																																		
																	340																345																350
Leu	Cys	Gly	Glu	Ile	Asn	Gln	Phe	Lys	Asp	Ala	Leu	Val	Ala	Phe	Met																																		
																	355																360																365
Leu	Val	Gly	Val	Leu	Lys	Pro	Val	Val	Gly	Asp	Lys	Ile	Asn	Tyr	Ile																																		
																	370																375																380
Asn	Ala	Pro	Phe	Val	Ala	Lys	Glu	Arg	Gly	Ile	Glu	Ile	Lys	Val	Ser																																		
																	385																390																395
Leu	Lys	Glu	Ser	Ala	Ser	Pro	Tyr	Lys	Asn	Met	Leu	Ser	Leu	Thr	Leu																																		
																	405																410																415
Asn	Ala	Ala	Asn	Gly	Thr	Ile	Ser	Val	Ser	Gly	Thr	Val	Phe	Glu	Glu																																		
																	420																425																430
Asp	Ile	Leu	Lys	Leu	Thr	Glu	Ile	Asp	Gly	Phe	His	Ile	Asp	Ile	Glu																																		
																	435																440																445
Pro	Lys	Gly	Lys	Met	Leu	Leu	Phe	Arg	Asn	Thr																																							

-774-

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...1701
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

GGATTTTATA TTTATTTTAT AGTAAGGCAG TCA ATG AGC AAG ATA GCA GAT GAT	54
Met Ser Lys Ile Ala Asp Asp	
1 5	
CAG AAC TTT AAT GAC GAG GAG GAA AAC TTC GCA AAA CTC TTT AAA AAA	102
Gln Asn Phe Asn Asp Glu Glu Asn Phe Ala Lys Leu Phe Lys Lys	
10 15 20	
GAA TTA GAA AAA GAA GAA ACC CTA GAA AAA GGC ACT ATC AAA GAA GGG	150
Glu Leu Glu Lys Glu Glu Thr Leu Glu Lys Gly Thr Ile Lys Glu Gly	
25 30 35	
CTA GTC GTT TCC ATC AAT GAG AAT GAT GGT TAT GCC ATG GTG AGC GTG	198
Leu Val Val Ser Ile Asn Glu Asn Asp Gly Tyr Ala Met Val Ser Val	
40 45 50 55	
GGC GGT AAG ACA GAA GGC CGT TTG GCT TTG AAT GAG ATC ACC GAT GAA	246
Gly Gly Lys Thr Glu Gly Arg Leu Ala Leu Asn Glu Ile Thr Asp Glu	
60 65 70	
AAG GGG CAG TTG CTG TAT CAA AAA AAT GAC CCC ATT ATC GTG CAT GTG	294
Lys Gly Gln Leu Leu Tyr Gln Lys Asn Asp Pro Ile Ile Val His Val	
75 80 85	
TCC GAA AAA GGT GAA CAC CCT AGC GTT TCC TAC AAA AAG GCC ATT TCC	342
Ser Glu Lys Gly Glu His Pro Ser Val Ser Tyr Lys Lys Ala Ile Ser	
90 95 100	
CAA CAA AAG ATT CAA GCT AAA ATT GAA GAA TTA GGC GAA AAC TAT GAA	390
Gln Gln Lys Ile Gln Ala Lys Ile Glu Glu Leu Gly Glu Asn Tyr Glu	
105 110 115	
AAC GCC ATT ATT GAA GGC AAG ATT GTA GGC AAG AAT AAA GGG GGT TAT	438
Asn Ala Ile Ile Glu Gly Lys Ile Val Gly Lys Asn Lys Gly Gly Tyr	
120 125 130 135	
ATC GTG GAG TCT CAA GGC GTG GAG TAT TTC CTC TCC CGC TCG CAC TCT	486
Ile Val Glu Ser Gln Gly Val Glu Tyr Phe Leu Ser Arg Ser His Ser	
140 145 150	
TCT TTA AAG AAT GAC GCA AAC CAT ATC GGC AAA CGC GTT AAA GCG TGC	534
Ser Leu Lys Asn Asp Ala Asn His Ile Gly Lys Arg Val Lys Ala Cys	

155					160					165						
ATC Ile	ATT Ile	CGT Arg 170	GTG Val	GAT Asp	AAG Lys	GAA Glu	AAC Asn 175	CAT His	TCT Ser	ATC Ile	AAT Asn 180	ATT Ile	TCT Ser	CGC Arg	AAA Lys	582
CGA Arg 185	TTC Phe	TTT Phe	GAA Glu	GTC Val	AAT Asn	GAC Asp 190	AAA Lys	CGA Arg	CAA Gln	CTT Leu	GAG Glu 195	GTT Val	TCT Ser	AAG Lys	GAA Glu	630
TTG Leu 200	TTA Leu	GAA Glu	GCC Ala	ACA Thr	GAG Glu 205	CCG Pro	GTG Val	TTA Leu	GGG Gly	GTT Val 210	GTG Val	CGC Arg	CAG Gln	ATC Ile	ACC Thr 215	678
CCT Pro	TTT Phe	GGC Gly	ATT Ile	TTT Phe 220	GTA Val	GAA Glu	GCT Ala	AAG Lys	GGG Gly 225	ATT Ile	GAG Glu	GGC Gly	TTG Leu	GTC Val 230	CAT His	726
TAT Tyr	TCT Ser	GAA Glu 235	ATC Ile	AGC Ser	CAT His	AAG Lys	GGA Gly 240	CCA Pro	GTC Val	AAT Asn	CCT Pro	GAA Glu 245	AAA Lys	TAC Tyr	TAC Tyr	774
AAA Lys	GAG Glu 250	GGC Gly	GAT Asp	GAA Glu	GTC Val	TAT Tyr 255	GTC Val	AAA Lys	GCC Ala	ATC Ile	GCT Ala 260	TAT Tyr	GAT Asp	GCA Ala	GAA Glu	822
AAA Lys 265	AGA Arg	CGC Arg	CTT Leu	TCA Ser	CTC Leu	TCC Ser 270	ATA Ile	AAA Lys	GCG Ala	ACT Thr 275	ATA Ile	GAA Glu	GAC Asp	CCA Pro	TGG Trp	870
GAA Glu 280	GAG Glu	ATT Ile	CAA Gln	GAC Asp	AAG Lys 285	CTA Leu	AAA Lys	CCC Pro	GGA Gly 290	TAC Tyr 290	GCC Ala	ATT Ile	AAG Lys	GTA Val	GTG Val 295	918
GTG Val	AGC Ser	AAC Asn	ATT Ile	GAA Glu 300	CAT His	TAT Tyr	GGG Gly 305	GTG Val	TTT Phe 305	GTG Val	GAT Asp	ATT Ile	GGT Gly 310	AAT Asn 310	GAT Asp	966
ATT Ile	GAA Glu	GGC Gly 315	TTT Phe	TTG Leu	CAT His	GTT Val	TCT Ser 320	GAA Glu 320	ATC Ile	TCT Ser	TGG Trp	GAT Asp 325	AAA Lys 325	AAT Asn 325	GTC Val	1014
AGC Ser	CAC His 330	CCT Pro	AAC Asn	AAT Asn	TAC Tyr	TTG Leu	AGC Ser 335	GTG Val	GGG Gly	CAA Gln	GAG Glu 340	ATT Ile 340	GAT Asp 340	GTG Val	AAA Lys	1062
ATC Ile 345	ATT Ile	GAC Asp	ATT Ile	GAT Asp	CCA Pro	AAA Lys 350	AAT Asn	CGC Arg	CGC Arg	TTA Leu	AGG Arg 355	GTT Val	TCT Ser	TTA Leu	AAG Lys	1110
CAA Gln 360	CTC Leu	ACT Thr	AAC Asn	AGG Arg	CCT Pro 365	TTT Phe	GAT Asp	GTT Val	TTT Phe	GAA Glu 370	TCT Ser	AAA Lys	CAC His	CAA Gln	GTG Val 375	1158
GGG Gly	GAT Asp	GTT Val	TTA Leu 380	GAA Glu	GGC Gly	AAA Lys	GTG Val	GCG Ala	ACT Thr 385	TTA Leu	ACG Thr	GAT Asp	TTT Phe 390	GGG Gly	GCG Ala	1206

[illegible]

Met 1	Ser	Lys	Ile	Ala 5	Asp	Asp	Gln	Asn	Phe 10	Asn	Asp	Glu	Glu	Glu	Asn 15
Phe	Ala	Lys	Leu	Phe 20	Lys	Lys	Glu	Leu	Glu	Lys	Glu	Glu	Thr	Leu	Glu
Lys	Gly	Thr	Ile	Lys	Glu	Gly	Leu	Val	Val	Ser	Ile	Asn	Glu	Asn	Asp
Gly	Tyr	Ala	Met	Val	Ser	Val	Gly	Gly	Lys	Thr	Glu	Gly	Arg	Leu	Ala
Leu 65	Asn	Glu	Ile	Thr	Asp 70	Glu	Lys	Gly	Gln	Leu	Leu	Tyr	Gln	Lys	Asn 80
Asp	Pro	Ile	Ile	Val	His	Val	Ser	Glu	Lys	Gly	Glu	His	Pro	Ser	Val
Ser	Tyr	Lys	Lys	Ala	Ile	Ser	Gln	Gln	Lys	Ile	Gln	Ala	Lys	Ile	Glu
Glu	Leu	Gly	Glu	Asn	Tyr	Glu	Asn	Ala	Ile	Ile	Glu	Gly	Lys	Ile	Val
Gly	Lys	Asn	Lys	Gly	Gly	Tyr	Ile	Val	Glu	Ser	Gln	Gly	Val	Glu	Tyr
Phe 145	Leu	Ser	Arg	Ser	His 150	Ser	Ser	Leu	Lys	Asn	Asp	Ala	Asn	His	Ile 160
Gly	Lys	Arg	Val	Lys	Ala	Cys	Ile	Ile	Arg	Val	Asp	Lys	Glu	Asn	His
Ser	Ile	Asn	Ile	Ser	Arg	Lys	Arg	Phe	Phe	Glu	Val	Asn	Asp	Lys	Arg
Gln	Leu	Glu	Val	Ser	Lys	Glu	Leu	Leu	Glu	Ala	Thr	Glu	Pro	Val	Leu
Gly	Val	Val	Arg	Gln	Ile	Thr	Pro	Phe	Gly	Ile	Phe	Val	Glu	Ala	Lys
Gly 225	Ile	Glu	Gly	Leu	Val	His	Tyr	Ser	Glu	Ile	Ser	His	Lys	Gly	Pro 240
Val	Asn	Pro	Glu	Lys	Tyr	Tyr	Lys	Glu	Gly	Asp	Glu	Val	Tyr	Val	Lys
Ala	Ile	Ala	Tyr	Asp	Ala	Glu	Lys	Arg	Arg	Leu	Ser	Leu	Ser	Ile	Lys
Ala	Thr	Ile	Glu	Asp	Pro	Trp	Glu	Glu	Ile	Gln	Asp	Lys	Leu	Lys	Pro
Gly	Tyr	Ala	Ile	Lys	Val	Val	Val	Ser	Asn	Ile	Glu	His	Tyr	Gly	Val
Phe 305	Val	Asp	Ile	Gly	Asn	Asp	Ile	Glu	Gly	Phe	Leu	His	Val	Ser	Glu 320
Ile	Ser	Trp	Asp	Lys	Asn	Val	Ser	His	Pro	Asn	Asn	Tyr	Leu	Ser	Val
Gly	Gln	Glu	Ile	Asp	Val	Lys	Ile	Ile	Asp	Ile	Asp	Pro	Lys	Asn	Arg
Arg	Leu	Arg	Val	Ser	Leu	Lys	Gln	Leu	Thr	Asn	Arg	Pro	Phe	Asp	Val
Phe	Glu	Ser	Lys	His	Gln	Val	Gly	Asp	Val	Leu	Glu	Gly	Lys	Val	Ala
Thr 385	Leu	Thr	Asp	Phe	Gly	Ala	Phe	Leu	Asn	Leu	Gly	Gly	Val	Asp	Gly 400
Leu	Leu	His	Asn	His	Asp	Ala	Phe	Trp	Asp	Lys	Asp	Lys	Lys	Cys	Lys
Asp	His	Tyr	Lys	Ile	Gly	Asp	Val	Ile	Lys	Val	Lys	Ile	Leu	Lys	Ile
Asn	Lys	Lys	Asp	Lys	Lys	Ile	Ser	Leu	Ser	Ala	Lys	His	Leu	Val	Thr
Ser	Pro	Thr	Glu	Glu	Phe	Ala	Gln	Lys	His	Lys	Thr	Asp	Ser	Val	Ile

CGC Arg	GGG Gly	AGA Arg	GAA Glu	GAG Glu	TTT Phe	GTG Val	CGT Arg	GTG Val	AGT Ser	TGG Trp	GAT Asp	GTG Val	GCG Ala	TTG Leu	GAT Asp	390
105																
TTA Leu	GCG Ala	GCT Ala	AAA Lys	AAG Lys	CTT Leu	AAA Lys	GAA Glu	ATC Ile	CCT Pro	AAA Lys	GAA Glu	AAC Asn	ATT Ile	TAT Tyr	AAT Asn	438
120																
GCC Ala	AGT Ser	TAT Tyr	GGT Gly	GGC Gly	TGG Trp	GGG Gly	CAT His	GCG Ala	GGC Gly	AGC Ser	TTG Leu	CAT His	CGT Arg	TGC Cys	CAT His	486
140																
CAT His	TTA Leu	GCA Ala	TGG Trp	CGT Arg	TTT Phe	TTT Phe	AAC Asn	ACG Thr	ACT Thr	TTA Leu	GGA Gly	GGG Gly	GCT Ala	ATT Ile	GGC Gly	534
155																
ACT Thr	GAT Asp	GGG Gly	GAA Glu	TAT Tyr	AGT Ser	AAT Asn	GGC Gly	GCG Ala	GCC Ala	GCA Ala	AGA Arg	ATA Ile	AAC Asn	CCT Pro	ATG Met	582
170																
ATT Ile	GTA Val	GGG Gly	GAT Asp	ATG Met	GAA Glu	GTT Val	TAT Tyr	TCG Ser	CAA Gln	CAA Gln	ACC Thr	ACG Thr	CAT His	GAA Glu	GAG Glu	630
185																
ATG Met	ATT Ile	AAA Lys	AAT Asn	TGT Cys	AAG Lys	GTG Val	TAT Tyr	GTC Val	ATG Met	TGG Trp	GGG Gly	GCG Ala	GAT Asp	TTA Leu	CTC Leu	678
200																
AAG Lys	TGC Cys	AAC Asn	CGC Arg	ATT Ile	GAT Asp	TAT Tyr	TTT Phe	GTG Val	CCA Pro	AAC Asn	CAT His	GTC Val	AAT Asn	GAC Asp	AGC Ser	726
220																
TAC Tyr	TAC Tyr	CCC Pro	AAG Lys	TAT Tyr	AAA Lys	AGA Arg	GCT Ala	GGT Gly	ATT Ile	AAA Lys	TTC Phe	ATT Ile	AGT Ser	ATC Ile	GAT Asp	774
230																
CCC Pro	ATT Ile	TAT Tyr	ACC Thr	GAA Glu	ACC Thr	GCT Ala	CAA Gln	GCC Ala	TTT Phe	AGT Ser	GCT Ala	GAA Glu	TGG Trp	ATA Ile	CCC Pro	822
245																
ATT Ile	CGC Arg	CCT Pro	AAC Asn	ACT Thr	GAT Asp	GTA Val	GCG Ala	TTA Leu	ATG Met	CTA Leu	GGC Gly	ATG Met	ATG Met	CAT His	TAT Tyr	870
265																
CTT Leu	TAT Tyr	ACG Thr	AGC Ser	AAT Asn	CAA Gln	TAT Tyr	GAT Asp	AAA Lys	GCG Ala	TTT Phe	ATC Ile	GCT Ala	AAA Lys	TAC Tyr	ACT Thr	918
280																
GAT Asp	GGT Gly	TTT Phe	GAT Asp	AAA Lys	TTT Phe	TTA Leu	CCC Pro	TAT Tyr	TTG Leu	CTA Leu	GGA Gly	GAG Glu	AGC Ser	GAT Asp	AAT Asn	966
295																
GCG Ala	CCT Pro	AAG Lys	ACT Thr	TTA Leu	GAA Glu	TGG Trp	GCG Ala	TCT Ser	CAA Gln	ATC Ile	ACT Thr	GGA Gly	GTG Val	AGC Ser	GCA Ala	1014
310																
GAA Glu	AAA Lys	ATC Ile	AAA Lys	GAA Glu	TTA Leu	GCG Ala	GAT Asp	TTG Leu	TTT Phe	GTT Val	TCT Ser	AAA Lys	CGC Arg	ACT Thr	TTT Phe	1062
315																

325	330							335							340					
TTA Leu	GCG Ala	GGT Gly	AAT Asn	TGG Trp	GCC Ala	ATG Met	CAA Gln	AGA Arg	GCT Ala	CAG Gln	TAT Tyr	GGC Gly	GAG Glu	CAA Gln	CCG Pro	1110				
				345					350					355						
GAT Asp	TGG Trp	GCG Ala	TTA Leu	ATT Ile	GTT Val	TTA Leu	GCT Ala	AGC Ser	ATG Met	ATT Ile	GGT Gly	CAA Gln	GTG Val	GGC Gly	TTA Leu	1158				
				360					365					370						
TCG Ser	GGT Gly	GGG Gly	GGC Gly	TTT Phe	GGC Gly	TTT Phe	TCT Ser	ATG Met	CAT His	TAT Tyr	GGA Gly	GGG Gly	AAC Asn	GCT Ala	CAA Gln	1206				
				375					380					385						
GCA Ala	AGC Ser	TCA Ser	GGG Gly	GCA Ala	AGA Arg	ATT Ile	GTT Val	CCT Pro	ATG Met	ATT Ile	TCA Ser	CAA Gln	GGG Gly	CAT His	AAT Asn	1254				
				390					395					400						
TCT Ser	GTA Val	AAA Lys	AGC Ser	GTT Val	ATT Ile	CCA Pro	GCA Ala	TCT Ser	AGG Arg	GTT Val	TCT Ser	GAA Glu	GCG Ala	ATT Ile	TTA Leu	1302				
				405					410					415						
AAT Asn	CCG Pro	GAT Asp	AAA Lys	GAA Glu	ATT Ile	GAT Asp	TTT Phe	ATG Met	GGC Gly	AAA Lys	AAA Lys	CTC Leu	AAA Lys	TTG Leu	CCT Pro	1350				
				425					430					435						
AAA Lys	ATC Ile	AAA Lys	ATG Met	ATT Ile	TAT Tyr	AAT Asn	TGT Cys	GGG Gly	GCG Ala	GAT Asp	TTA Leu	TTA Leu	GGG Gly	CAT His	GAA Glu	1398				
				440					445					450						
ACT Thr	GAT Asp	ACA Thr	AAC Asn	GAG Glu	CTG Leu	ATT Ile	CGC Arg	GCT Ala	TTA Leu	AGG Arg	ACC Thr	TTA Leu	GAT Asp	TGC Cys	GTG Val	1446				
				455					460					465						
ATC Ile	GTG Val	CAT His	GAG Glu	CCT Pro	TGG Trp	TGG Trp	CGC Arg	CTA Leu	CGG Arg	CAA Gln	AAT Asn	TTG Leu	CTG Leu	ATA Ile	TTG Leu	1494				
				470					475					480						
TCT Ser	TTG Leu	CTT Leu	CCA Pro	CTA Leu	GCA Ala	CTG Leu	TGG Trp	AAA Lys	GAG Glu	ATG Met	ATA Ile	TTG Leu	CTT Leu	TTG Leu	GAG Glu	1542				
				485					490					495						
GGA Gly	GTT Val	ATT Ile	CTA Leu	AGA Arg	ATG Met	TGG Trp	TTT Phe	ATG Met	CCA Pro	TGC Cys	GTA Val	AGG Arg	TGG Trp	TAGAGCCTG		1593				
				505					510											
TTTATGAATC TAAAGACGAT TATGAGATTT TCAGACAGCT TGC																1636				

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

Met	Ser	Ile	Ser	Arg	Arg	Ser	Ile	Leu	Thr	Lys	Ile	Pro	Ile	Ala	Leu	1	5	10	15
Ala	Ser	Ala	Asn	Val	Leu	Lys	Ala	Val	Gly	Val	Phe	Glu	Lys	Val	Glu	20	25	30	
Ser	Ile	Pro	His	Ala	Thr	His	Phe	Gly	Pro	Phe	Ile	Ala	Lys	Val	Gln	35	40	45	
Asn	Gly	Val	Ile	Lys	Asp	Ile	Val	Pro	Gln	Lys	Ser	Asp	Tyr	Asn	Pro	50	55	60	
Thr	Met	Met	Leu	Lys	Ala	Met	Val	Asp	Arg	Val	Tyr	Ser	Asp	Ser	Arg	65	70	75	80
Val	Lys	Tyr	Pro	Cys	Val	Arg	Lys	Ser	Phe	Leu	Glu	Asn	Lys	Lys	Asn	85	90	95	
His	Lys	Glu	Leu	Arg	Gly	Arg	Glu	Glu	Phe	Val	Arg	Val	Ser	Trp	Asp	100	105	110	
Val	Ala	Leu	Asp	Leu	Ala	Ala	Lys	Lys	Leu	Lys	Glu	Ile	Pro	Lys	Glu	115	120	125	
Asn	Ile	Tyr	Asn	Ala	Ser	Tyr	Gly	Gly	Trp	Gly	His	Ala	Gly	Ser	Leu	130	135	140	
His	Arg	Cys	His	His	Leu	Ala	Trp	Arg	Phe	Phe	Asn	Thr	Thr	Leu	Gly	145	150	155	160
Gly	Ala	Ile	Gly	Thr	Asp	Gly	Glu	Tyr	Ser	Asn	Gly	Ala	Ala	Ala	Arg	165	170	175	
Ile	Asn	Pro	Met	Ile	Val	Gly	Asp	Met	Glu	Val	Tyr	Ser	Gln	Gln	Thr	180	185	190	
Thr	His	Glu	Glu	Met	Ile	Lys	Asn	Cys	Lys	Val	Tyr	Val	Met	Trp	Gly	195	200	205	
Ala	Asp	Leu	Leu	Lys	Cys	Asn	Arg	Ile	Asp	Tyr	Phe	Val	Pro	Asn	His	210	215	220	
Val	Asn	Asp	Ser	Tyr	Tyr	Pro	Lys	Tyr	Lys	Arg	Ala	Gly	Ile	Lys	Phe	225	230	235	240
Ile	Ser	Ile	Asp	Pro	Ile	Tyr	Thr	Glu	Thr	Ala	Gln	Ala	Phe	Ser	Ala	245	250	255	
Glu	Trp	Ile	Pro	Ile	Arg	Pro	Asn	Thr	Asp	Val	Ala	Leu	Met	Leu	Gly	260	265	270	
Met	Met	His	Tyr	Leu	Tyr	Thr	Ser	Asn	Gln	Tyr	Asp	Lys	Ala	Phe	Ile	275	280	285	
Ala	Lys	Tyr	Thr	Asp	Gly	Phe	Asp	Lys	Phe	Leu	Pro	Tyr	Leu	Leu	Gly	290	295	300	
Glu	Ser	Asp	Asn	Ala	Pro	Lys	Thr	Leu	Glu	Trp	Ala	Ser	Gln	Ile	Thr	305	310	315	320
Gly	Val	Ser	Ala	Glu	Lys	Ile	Lys	Glu	Leu	Ala	Asp	Leu	Phe	Val	Ser	325	330	335	
Lys	Arg	Thr	Phe	Leu	Ala	Gly	Asn	Trp	Ala	Met	Gln	Arg	Ala	Gln	Tyr	340	345	350	
Gly	Glu	Gln	Pro	Asp	Trp	Ala	Leu	Ile	Val	Leu	Ala	Ser	Met	Ile	Gly	355	360	365	
Gln	Val	Gly	Leu	Ser	Gly	Gly	Gly	Phe	Gly	Phe	Ser	Met	His	Tyr	Gly	370	375	380	
Gly	Asn	Ala	Gln	Ala	Ser	Ser	Gly	Ala	Arg	Ile	Val	Pro	Met	Ile	Ser	385	390	395	400
Gln	Gly	His	Asn	Ser	Val	Lys	Ser	Val	Ile	Pro	Ala	Ser	Arg	Val	Ser	405	410	415	
Glu	Ala	Ile	Leu	Asn	Pro	Asp	Lys	Glu	Ile	Asp	Phe	Met	Gly	Lys	Lys	420	425	430	
Leu	Lys	Leu	Pro	Lys	Ile	Lys	Met	Ile	Tyr	Asn	Cys	Gly	Ala	Asp	Leu	435	440	445	

Leu Gly His Glu Thr Asp Thr Asn Glu Leu Ile Arg Ala Leu Arg Thr
 450 455 460
 Leu Asp Cys Val Ile Val His Glu Pro Trp Trp Arg Leu Arg Gln Asn
 465 470 475 480
 Leu Leu Ile Leu Ser Leu Leu Pro Leu Ala Leu Trp Lys Glu Met Ile
 485 490 495
 Leu Leu Leu Glu Gly Val Ile Leu Arg Met Trp Phe Met Pro Cys Val
 500 505 510
 Arg Trp

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 24...509
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

ATTGACGCTT ATAAGGATAA AAG ATG AAT ATT TTT CAA ACG AGT TTG AAA TGT	53
Met Asn Ile Phe Gln Thr Ser Leu Lys Cys	
1 5 10	
TGC GTG GGG TTG GTT TTG TCT GTG GGG GTC TTA TTA GGG GAT TCT AAA	101
Cys Val Gly Leu Val Leu Ser Val Gly Val Leu Leu Gly Asp Ser Lys	
15 20 25	
GCT TTT AAG GTT AGG GTG GAT AAA AGT TTA ACC CCG CCT TTT TTG AAT	149
Ala Phe Lys Val Arg Val Asp Lys Ser Leu Thr Pro Pro Phe Leu Asn	
30 35 40	
GTG CTT TCA TTA GCT TTT AAA CAA GAC ATG AAA AAA GAG GTC ATT TTT	197
Val Leu Ser Leu Ala Phe Lys Gln Asp Met Lys Lys Glu Val Ile Phe	
45 50 55	
GTG ATT ACC AAA AGC AAT AAG TTG AGT AAA AAA GTG CTT TGT GAT TTT	245
Val Ile Thr Lys Ser Asn Lys Leu Ser Lys Lys Val Leu Cys Asp Phe	
60 65 70	
GAC GCT TTT TTA TTG CCT GAG ACT CTG ATG AGC GGC ATG CCT AAA AAA	293
Asp Ala Phe Leu Leu Pro Glu Thr Leu Met Ser Gly Met Pro Lys Lys	
75 80 85 90	
GCA CTA TTC CAT AAA GAG TTT TTA TTC CAA TCT AAA GAA AAT AAA ACG	341
Ala Leu Phe His Lys Glu Phe Leu Phe Gln Ser Lys Glu Asn Lys Thr	
95 100 105	
CTC TAT GCG TTT TCG CTG ATT GAT TCT CAA TAT TGC TCA AAA GGT GGA	389

Leu	Tyr	Ala	Phe	Ser	Leu	Ile	Asp	Ser	Gln	Tyr	Cys	Ser	Lys	Gly	Gly		
			110					115					120				
AAT	TAC	AGA	TAC	GAA	CTA	GAA	AAA	TTA	GAA	CGC	TGG	TTT	GTG	CAA	AAA	437	
Asn	Tyr	Arg	Tyr	Glu	Leu	Glu	Lys	Leu	Glu	Arg	Trp	Phe	Val	Gln	Lys		
		125					130					135					
GCA	CCT	GAG	TTG	GCT	GAA	AGC	TAT	AGG	GTG	AAT	TAC	AAA	AAT	CAA	TAC	485	
Ala	Pro	Glu	Leu	Ala	Glu	Ser	Tyr	Arg	Val	Asn	Tyr	Lys	Asn	Gln	Tyr		
	140					145					150						
AAT	AAA	ACA	CAG	ATC	TCA	CAA	AAA	TAAAGAATGA	GCGATGATTT	TAGTATTAGA	539						
Asn	Lys	Thr	Gln	Ile	Ser	Gln	Lys										
155					160												
T																	540

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

Met	Asn	Ile	Phe	Gln	Thr	Ser	Leu	Lys	Cys	Cys	Val	Gly	Leu	Val	Leu		
1				5					10				15				
Ser	Val	Gly	Val	Leu	Leu	Gly	Asp	Ser	Lys	Ala	Phe	Lys	Val	Arg	Val		
			20					25					30				
Asp	Lys	Ser	Leu	Thr	Pro	Pro	Phe	Leu	Asn	Val	Leu	Ser	Leu	Ala	Phe		
		35					40					45					
Lys	Gln	Asp	Met	Lys	Lys	Glu	Val	Ile	Phe	Val	Ile	Thr	Lys	Ser	Asn		
	50					55					60						
Lys	Leu	Ser	Lys	Lys	Val	Leu	Cys	Asp	Phe	Asp	Ala	Phe	Leu	Leu	Pro		
65					70					75					80		
Glu	Thr	Leu	Met	Ser	Gly	Met	Pro	Lys	Lys	Ala	Leu	Phe	His	Lys	Glu		
			85						90					95			
Phe	Leu	Phe	Gln	Ser	Lys	Glu	Asn	Lys	Thr	Leu	Tyr	Ala	Phe	Ser	Leu		
			100					105					110				
Ile	Asp	Ser	Gln	Tyr	Cys	Ser	Lys	Gly	Gly	Asn	Tyr	Arg	Tyr	Glu	Leu		
	115						120					125					
Glu	Lys	Leu	Glu	Arg	Trp	Phe	Val	Gln	Lys	Ala	Pro	Glu	Leu	Ala	Glu		
	130					135					140						
Ser	Tyr	Arg	Val	Asn	Tyr	Lys	Asn	Gln	Tyr	Asn	Lys	Thr	Gln	Ile	Ser		
145					150					155					160		
Gln	Lys																

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 25...1548

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

TCTCACAAAA ATAAAGAATG AGCG ATG ATT TTA GTA TTA GAT TTT GGG AGT	51
Met Ile Leu Val Leu Asp Phe Gly Ser	
1 5	
CAA TAC ACA CAG CTG ATT GCT AGA AGA TTG AGA GAG AGA GGG ATT TAT	99
Gln Tyr Thr Gln Leu Ile Ala Arg Arg Leu Arg Glu Arg Gly Ile Tyr	
10 15 20 25	
ACA GAA ATA GTC CCT TTT TTT GAA AGC ATA GAA AAC ATT CAA AAA AAA	147
Thr Glu Ile Val Pro Phe Phe Glu Ser Ile Glu Asn Ile Gln Lys Lys	
30 35 40	
GCC CCC AAA GGT TTG ATT TTG AGT GGG GGG CCA GCG AGC GTG TAT GCT	195
Ala Pro Lys Gly Leu Ile Leu Ser Gly Gly Pro Ala Ser Val Tyr Ala	
45 50 55	
AAA GAC GCT TAC AAG CCT AGT GGG AAA ATC TTT GAT TTG AAT GTG CCG	243
Lys Asp Ala Tyr Lys Pro Ser Gly Lys Ile Phe Asp Leu Asn Val Pro	
60 65 70	
ATT TTA GGG ATT TGC TAC GGC ATG CAG TAT TTG GTG GAT TTT TTT GGG	291
Ile Leu Gly Ile Cys Tyr Gly Met Gln Tyr Leu Val Asp Phe Phe Gly	
75 80 85	
GGG GTA GTG GTT GGT GCG AAT GAG CAA GAA TTT GGT AAG GCT GTT TTA	339
Gly Val Val Val Gly Ala Asn Glu Gln Glu Phe Gly Lys Ala Val Leu	
90 95 100 105	
GAA ATC ACT CAA AAT TCT GTG ATT TTT GAA GGC GTG AAG ATT AAA AGC	387
Glu Ile Thr Gln Asn Ser Val Ile Phe Glu Gly Val Lys Ile Lys Ser	
110 115 120	
CTT GTG TGG ATG AGC CAT ATG GAT AAA GTC ATA GAA CTG CCT AAA GGC	435
Leu Val Trp Met Ser His Met Asp Lys Val Ile Glu Leu Pro Lys Gly	
125 130 135	
TTT ACT ACC CTT GCA AAA AGC CCT AAT TCC CCC CAT TGC GCG ATT GAA	483
Phe Thr Thr Leu Ala Lys Ser Pro Asn Ser Pro His Cys Ala Ile Glu	
140 145 150	
AAC GGC AAG ATT TTT GGC TTG CAA TTC CAC CCA GAA GTC GTT CAA AGC	531
Asn Gly Lys Ile Phe Gly Leu Gln Phe His Pro Glu Val Val Gln Ser	
155 160 165	
GAA GAA GGG GGT AAG ATT TTA GAA AAT TTT GCC CTT TTA GTT TGC GGC	579
Glu Glu Gly Gly Lys Ile Leu Glu Asn Phe Ala Leu Leu Val Cys Gly	

170	175	180	185	
TGT GAA AAA ACT	TGG GGG ATG CAG CAT	TTC GCT CAA AGA GAA ATC GCA	627	
Cys Glu Lys Thr	Trp Gly Met Gln His	Phe Ala Gln Arg Glu Ile Ala		
	190	195 200		
CGA TTG AAA GAA AAA ATC	GCT AAC GCT AAG GTT TTG TGC GCG GTG AGT	675		
Arg Leu Lys Glu Lys Ile Ala Asn Ala Lys Val Leu Cys Ala Val Ser				
	205 210	215		
GGG GGC GTG GAT TCT ACG GTG GTC GCT ACG CTG TTG CAC AGA GCC ATT	723			
Gly Gly Val Asp Ser Thr Val Val Ala Thr Leu Leu His Arg Ala Ile				
	220 225 230			
AAG GAT AAT TTG ATC GCT GTT TTT GTG GAT CAT GGC TTG TTG CGT AAA	771			
Lys Asp Asn Leu Ile Ala Val Phe Val Asp His Gly Leu Leu Arg Lys				
	235 240 245			
AAT GAA AAA GAA AGG GTG CAA GCG ATG TTT AAG GAC TTG AAA ATC CCT	819			
Asn Glu Lys Glu Arg Val Gln Ala Met Phe Lys Asp Leu Lys Ile Pro				
	250 255 260 265			
TTA AAC ACG ATA GAC GCT AAA GAA GTC TTT TTG TCT AAA TTA AAG GGC	867			
Leu Asn Thr Ile Asp Ala Lys Glu Val Phe Leu Ser Lys Leu Lys Gly				
	270 275 280			
GTG AGC GAG CCT GAA TTG AAG CGA AAA ATC ATC GGC GAG ACC TTT ATT	915			
Val Ser Glu Pro Glu Leu Lys Arg Lys Ile Ile Gly Glu Thr Phe Ile				
	285 290 295			
GAA GTG TTT GAA AAA GAA GCC AAA AAG CAC CAT TTA AAA GGC AAA ATT	963			
Glu Val Phe Glu Lys Glu Ala Lys Lys His His Leu Lys Gly Lys Ile				
	300 305 310			
GAA TTT TTA GCC CAA GGC ACT TTA TAC CCT GAT GTG ATT GAA TCC GTG	1011			
Glu Phe Leu Ala Gln Gly Thr Leu Tyr Pro Asp Val Ile Glu Ser Val				
	315 320 325			
AGC GTT AAA GGG CCT TCA AAA GTG ATC AAA ACC CAT CAT AAT GTG GGC	1059			
Ser Val Lys Gly Pro Ser Lys Val Ile Lys Thr His His Asn Val Gly				
	330 335 340 345			
GGA CTG CCT GAA TGG ATG GAT TTT AAA CTC ATA GAG CCT TTA AGG GAG	1107			
Gly Leu Pro Glu Trp Met Asp Phe Lys Leu Ile Glu Pro Leu Arg Glu				
	350 355 360			
TTG TTT AAA GAT GAG GTG CGC TTA CTG GGT AAA GAA TTG GGC GTT AGT	1155			
Leu Phe Lys Asp Glu Val Arg Leu Leu Gly Lys Glu Leu Gly Val Ser				
	365 370 375			
CAG GAT TTT TTA ATG CGC CAC CCT TTT CCA GGG CCT GGG CTT GCT GTA	1203			
Gln Asp Phe Leu Met Arg His Pro Phe Pro Gly Pro Gly Leu Ala Val				
	380 385 390			
AGG ATT TTA GGC GAA ATC AGT GAG AGT AAG ATC AAA CGC TTG CAA GAA	1251			
Arg Ile Leu Gly Glu Ile Ser Glu Ser Lys Ile Lys Arg Leu Gln Glu				
	395 400 405			

GCG GAT TTT ATT TTT ATA GAG GAA CTT AAA AAA GCC AAT TTG TAT GAC	1299
Ala Asp Phe Ile Phe Ile Glu Glu Leu Lys Lys Ala Asn Leu Tyr Asp	
410 415 420 425	
AAG GTT TGG CAA GCT TTT TGC GTG CTG TTG AAT GTC AAT TCT GTG GGG	1347
Lys Val Trp Gln Ala Phe Cys Val Leu Leu Asn Val Asn Ser Val Gly	
430 435 440	
GTT ATG GGG GAT AAC CGC ACT TAT GAA AAC GCT ATT TGC TTA AGA GCG	1395
Val Met Gly Asp Asn Arg Thr Tyr Glu Asn Ala Ile Cys Leu Arg Ala	
445 450 455	
GTA AAT GCG AGC GAT GGC ATG ACG GCG AGC TTT TCA TTT TTA GAG CAT	1443
Val Asn Ala Ser Asp Gly Met Thr Ala Ser Phe Ser Phe Leu Glu His	
460 465 470	
TCT TTT TTA GAA AAG GTT TCT AAC CGT ATC ACT AAT GAA GTG AGC GGT	1491
Ser Phe Leu Glu Lys Val Ser Asn Arg Ile Thr Asn Glu Val Ser Gly	
475 480 485	
ATC AAT AGG GTG GTG TAT GAC ATT ACC TCT AAA CCA CCA GGA ACG ATT	1539
Ile Asn Arg Val Val Tyr Asp Ile Thr Ser Lys Pro Pro Gly Thr Ile	
490 495 500 505	
GAA TGG GAA TGATTATCTT AAAAAATAGC ACTA	1572
Glu Trp Glu	

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

Met	Ile	Leu	Val	Leu	Asp	Phe	Gly	Ser	Gln	Tyr	Thr	Gln	Leu	Ile	Ala
1				5					10					15	
Arg	Arg	Leu	Arg	Glu	Arg	Gly	Ile	Tyr	Thr	Glu	Ile	Val	Pro	Phe	Phe
			20					25					30		
Glu	Ser	Ile	Glu	Asn	Ile	Gln	Lys	Lys	Ala	Pro	Lys	Gly	Leu	Ile	Leu
		35				40						45			
Ser	Gly	Gly	Pro	Ala	Ser	Val	Tyr	Ala	Lys	Asp	Ala	Tyr	Lys	Pro	Ser
	50					55				60					
Gly	Lys	Ile	Phe	Asp	Leu	Asn	Val	Pro	Ile	Leu	Gly	Ile	Cys	Tyr	Gly
65				70				75					80		
Met	Gln	Tyr	Leu	Val	Asp	Phe	Phe	Gly	Gly	Val	Val	Val	Gly	Ala	Asn
			85					90					95		
Glu	Gln	Glu	Phe	Gly	Lys	Ala	Val	Leu	Glu	Ile	Thr	Gln	Asn	Ser	Val
			100					105					110		
Ile	Phe	Glu	Gly	Val	Lys	Ile	Lys	Ser	Leu	Val	Trp	Met	Ser	His	Met
		115					120					125			
Asp	Lys	Val	Ile	Glu	Leu	Pro	Lys	Gly	Phe	Thr	Thr	Leu	Ala	Lys	Ser

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 26...808
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

AAAAACCCCC	ACGCTATGGT	AAATC	ATG	CTC	ATT	TGT	AAC	GAT	AAA	TCC	AAT	52
			Met	Leu	Ile	Cys	Asn	Asp	Lys	Ser	Asn	
			1				5					
CCA AAA ACC CTT TTA GAA GAA ATC ATG GCG TTA AGG CCA TGG CGT AAA	100											
Pro Lys Thr Leu Leu Glu Glu Ile Met Ala Leu Arg Pro Trp Arg Lys												
10 15 20 25												
GGC CCT TTT GAA ATT TCT CAA ATC AAG ATT GAT AGC GAA TGG GAT AGC	148											
Gly Pro Phe Glu Ile Ser Gln Ile Lys Ile Asp Ser Glu Trp Asp Ser												
30 35 40												
TCC ATT AAA TGG GAT CTA GTT AAA AAC GCC ACT CCT TTA AAA GAT AAG	196											
Ser Ile Lys Trp Asp Leu Val Lys Asn Ala Thr Pro Leu Lys Asp Lys												
45 50 55												
GTT GTG GCT GAT GTG GGT TGC AAT AAC GGC TAT TAC TTG TTT AAA ATG	244											
Val Val Ala Asp Val Gly Cys Asn Asn Gly Tyr Tyr Leu Phe Lys Met												
60 65 70												
CTA GAA CAT GGG CCT AAA AGT TTG GTG GGG TTT GAT CCG GGC GTT TTA	292											
Leu Glu His Gly Pro Lys Ser Leu Val Gly Phe Asp Pro Gly Val Leu												
75 80 85												
GTC AAA AAA CAA TTT GAA TTT TTA GCC CCC TTT TTT GAT AAA GAA AAA	340											
Val Lys Lys Gln Phe Glu Phe Leu Ala Pro Phe Phe Asp Lys Glu Lys												
90 95 100 105												
AAA ATC ATT TAT GAG TCT TTG GGG GTA GAG GAT TTG CAT GAA AAA TAC	388											
Lys Ile Ile Tyr Glu Ser Leu Gly Val Glu Asp Leu His Glu Lys Tyr												
110 115 120												
CCT AAC GCT TTT GAT GTC ATT TTT TGC TTA GGG GTG CTA TAC CAC AGA	436											
Pro Asn Ala Phe Asp Val Ile Phe Cys Leu Gly Val Leu Tyr His Arg												
125 130 135												
AAA AGC CCG CTA GAG GCT TTA AAA GCC TTG TAT CAC GCT TTG AAA ATA	484											
Lys Ser Pro Leu Glu Ala Leu Lys Ala Leu Tyr His Ala Leu Lys Ile												
140 145 150												
AAA GGG GAG CTG GTG TTG GAT ACC TTA ATC ATT GAT TCG CCC TTA GAC	532											
Lys Gly Glu Leu Val Leu Asp Thr Leu Ile Ile Asp Ser Pro Leu Asp												
155 160 165												
ATC GCC CTT TGC CCT AAA AAA ACT TAT GCT AAA ATG AAA AAT GTT TAT	580											
Ile Ala Leu Cys Pro Lys Lys Thr Tyr Ala Lys Met Lys Asn Val Tyr												
170 175 180 185												
TTT ATC CCC AGT GTT AGC GCG TTA AAA GGG TGG TGC GAA AGG GTA GGG	628											
Phe Ile Pro Ser Val Ser Ala Leu Lys Gly Trp Cys Glu Arg Val Gly												
190 195 200												

TTT GAA AAT TTT GAG ATT CTT AGC GTT TTA AAG ACC ACG CCT AAA GAA	676
Phe Glu Asn Phe Glu Ile Leu Ser Val Leu Lys Thr Thr Pro Lys Glu	
205 210 215	
CAG CGT AAA ACG GAT TTT ATT TTG GGG CAG AGT TTG GAA GAT TTT TTG	724
Gln Arg Lys Thr Asp Phe Ile Leu Gly Gln Ser Leu Glu Asp Phe Leu	
220 225 230	
GAT AAA ACA GAT CCC TCT AAA ACT TTA GAG GGG TAT GAC GCC CCT TTA	772
Asp Lys Thr Asp Pro Ser Lys Thr Leu Glu Gly Tyr Asp Ala Pro Leu	
235 240 245	
AGG GGG TAT TTT AAA ATG CTT AAA CCA AGC AAG CGT TAAATAAAGG ATTAAG	824
Arg Gly Tyr Phe Lys Met Leu Lys Pro Ser Lys Arg	
250 255 260	
ATAGTGCAAG	834

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

Met	Leu	Ile	Cys	Asn	Asp	Lys	Ser	Asn	Pro	Lys	Thr	Leu	Leu	Glu	Glu
1				5				10						15	
Ile	Met	Ala	Leu	Arg	Pro	Trp	Arg	Lys	Gly	Pro	Phe	Glu	Ile	Ser	Gln
		20						25					30		
Ile	Lys	Ile	Asp	Ser	Glu	Trp	Asp	Ser	Ser	Ile	Lys	Trp	Asp	Leu	Val
		35					40					45			
Lys	Asn	Ala	Thr	Pro	Leu	Lys	Asp	Lys	Val	Val	Ala	Asp	Val	Gly	Cys
		50				55				60					
Asn	Asn	Gly	Tyr	Tyr	Leu	Phe	Lys	Met	Leu	Glu	His	Gly	Pro	Lys	Ser
65					70					75				80	
Leu	Val	Gly	Phe	Asp	Pro	Gly	Val	Leu	Val	Lys	Lys	Gln	Phe	Glu	Phe
			85					90						95	
Leu	Ala	Pro	Phe	Phe	Asp	Lys	Glu	Lys	Lys	Ile	Ile	Tyr	Glu	Ser	Leu
			100					105					110		
Gly	Val	Glu	Asp	Leu	His	Glu	Lys	Tyr	Pro	Asn	Ala	Phe	Asp	Val	Ile
		115					120					125			
Phe	Cys	Leu	Gly	Val	Leu	Tyr	His	Arg	Lys	Ser	Pro	Leu	Glu	Ala	Leu
		130					135				140				
Lys	Ala	Leu	Tyr	His	Ala	Leu	Lys	Ile	Lys	Gly	Glu	Leu	Val	Leu	Asp
145					150					155				160	
Thr	Leu	Ile	Ile	Asp	Ser	Pro	Leu	Asp	Ile	Ala	Leu	Cys	Pro	Lys	Lys
				165				170						175	
Thr	Tyr	Ala	Lys	Met	Lys	Asn	Val	Tyr	Phe	Ile	Pro	Ser	Val	Ser	Ala
			180					185					190		
Leu	Lys	Gly	Trp	Cys	Glu	Arg	Val	Gly	Phe	Glu	Asn	Phe	Glu	Ile	Leu
		195					200					205			
Ser	Val	Leu	Lys	Thr	Thr	Pro	Lys	Glu	Gln	Arg	Lys	Thr	Asp	Phe	Ile
		210				215					220				

Leu Gly Gln Ser Leu Glu Asp Phe Leu Asp Lys Thr Asp Pro Ser Lys
 225 230 235 240
 Thr Leu Glu Gly Tyr Asp Ala Pro Leu Arg Gly Tyr Phe Lys Met Leu
 245 250 255
 Lys Pro Ser Lys Arg
 260

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 31...1197
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

TTAAATTCAA TTTTAAAGAA GAGTAGTTAA	ATG GTT ATT GTT TTA GTC GTG GAT	54
	Met Val Ile Val Leu Val Val Asp	
	1 5	
AGT TTT AAA GAC ACC AGT AAT GGC ACT TCT ATG ACA GCG TTT CGT TTT		102
Ser Phe Lys Asp Thr Ser Asn Gly Thr Ser Met Thr Ala Phe Arg Phe		
10 15 20		
TTT GAA GCG CTG AAA AAA AGA GGG CAT GTG ATG AGA GTG GTC GCC CCT		150
Phe Glu Ala Leu Lys Lys Arg Gly His Val Met Arg Val Val Ala Pro		
25 30 35 40		
CAT GTG GAT AAT TTA GGG AGT GAA GAA GAG GGG TAT TAC AAC CTT AAA		198
His Val Asp Asn Leu Gly Ser Glu Glu Gly Tyr Tyr Asn Leu Lys		
45 50 55		
GAG CGC TAC ATC CCC CTA GTT ACA GAA ATT TCA CAC AAA CAA CAC ATC		246
Glu Arg Tyr Ile Pro Leu Val Thr Glu Ile Ser His Lys Gln His Ile		
60 65 70		
CTT TTT GCT AAA CCC GAT GAA AAA ATC TTA AGA AAG GCT TTT AAG GGA		294
Leu Phe Ala Lys Pro Asp Glu Lys Ile Leu Arg Lys Ala Phe Lys Gly		
75 80 85		
GCG GAT ATG ATC CAT ACT TAT TTG CCT TTT TTG CTA GAA AAA ACA GCC		342
Ala Asp Met Ile His Thr Tyr Leu Pro Phe Leu Leu Glu Lys Thr Ala		
90 95 100		
GTA AAA ATC GCG CGA GAA ATG CAA GTG CCT TAT ATT GGC TCT TTC CAT		390
Val Lys Ile Ala Arg Glu Met Gln Val Pro Tyr Ile Gly Ser Phe His		
105 110 115 120		
TTA CAG CCA GAG CAT ATT TCT TAT AAC ATG AAA TTG GGG TGG TTT TCT		438

GAA AAT TCA GTC ATT CAA ATT GAA AAA GTT TAT GAA GAA GCG ATC AGA 1158
 Glu Asn Ser Val Ile Gln Ile Glu Lys Val Tyr Glu Glu Ala Ile Arg
 365 370 375

GAT TTT AAA AAT AAC CCC CAT CTC TTT AAA ACC TTA TCA TAATGAAAGG AT 1209
 Asp Phe Lys Asn Asn Pro His Leu Phe Lys Thr Leu Ser
 380 385

AAAAAATGCA AGAAG 1224

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

Met	Val	Ile	Val	Leu	Val	Val	Asp	Ser	Phe	Lys	Asp	Thr	Ser	Asn	Gly
1				5					10					15	
Thr	Ser	Met	Thr	Ala	Phe	Arg	Phe	Phe	Glu	Ala	Leu	Lys	Lys	Arg	Gly
			20					25					30		
His	Val	Met	Arg	Val	Val	Ala	Pro	His	Val	Asp	Asn	Leu	Gly	Ser	Glu
		35					40					45			
Glu	Glu	Gly	Tyr	Tyr	Asn	Leu	Lys	Glu	Arg	Tyr	Ile	Pro	Leu	Val	Thr
	50					55					60				
Glu	Ile	Ser	His	Lys	Gln	His	Ile	Leu	Phe	Ala	Lys	Pro	Asp	Glu	Lys
65					70					75				80	
Ile	Leu	Arg	Lys	Ala	Phe	Lys	Gly	Ala	Asp	Met	Ile	His	Thr	Tyr	Leu
				85					90					95	
Pro	Phe	Leu	Leu	Glu	Lys	Thr	Ala	Val	Lys	Ile	Ala	Arg	Glu	Met	Gln
			100					105					110		
Val	Pro	Tyr	Ile	Gly	Ser	Phe	His	Leu	Gln	Pro	Glu	His	Ile	Ser	Tyr
		115					120					125			
Asn	Met	Lys	Leu	Gly	Trp	Phe	Ser	Trp	Phe	Asn	Met	Met	Leu	Phe	Ser
	130					135				140					
Trp	Phe	Lys	Ser	Ser	His	Tyr	Arg	Tyr	Ile	His	His	Ile	His	Cys	Pro
145					150					155				160	
Ser	Lys	Phe	Ile	Val	Glu	Glu	Leu	Glu	Lys	Tyr	Asn	Tyr	Gly	Gly	Lys
				165					170					175	
Lys	Tyr	Ala	Ile	Ser	Asn	Gly	Phe	Asp	Pro	Met	Phe	Arg	Phe	Glu	His
			180					185					190		
Pro	Gln	Lys	Ser	Leu	Phe	Asp	Thr	Thr	Pro	Phe	Lys	Ile	Ala	Met	Val
		195					200					205			
Gly	Arg	Tyr	Ser	Asn	Glu	Lys	Asn	Gln	Ser	Val	Leu	Ile	Lys	Ala	Val
	210					215					220				
Ala	Leu	Ser	Lys	Tyr	Lys	Gln	Asp	Ile	Val	Leu	Leu	Leu	Lys	Gly	Lys
225					230					235				240	
Gly	Pro	Asp	Glu	Lys	Lys	Ile	Lys	Leu	Leu	Ala	Gln	Lys	Leu	Gly	Val
				245				250						255	
Lys	Ala	Glu	Phe	Gly	Phe	Val	Asn	Ser	Asn	Glu	Leu	Leu	Glu	Ile	Leu
			260				265						270		
Lys	Thr	Cys	Thr	Leu	Tyr	Val	His	Ala	Ala	Asn	Val	Glu	Ser	Glu	Ala
		275					280					285			

Ile	Ala	Cys	Leu	Glu	Ala	Ile	Ser	Val	Gly	Ile	Val	Pro	Val	Ile	Ala
290						295					300				
Asn	Ser	Pro	Leu	Ser	Ala	Thr	Arg	Gln	Phe	Ala	Leu	Asp	Glu	Arg	Ser
305					310					315					320
Leu	Phe	Glu	Pro	Asn	Ala	Lys	Asp	Leu	Ser	Ala	Lys	Ile	Asp	Trp	
				325				330					335		
Trp	Leu	Glu	Asn	Lys	Leu	Glu	Arg	Glu	Arg	Met	Gln	Asn	Glu	Tyr	Ala
			340					345					350		
Lys	Ser	Ala	Leu	Asn	Tyr	Thr	Leu	Glu	Asn	Ser	Val	Ile	Gln	Ile	Glu
		355					360					365			
Lys	Val	Tyr	Glu	Glu	Ala	Ile	Arg	Asp	Phe	Lys	Asn	Asn	Pro	His	Leu
	370					375					380				
Phe	Lys	Thr	Leu	Ser											
385															

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 947 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 16...903
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

TAGAAAAGGT	AGTTT	ATG	GAG	TTA	GAA	GAA	ATT	GTT	GAT	AGT	GAG	AGG	AAT		51	
	Met	Glu	Leu	Glu	Glu	Ile	Val	Asp	Ser	Glu	Arg	Asn				
	1					5					10					
ATC	CAT	AAG	ACT	ATA	GAA	GTT	TTA	GGA	AAA	GGC	GGA	CAG	GGT	ATA	GTG	99
Ile	His	Lys	Thr	Ile	Glu	Val	Leu	Gly	Lys	Gly	Gly	Gln	Gly	Ile	Val	
	15					20					25					
TAT	CGC	TGT	TTG	GAT	AAG	GAT	GTG	GCT	ATT	AAG	GTA	GTA	TTG	AGG	GAT	147
Tyr	Arg	Cys	Leu	Asp	Lys	Asp	Val	Ala	Ile	Lys	Val	Val	Leu	Arg	Asp	
	30				35					40						
GGA	GAT	TTT	ATT	AAA	GAC	AAA	GAA	TCC	CTC	AAA	CAA	TAT	GAA	AAA	AGC	195
Gly	Asp	Phe	Ile	Lys	Asp	Lys	Glu	Ser	Leu	Lys	Gln	Tyr	Glu	Lys	Ser	
	45				50				55					60		
GTT	CTA	AAC	TTA	TCT	TTT	AAG	CCG	ATA	GAG	AGT	CAT	TTC	CCT	ATG	TCA	243
Val	Leu	Asn	Leu	Ser	Phe	Lys	Pro	Ile	Glu	Ser	His	Phe	Pro	Met	Ser	
			65					70					75			
ATT	CCA	CTG	GTA	ACT	TTG	AAA	GAA	AAA	CAA	GGC	TAT	GTG	ATG	AAA	ATG	291
Ile	Pro	Leu	Val	Thr	Leu	Lys	Glu	Lys	Gln	Gly	Tyr	Val	Met	Lys	Met	
			80					85					90			
GCT	GAG	GGC	TAT	GAA	CCA	CTA	AAA	ACT	TTT	TTA	AAG	AAG	CCC	AGC	ATT	339

Ala	Glu	Gly	Tyr	Glu	Pro	Leu	Lys	Thr	Phe	Leu	Lys	Lys	Pro	Ser	Ile		
		95					100					105					
TTA	GAA	AAC	GAA	GAA	AAA	GAT	GGG	ATT	TTT	AGG	ATC	AAT	AAT	GCC	ATT	387	
Leu	Glu	Asn	Glu	Glu	Lys	Asp	Gly	Ile	Phe	Arg	Ile	Asn	Asn	Ala	Ile		
	110					115					120						
CAA	GAA	CTT	TGC	AAA	GAT	AAC	CAT	TAT	ATG	ACT	TTA	AGT	TTA	AGT	TAT	435	
Gln	Glu	Leu	Cys	Lys	Asp	Asn	His	Tyr	Met	Thr	Leu	Ser	Leu	Ser	Tyr		
	125				130					135					140		
TAC	TCA	CAA	ACA	CAA	GGA	TTG	AGA	TCA	CGA	TTA	AAA	ATA	CTC	ACC	CAT	483	
Tyr	Ser	Gln	Thr		Gln	Gly	Leu	Arg	Ser	Arg	Leu	Lys	Ile	Leu	Thr	His	
				145					150						155		
TTA	GCA	AAA	CTT	CTA	TTC	AGA	TTG	CAA	AGT	AAG	GGT	TTG	GTG	TAT	GGG	531	
Leu	Ala	Lys	Leu	Leu	Phe	Arg	Leu	Gln	Ser	Lys	Gly	Leu	Val	Tyr	Gly		
			160					165					170				
GAC	TTG	AAT	TTA	AAC	AAT	GTT	TTT	TAT	AAA	GAC	AAT	TCA	GCG	TTT	TTA	579	
Asp	Leu	Asn	Leu	Asn	Asn	Val	Phe	Tyr	Lys	Asp	Asn	Ser	Ala	Phe	Leu		
		175					180					185					
ATT	GAT	GCG	GAT	AAT	GTG	CGT	TAT	GAG	AGC	GAA	AAA	GCC	CTG	TGT	GTT	627	
Ile	Asp	Ala	Asp	Asn	Val	Arg	Tyr	Glu	Ser	Glu	Lys	Ala	Leu	Cys	Val		
	190					195					200						
ATT	TTT	ACG	CCT	AAC	TAT	GGG	GCT	TTA	GAG	ATT	AGC	CAA	ACC	TCT	AAA	675	
Ile	Phe	Thr	Pro	Asn	Tyr	Gly	Ala	Leu	Glu	Ile	Ser	Gln	Thr	Ser	Lys		
	205				210					215					220		
AAT	AGC	GAT	ACA	ACC	AAT	TAC	AAC	ACC	ATG	CTT	AGC	GAT	ACC	TTT	TCT	723	
Asn	Ser	Asp	Thr	Thr	Asn	Tyr	Asn	Thr	Met	Leu	Ser	Asp	Thr	Phe	Ser		
				225					230					235			
TTT	GCT	ATC	ATA	ACT	TAT	GAA	CTT	TTA	AAT	ATG	GTT	CAT	CCT	TTT	GAT	771	
Phe	Ala	Ile	Ile	Thr	Tyr	Glu	Leu	Leu	Asn	Met	Val	His	Pro	Phe	Asp		
			240					245					250				
GGG	AAT	AAG	GCA	GAT	GAT	AGT	GTA	GAA	AAT	TTT	ATA	GAA	TTG	CCT	TGG	819	
Gly	Asn	Lys	Ala	Asp	Asp	Ser	Val	Glu	Asn	Phe	Ile	Glu	Leu	Pro	Trp		
		255					260					265					
ATT	GAA	GAT	AGA	AAG	GAT	GAT	AGC	AAT	CGT	TCT	TGT	GGC	TTA	CTG	CCT	867	
Ile	Glu	Asp	Arg	Lys	Asp	Asp	Ser	Asn	Arg	Ser	Cys	Gly	Leu	Leu	Pro		
	270					275					280						
TTT	TTC	TTA	ACA	AGG	GAT	TTA	AAA	AAT	TTA	TTA	GCG	TAATGCTTTG	AAGAAG			919	
Phe	Phe	Leu	Thr	Arg	Asp	Leu	Lys	Asn	Leu	Leu	Ala						
	285				290				295								
GCAAAAAAGA	TCCTTTGAAA	CGCCCTAC														947	

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 296 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

Met	Glu	Leu	Glu	Glu	Ile	Val	Asp	Ser	Glu	Arg	Asn	Ile	His	Lys	Thr
1				5					10					15	
Ile	Glu	Val	Leu	Gly	Lys	Gly	Gly	Gln	Gly	Ile	Val	Tyr	Arg	Cys	Leu
			20					25					30		
Asp	Lys	Asp	Val	Ala	Ile	Lys	Val	Val	Leu	Arg	Asp	Gly	Asp	Phe	Ile
		35				40						45			
Lys	Asp	Lys	Glu	Ser	Leu	Lys	Gln	Tyr	Glu	Lys	Ser	Val	Leu	Asn	Leu
	50					55					60				
Ser	Phe	Lys	Pro	Ile	Glu	Ser	His	Phe	Pro	Met	Ser	Ile	Pro	Leu	Val
65					70				75					80	
Thr	Leu	Lys	Glu	Lys	Gln	Gly	Tyr	Val	Met	Lys	Met	Ala	Glu	Gly	Tyr
				85					90					95	
Glu	Pro	Leu	Lys	Thr	Phe	Leu	Lys	Lys	Pro	Ser	Ile	Leu	Glu	Asn	Glu
			100					105					110		
Glu	Lys	Asp	Gly	Ile	Phe	Arg	Ile	Asn	Asn	Ala	Ile	Gln	Glu	Leu	Cys
		115					120					125			
Lys	Asp	Asn	His	Tyr	Met	Thr	Leu	Ser	Leu	Ser	Tyr	Tyr	Ser	Gln	Thr
	130					135					140				
Gln	Gly	Leu	Arg	Ser	Arg	Leu	Lys	Ile	Leu	Thr	His	Leu	Ala	Lys	Leu
145					150					155				160	
Leu	Phe	Arg	Leu	Gln	Ser	Lys	Gly	Leu	Val	Tyr	Gly	Asp	Leu	Asn	Leu
				165					170					175	
Asn	Asn	Val	Phe	Tyr	Lys	Asp	Asn	Ser	Ala	Phe	Leu	Ile	Asp	Ala	Asp
		180						185					190		
Asn	Val	Arg	Tyr	Glu	Ser	Glu	Lys	Ala	Leu	Cys	Val	Ile	Phe	Thr	Pro
		195					200					205			
Asn	Tyr	Gly	Ala	Leu	Glu	Ile	Ser	Gln	Thr	Ser	Lys	Asn	Ser	Asp	Thr
	210					215					220				
Thr	Asn	Tyr	Asn	Thr	Met	Leu	Ser	Asp	Thr	Phe	Ser	Phe	Ala	Ile	Ile
225					230					235				240	
Thr	Tyr	Glu	Leu	Leu	Asn	Met	Val	His	Pro	Phe	Asp	Gly	Asn	Lys	Ala
				245					250					255	
Asp	Asp	Ser	Val	Glu	Asn	Phe	Ile	Glu	Leu	Pro	Trp	Ile	Glu	Asp	Arg
			260					265					270		
Lys	Asp	Asp	Ser	Asn	Arg	Ser	Cys	Gly	Leu	Leu	Pro	Phe	Phe	Leu	Thr
	275						280					285			
Arg	Asp	Leu	Lys	Asn	Leu	Leu	Ala								
290						295									

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 509 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 44...469
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

ATGCTTTGAA	GAAGGCAAAA	AAGATCCTTT	GAAACGCCCT	ACT	ATG	CCC	TTA	TTT	55
					Met	Pro	Leu	Phe	
					1				
ATA GAG AGC TTA GAA AAA GCT AGC TTG CAA GTG TTA GAA TGT GAA AAT	103								
Ile Glu Ser Leu Glu Lys Ala Ser Leu Gln Val Leu Glu Cys Glu Asn									
5 10 15 20									
TGT TCA ATG ACT TAT TAT GAT AGA GAT TAT AAT AGA GAA TGT GAG ATT	151								
Cys Ser Met Thr Tyr Tyr Asp Arg Asp Tyr Asn Arg Glu Cys Glu Ile									
25 30 35									
TGC CCT TAT TGC GAT GCT AAA AAA CCT GTC AGA CTT GTA GCA ACA AGT	199								
Cys Pro Tyr Cys Asp Ala Lys Lys Pro Val Arg Leu Val Ala Thr Ser									
40 45 50									
TAT TAC CAA AAG AGC GAA GTT TTT TAT TTT GTC TCG AAT TTT ACA GAC	247								
Tyr Tyr Gln Lys Ser Glu Val Phe Tyr Phe Val Ser Asn Phe Thr Asp									
55 60 65									
CCT ATT TTT TTA CCG ACA ACC TTA TTT AAG GGG ATT GAA GTG GTT AAA	295								
Pro Ile Phe Leu Pro Thr Thr Leu Phe Lys Gly Ile Glu Val Val Lys									
70 75 80									
AGC GAA TGG GAG TTT GCA GAG ATT GCT AAT AAT ATA TTG ATT TTT CAT	343								
Ser Glu Trp Glu Phe Ala Glu Ile Ala Asn Asn Ile Leu Ile Phe His									
85 90 95 100									
CAT GAC ATA CAA CAA GAA AAG ATT CTC ATT AAT AAT AAA AGA TTG GAT	391								
His Asp Ile Gln Gln Glu Lys Ile Leu Ile Asn Asn Lys Arg Leu Asp									
105 110 115									
CAC TAT AGG ATA GAA ATA GAT TTA GAA AAA GAA TTG ACT ATT TCA TAC	439								
His Tyr Arg Ile Glu Ile Asp Leu Glu Lys Glu Leu Thr Ile Ser Tyr									
120 125 130									
AAT GGT TTT TTA ATT AAG GTT CAA AAA TGC TGAGTTTAT CAAAGAAGAT AGC	492								
Asn Gly Phe Leu Ile Lys Val Gln Lys Cys									
135 140									
ATCATCAAGG CTTATAA	509								

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

Met	Pro	Leu	Phe	Ile	Glu	Ser	Leu	Glu	Lys	Ala	Ser	Leu	Gln	Val	Leu
1				5					10					15	
Glu	Cys	Glu	Asn	Cys	Ser	Met	Thr	Tyr	Tyr	Asp	Arg	Asp	Tyr	Asn	Arg
			20					25					30		
Glu	Cys	Glu	Ile	Cys	Pro	Tyr	Cys	Asp	Ala	Lys	Lys	Pro	Val	Arg	Leu
		35					40					45			
Val	Ala	Thr	Ser	Tyr	Tyr	Gln	Lys	Ser	Glu	Val	Phe	Tyr	Phe	Val	Ser
		50				55					60				
Asn	Phe	Thr	Asp	Pro	Ile	Phe	Leu	Pro	Thr	Thr	Leu	Phe	Lys	Gly	Ile
65					70				75						80
Glu	Val	Val	Lys	Ser	Glu	Trp	Glu	Phe	Ala	Glu	Ile	Ala	Asn	Asn	Ile
			85					90					95		
Leu	Ile	Phe	His	His	Asp	Ile	Gln	Gln	Glu	Lys	Ile	Leu	Ile	Asn	Asn
			100				105						110		
Lys	Arg	Leu	Asp	His	Tyr	Arg	Ile	Glu	Ile	Asp	Leu	Glu	Lys	Glu	Leu
		115					120					125			
Thr	Ile	Ser	Tyr	Asn	Gly	Phe	Leu	Ile	Lys	Val	Gln	Lys	Cys		
		130				135					140				

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 27...1193
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

AATGGTTTTT TAATTAAGGT TCAAAA ATG CTG AGT TTT ATC AAA GAA GAT AGC	53
Met Leu Ser Phe Ile Lys Glu Asp Ser	
1 5	
ATC ATC AAG GCT TAT AAC CTC AAT ACC GCA AAA CTA GAG CCA AAA GAT	101
Ile Ile Lys Ala Tyr Asn Leu Asn Thr Ala Lys Leu Glu Pro Lys Asp	
10 15 20 25	
AGA GAA AAA TTG GGA TTA TTA AAG ATT GAA AAA AAT AAA ATA TAT TTT	149
Arg Glu Lys Leu Gly Leu Leu Lys Ile Glu Lys Asn Lys Ile Tyr Phe	
30 35 40	
CAT CTA GAT GAA AAG CGT TAT TTG AAA TTA GAG ATC ATA GGC AAA ACC	197
His Leu Asp Glu Lys Arg Tyr Leu Lys Leu Glu Ile Ile Gly Lys Thr	
45 50 55	
AAA GAA AAA GAA ATT AAA AAC GCT TTT TGC AGT AAT GCT TTT CTT GCA	245
Lys Glu Lys Glu Ile Lys Asn Ala Phe Cys Ser Asn Ala Phe Leu Ala	
60 65 70	

GCT Ala	CAA Gln	GTC Val	CTA Leu	AAT Asn	TTA Leu	AAC Asn	CAA Gln	GAA Glu	AGA Arg	CAA Gln	GTT Val	TTA Leu	GAA Glu	TTG Leu	AAG Lys	293
758085																
TGC Cys	CAT His	TTC Phe	TTC Phe	AAG Lys	CAC His	CCT Pro	ATA Ile	AAA Lys	ATT Ile	CTT Leu	CCT Pro	GAA Glu	CCA Pro	TTA Leu	AAC Asn	341
9095100																
ATT Ile	AAT Asn	TTC Phe	AAA Lys	GAC Asp	ACA Thr	ATC Ile	ATA Ile	AAA Lys	AAG Lys	TTA Leu	CTA Leu	AAA Lys	GAT Asp	ATG Met	GGC Gly	389
110115120																
AAA Lys	GAT Asp	AAA Lys	AAA Lys	ATA Ile	GAA Glu	GAT Asp	TTT Phe	AAA Lys	GAA Glu	ACT Thr	TGT Cys	ATT Ile	TTA Leu	AAA Lys	ATA Ile	437
125130135																
GCT Ala	GGT Gly	TTT Phe	ACT Thr	TAT Tyr	TTT Phe	GTG Val	TGC Cys	GTA Val	TTG Leu	CCT Pro	TAT Tyr	GAA Glu	TAT Tyr	GAG Glu	AAT Asn	485
140145150																
AAA Lys	GAG Glu	GAT Asp	AAA Lys	GAG Glu	AAT Asn	AGT Ser	GAA Glu	GAG Glu	ATT Ile	TTA Leu	AAA Lys	GAA Glu	GAT Asp	TTC Phe	AGG Arg	533
155160165																
CTG Leu	TTA Leu	AAT Asn	ACC Thr	AAG Lys	GGG Gly	GGA Gly	TTA Leu	AGC Ser	GTT Val	AAG Lys	CGT Arg	GCT Ala	TTG Leu	ATA Ile	AAT Asn	581
170175180185																
AAC Asn	AGG Arg	CAT His	TCT Ser	TAT Tyr	GAA Glu	GCG Ala	ATA Ile	AAA Lys	TTA Leu	AGA Arg	CCC Pro	ATT Ile	AAA Lys	CAA Gln	GAG Glu	629
190195200																
TTA Leu	GTG Val	CCT Pro	GGT Gly	TTG Leu	TGT Cys	TTG Leu	TTT Phe	TTT Phe	CAA Gln	GGT Gly	TCA Ser	TTA Leu	GAA Glu	TTT Phe	AAT Asn	677
205210215																
GAT Asp	AAA Lys	ACC Thr	ACA Thr	AAA Lys	ACC Thr	ATG Met	CGA Arg	ACG Thr	AGC Ser	CTT Leu	TTA Leu	GAC Asp	CAG Gln	ATC Ile	CAG Gln	725
220225230																
CAA Gln	GAT Asp	GAC Asp	AAA Lys	TCT Ser	TAT Tyr	TTA Leu	AAA Lys	ATT Ile	TGG Trp	GAA Glu	AAA Lys	TAT Tyr	CTC Leu	ATC Ile	AAA Lys	773
235240245																
AGC Ser	GCT Ala	CAA Gln	AAA Lys	AGT Ser	TTT Phe	AAT Asn	GAG Glu	GCA Ala	AAA Lys	GAA Glu	GTG Val	GGG Gly	GTT Val	TTA Leu	GAG Glu	821
250255260265																
ATT Ile	GAA Glu	AGC Ser	GTG Val	AGT Ser	AAA Lys	GAA Glu	GGA Gly	GGG Gly	AAT Asn	TTA Leu	AGA Arg	ATT Ile	CGT Arg	TTT Phe	AAG Lys	869
270275280																
CCA Pro	GCT Ala	TTA Leu	GGC Gly	AAG Lys	AAT Asn	AAA Lys	ATG Met	GAA Glu	ATC Ile	TTA Leu	AAG Lys	AAA Lys	TCA Ser	CAA Gln	TTT Phe	917
285290295																
AAA Lys	AAG Lys	GGG Gly	AGT Ser	GAT Asp	TTA Leu	GGG Gly	GTT Val	TTA Leu	GAG Glu	GAT Asp	TTA Leu	GAC Asp	CCA Pro	CAA Gln	AAT Asn	965

ATT Ile 45	GAA Glu	AAT Asn	GAA Glu	TTA Leu	AAG Lys 50	CAA Gln	TTA Leu	GAA Glu	AAC Asn	AAA Lys 55	GAA Glu	AAT Asn	CTT Leu	AAA Lys	GCA Ala 60	195
GAC Asp	AAC Asn	AAC Asn	ACA Thr	GAA Glu 65	TTT Phe	AAA Lys	GAA Glu	GAA Glu	AAT Asn 70	CAA Gln	GAC Asp	ACT Thr	AAA Lys	GAA Glu 75	AAC Asn	243
CAG Gln	CCT Pro	AAC Asn	GAT Asp 80	TTG Leu	TTT Phe	TCT Ser	TTG Leu	CCA Pro 85	TTG Leu	CCC Pro	ACT Thr	CAA Gln 90	ACC Thr	ACC Thr	ATC Ile	291
AAT Asn	GGA Gly	ATT Ile 95	AAA Lys	GAA Glu	TTT Phe	GTA Val 100	GAA Glu	GAG Glu	CCT Pro	GTG Val	ATA Ile	GAA Glu 105	ACA Thr	GAG Glu	AAA Lys	339
AAA Lys 110	GAA Glu	ACA Thr	TCC Ser	CAA Gln	AAT Asn	GAG Glu 115	CCA Pro	ATC Ile	CAA Gln	GAA Glu 120	AAA Lys	AAA Lys	GAA Glu	AGA Arg	ATT Ile	387
TTT Phe 125	AAA Lys	AAC Asn	TTT Phe	TTC Phe	TCC Ser 130	AGA Arg	ATA Ile	GGC Gly	TTT Phe	GAT Asp 135	AAA Lys	AGT Ser	ATT Ile	GCC Ala	CCT Pro 140	435
ACA Thr	ATG Met	CTT Leu	TTT Phe	GAA Glu 145	GAA Glu	GTG Val	AGA Arg	GAT Asp	GCA Ala 150	AGC Ser	GTT Val	ATC Ile	TAT Tyr	CAT His 155	TTA Leu	483
GAG Glu	AAA Lys	AAA Lys	TTA Leu 160	GGC Gly	GAT Asp	TAT Tyr	ATC Ile	TTT Phe 165	TAT Tyr	GTA Val	GCG Ala	TGT Cys	TTC Phe 170	TTC Phe	TTT Phe	531
GGC Gly	ACA Thr	ACG Thr 175	GCA Ala	TTG Leu	CTT Leu	ATT Ile	ATC Ile 180	TTA Leu	CTG Leu	ACT Thr	ATT Ile	CTG Leu 185	TTG Leu	CCC Pro	TTA Leu	579
AAA Lys 190	CAA Gln	AAA Lys	GAG Glu	CCG Pro	TAT Tyr	TTA Leu 195	GTG Val	CAA Gln	TTT Phe	TCT Ser	AAC Asn 200	AAT Asn	AAA Lys	GAA Glu	AAT Asn	627
TTT Phe 205	GCT Ala	TTA Leu	GTT Val	CAA Gln 210	AAG Lys	GCA Ala	GAT Asp	AGC Ser	AGC Ser	ATT Ile 215	ACA Thr	GCC Ala	AAT Asn	AAA Lys	GCT Ala 220	675
CTT Leu	ATT Ile	CGT Arg	TCA Ser	TTA Leu 225	GTG Val	GGA Gly	GCG Ala	TAT Tyr	GTG Val 230	CTA Leu	AAC Asn	AGG Arg	GAA Glu	AGC Ser 235	ATT Ile	723
ACT Thr	CAT His	ATT Ile	GAG Glu 240	CAA Gln	CAT His	GAA Glu	AAA Lys	ATG Met 245	CGT Arg	CAA Gln	AAC Asn	ACC Thr	ATT Ile 250	AAA Lys	GAG Glu	771
CAA Gln	AGT Ser	TCC Ser 255	AAT Asn	GAA Glu	GTA Val	TGG Trp	TAT Tyr 260	GAA Glu	TTT Phe	GAA Glu	AAA Lys	CTC Leu 265	ATC Ile	GCT Ala	CAT His	819
TAT Tyr	GAC Asp	AGC Ser	ATT Ile	TAC Tyr	ACT Thr	AAT Asn	CCT Pro	TTA Leu	CTC Leu	ACA Thr	AGA Arg	AAA Lys	GTA Val	AAG Lys	ATT Ile	867

270	275	280	
GCA AAT ATT TAC TTA GAT AAA GAT TTA GCC TAT ATT GAC ATT GAA GTG			915
Ala Asn Ile Tyr Leu Asp Lys Asp Leu Ala Tyr Ile Asp Ile Glu Val			
285	290	295	300
AGC TTG TAT CAT AGT GGA GAA TTA GAG AGC TTG AAG CGC TAT AAA GTG			963
Ser Leu Tyr His Ser Gly Glu Leu Glu Ser Leu Lys Arg Tyr Lys Val			
	305	310	315
GTG ATG AGT TTT GAA TTT AAA AAA CAA GAA ATC AAT TTT GAC TCC ATG			1011
Val Met Ser Phe Glu Phe Lys Lys Gln Glu Ile Asn Phe Asp Ser Met			
	320	325	330
TCT TTA AAT CCT ACA GGC TTT ATG GTT ACA AGT TAT GAT GTA ACT GAA			1059
Ser Leu Asn Pro Thr Gly Phe Met Val Thr Ser Tyr Asp Val Thr Glu			
	335	340	345
ATT GCG ATT GTG AAT TAC CCA ACC GCT AAA GCG ATT GGG CTT TTT CTT			1107
Ile Ala Ile Val Asn Tyr Pro Thr Ala Lys Ala Ile Gly Leu Phe Leu			
	350	355	360
GCT TCA TAGCTCCATA ACTAGCTAGA TCCAATATGT TTCCATATTT AGAACTAACC CC			1165
Ala Ser			
365			
GTTAGAGGAA GCTCCACAAG			1185

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

Met	Ser	Lys	Arg	Ser	Glu	Val	Leu	Glu	Gln	Phe	His	Gly	Gly	Leu	Lys
1				5					10					15	
Asn	Leu	Glu	Leu	Gln	Thr	Lys	Arg	Arg	Met	Gly	Leu	Trp	Gly	Asp	Pro
			20					25					30		
Lys	Glu	Asn	Glu	Glu	Gln	Thr	Leu	Phe	Leu	Glu	Glu	Ile	Glu	Asn	Glu
		35					40					45			
Leu	Lys	Gln	Leu	Glu	Asn	Lys	Glu	Asn	Leu	Lys	Ala	Asp	Asn	Asn	Thr
		50				55				60					
Glu	Phe	Lys	Glu	Glu	Asn	Gln	Asp	Thr	Lys	Glu	Asn	Gln	Pro	Asn	Asp
65					70				75					80	
Leu	Phe	Ser	Leu	Pro	Leu	Pro	Thr	Gln	Thr	Thr	Ile	Asn	Gly	Ile	Lys
			85					90					95		
Glu	Phe	Val	Glu	Glu	Pro	Val	Ile	Glu	Thr	Glu	Lys	Lys	Glu	Thr	Ser
			100					105					110		
Gln	Asn	Glu	Pro	Ile	Gln	Glu	Lys	Lys	Glu	Arg	Ile	Phe	Lys	Asn	Phe
		115				120						125			
Phe	Ser	Arg	Ile	Gly	Phe	Asp	Lys	Ser	Ile	Ala	Pro	Thr	Met	Leu	Phe
		130				135					140				

GGG CAT TCT ATT AGC GTT CAT TCT ACC GAT GAA TAT TTC ATC CAA ACA	198
Gly His Ser Ile Ser Val His Ser Thr Asp Glu Tyr Phe Ile Gln Thr	
40 45 50	
GAT GAA GAG GGT ATC AGG CAT TAT GTT GTT GAT AAA AAG AAA CTC AAT	246
Asp Glu Glu Gly Ile Arg His Tyr Val Val Asp Lys Lys Lys Leu Asn	
55 60 65 70	
GAA TAC CAC CAA AAC AAT CAA GAA GCC TTC AAA CAA GCT TTA GAA AAT	294
Glu Tyr His Gln Asn Asn Gln Glu Ala Phe Lys Gln Ala Leu Glu Asn	
75 80 85	
CGT ATA GAT ATT GTA GTG TGC GAT AAC ACC AAT TTT GAA TCG TGG CAA	342
Arg Ile Asp Ile Val Val Cys Asp Asn Thr Asn Phe Glu Ser Trp Gln	
90 95 100	
AGC AAA CCA TAT ACA GAT ATG GCT AGA GAA TTT GGC TAT AAA ATT TTG	390
Ser Lys Pro Tyr Thr Asp Met Ala Arg Glu Phe Gly Tyr Lys Ile Leu	
105 110 115	
TTG ATT GAT TTT AAG AAT AGA CAC TTA GAA ACC CCC ATG GAT TAT GGA	438
Leu Ile Asp Phe Lys Asn Arg His Leu Glu Thr Pro Met Asp Tyr Gly	
120 125 130	
TGG GAT GTT GCG CAA TGC ATC AAG AAG CCA CGA GGT ATT GCA AAG CAT	486
Trp Asp Val Ala Gln Cys Ile Lys Lys Pro Arg Gly Ile Ala Lys His	
135 140 145 150	
TAT GAC TAT GAT TTT TAT TTG GAG AGG GTT TTG GTT GAG CCA CAG GAT	534
Tyr Asp Tyr Asp Phe Tyr Leu Glu Arg Val Leu Val Glu Pro Gln Asp	
155 160 165	
TAT GAG AAA CAA AAT AGA GAG TTG AGC TTA AAA GCC TTA GAA TTT TTG	582
Tyr Glu Lys Gln Asn Arg Glu Leu Ser Leu Lys Ala Leu Glu Phe Leu	
170 175 180	
AAA TAC AAT TTT GAT TTT GAT GTG ATT TTT TAT TCT TTT GGG GAG CAA	630
Lys Tyr Asn Phe Asp Phe Asp Val Ile Phe Tyr Ser Phe Gly Glu Gln	
185 190 195	
TTA ATG CCT ATT CTT ACT AGA ATG TTA GTT TCT GTC TCT AAG TCT CAT	678
Leu Met Pro Ile Leu Thr Arg Met Leu Val Ser Val Ser Lys Ser His	
200 205 210	
AGA AAG AGA CTT GAA AAC TAT GGC AAA GAC ATT AAA ACC TAATTTAGAT AA	729
Arg Lys Arg Leu Glu Asn Tyr Gly Lys Asp Ile Lys Thr	
215 220 225	
AGATGAGTTA AACACA	745

(2) INFORMATION FOR SEQ ID NO:584:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 227 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

Met Gly Gln Lys Arg Met Asn Lys Ser Asn Lys Leu Val Ile Ile Asn
1 5 10 15
Arg Ala Ile Pro Gly Gly Gly Lys Thr Ser Leu Ile Lys Gln Ile Glu
20 25 30
Glu Leu Ala Lys Ser Leu Gly His Ser Ile Ser Val His Ser Thr Asp
35 40 45
Glu Tyr Phe Ile Gln Thr Asp Glu Glu Gly Ile Arg His Tyr Val Val
50 55 60
Asp Lys Lys Lys Leu Asn Glu Tyr His Gln Asn Asn Gln Glu Ala Phe
65 70 75 80
Lys Gln Ala Leu Glu Asn Arg Ile Asp Ile Val Val Cys Asp Asn Thr
85 90 95
Asn Phe Glu Ser Trp Gln Ser Lys Pro Tyr Thr Asp Met Ala Arg Glu
100 105 110
Phe Gly Tyr Lys Ile Leu Leu Ile Asp Phe Lys Asn Arg His Leu Glu
115 120 125
Thr Pro Met Asp Tyr Gly Trp Asp Val Ala Gln Cys Ile Lys Lys Pro
130 135 140
Arg Gly Ile Ala Lys His Tyr Asp Tyr Asp Phe Tyr Leu Glu Arg Val
145 150 155 160
Leu Val Glu Pro Gln Asp Tyr Glu Lys Gln Asn Arg Glu Leu Ser Leu
165 170 175
Lys Ala Leu Glu Phe Leu Lys Tyr Asn Phe Asp Phe Asp Val Ile Phe
180 185 190
Tyr Ser Phe Gly Glu Gln Leu Met Pro Ile Leu Thr Arg Met Leu Val
195 200 205
Ser Val Ser Lys Ser His Arg Lys Arg Leu Glu Asn Tyr Gly Lys Asp
210 215 220
Ile Lys Thr
225

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...468
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

ATTTACTAAA GGAAAACA ATG ATT AAA CTA ATC TTA CAC AAG AAG TCC ATA 51
Met Ile Lys Leu Ile Leu His Lys Lys Ser Ile
1 5 10
CAA ATT GAT GAA ACA TTG CTG AAT GTA AAA GAG CAT TTA GAA AAG TTT 99

Gln	Ile	Asp	Glu	Thr	Leu	Leu	Asn	Val	Lys	Glu	His	Leu	Glu	Lys	Phe		
			15					20					25				
TAT	TCA	AAT	AAA	GAA	CAA	GAG	ACA	ATC	GCT	CAA	ACT	TTA	GAG	AAT	GAA		147
Tyr	Ser	Asn	Lys	Glu	Gln	Glu	Thr	Ile	Ala	Gln	Thr	Leu	Glu	Asn	Glu		
		30					35					40					
ACA	GAA	ATT	TCT	TGT	AGC	TAT	TTT	TGG	GAC	AAA	GAC	TTC	TTG	TTG	TTA		195
Thr	Glu	Ile	Ser	Cys	Ser	Tyr	Phe	Trp	Asp	Lys	Asp	Phe	Leu	Leu	Leu		
	45					50					55						
GAG	CAA	CTT	TTA	GAA	AAT	RAT	TTA	GGT	CAT	TTT	ACC	TTT	GAG	AGC	GAG		243
Glu	Gln	Leu	Leu	Glu	Asn	Xaa	Leu	Gly	His	Phe	Thr	Phe	Glu	Ser	Glu		
60					65					70					75		
TTT	GCC	CTA	CTA	AAA	GAT	AAA	GAG	ACT	TTA	AAC	CTA	TCT	CAA	ATC	AAA		291
Phe	Ala	Leu	Leu	Lys	Asp	Lys	Glu	Thr	Leu	Asn	Leu	Ser	Gln	Ile	Lys		
				80					85					90			
CAA	ATC	GGT	GTC	TTA	AAG	GTT	CTT	ACC	TAT	GAR	ATG	ATA	CAA	ACC	TTA		339
Gln	Ile	Gly	Val	Leu	Lys	Val	Leu	Thr	Tyr	Xaa	Met	Ile	Gln	Thr	Leu		
			95					100					105				
AAA	AAT	CAA	ATC	ATT	CAT	TTA	GCA	CAA	GTT	GTC	AAT	GAA	GAA	AAT	TTA		387
Lys	Asn	Gln	Ile	Ile	His	Leu	Ala	Gln	Val	Val	Asn	Glu	Glu	Asn	Leu		
		110					115					120					
GAA	AAA	GAT	GAA	GAA	CTT	GTT	GTC	TAC	CAC	CTA	AAT	TTC	ACG	TCA	CGC		435
Glu	Lys	Asp	Glu	Glu	Leu	Val	Val	Tyr	His	Leu	Asn	Phe	Thr	Ser	Arg		
	125					130					135						
AAC	AAT	CTT	ACA	AAA	TAT	TAT	CCA	AGT	TCT	GTG	TGATTAAAAA	AGAAAGAAAT					488
Asn	Asn	Leu	Thr	Lys	Tyr	Tyr	Pro	Ser	Ser	Val							
140					145					150							
ATCGCATGAA	AAAATTAAGT	CATTTTAGAA	AGCTTATCGC	CTT													531

(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

Met	Ile	Lys	Leu	Ile	Leu	His	Lys	Lys	Ser	Ile	Gln	Ile	Asp	Glu	Thr		
1				5					10					15			
Leu	Leu	Asn	Val	Lys	Glu	His	Leu	Glu	Lys	Phe	Tyr	Ser	Asn	Lys	Glu		
		20						25					30				
Gln	Glu	Thr	Ile	Ala	Gln	Thr	Leu	Glu	Asn	Glu	Thr	Glu	Ile	Ser	Cys		
		35					40					45					
Ser	Tyr	Phe	Trp	Asp	Lys	Asp	Phe	Leu	Leu	Leu	Glu	Gln	Leu	Leu	Glu		
	50					55					60						
Asn	Xaa	Leu	Gly	His	Phe	Thr	Phe	Glu	Ser	Glu	Phe	Ala	Leu	Leu	Lys		

65		70		75		80
Asp	Lys	Glu	Thr	Leu	Asn	Leu
		85		90		95
Lys	Val	Leu	Thr	Xaa	Met	Ile
		100		105		110
His	Leu	Ala	Gln	Val	Val	Asn
		115		120		125
Leu	Val	Val	Tyr	His	Leu	Asn
		130		135		140
Tyr	Tyr	Pro	Ser	Ser	Val	
145					150	

(2) INFORMATION FOR SEQ ID NO:587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...294
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

CTGGTTTATG AGTATTTTTT AAAAGAAGTC CCC ATG CAA TTA GTT GGT ATT TCA	54
Met Gln Leu Val Gly Ile Ser	
1 5	
GTT TCT AAT CTC AAA GAA ATC AGC TCC AAA GAA AAA TTT CTT TGG CTC	102
Val Ser Asn Leu Lys Glu Ile Ser Ser Lys Glu Lys Phe Leu Trp Leu	
10 15 20	
AAT GCT AAG AGT TTT TTA CTC TCA GGA TTT GTG CCT TTT ATT ATG ATA	150
Asn Ala Lys Ser Phe Leu Leu Ser Gly Phe Val Pro Phe Ile Met Ile	
25 30 35	
CCT TGG CTA GAT ATA TTG AAC TCT TTT GTG CTT TAT GTG TGC TTT CTC	198
Pro Trp Leu Asp Ile Leu Asn Ser Phe Val Leu Tyr Val Cys Phe Leu	
40 45 50 55	
TTA ATT TTT AGC ATA GCG GAG TTC TTT GAT GAA GAT ATA AGT GAC ATT	246
Leu Ile Phe Ser Ile Ala Glu Phe Phe Asp Glu Asp Ile Ser Asp Ile	
60 65 70	
TTA ATC GCT CAT TCC AAA ATT AAA ACC AAA GCT AAT TCA TTT TAC GCT T	295
Leu Ile Ala His Ser Lys Ile Lys Thr Lys Ala Asn Ser Phe Tyr Ala	
75 80 85	
AAAAGGAAAA AATATGCAAA AAGAAGTCTT AGTAGAAAA	334

(2) INFORMATION FOR SEQ ID NO:588:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

```

Met Gln Leu Val Gly Ile Ser Val Ser Asn Leu Lys Glu Ile Ser Ser
 1           5           10           15
Lys Glu Lys Phe Leu Trp Leu Asn Ala Lys Ser Phe Leu Leu Ser Gly
      20           25           30
Phe Val Pro Phe Ile Met Ile Pro Trp Leu Asp Ile Leu Asn Ser Phe
      35           40           45
Val Leu Tyr Val Cys Phe Leu Leu Ile Phe Ser Ile Ala Glu Phe Phe
      50           55           60
Asp Glu Asp Ile Ser Asp Ile Leu Ile Ala His Ser Lys Ile Lys Thr
      65           70           75           80
Lys Ala Asn Ser Phe Tyr Ala
              85
  
```

(2) INFORMATION FOR SEQ ID NO:589:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 995 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 37...948
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

```

TAAAAACACC CCTAAAAGAA AAAGAAAGTC TTCTTA ATG TTA GAA AGC GCC CTT      54
                               Met Leu Glu Ser Ala Leu
                               1           5

AAA TAT TGC AAG GAA AAA GCC ATA GAC CTT TTA GTA GGG TTT GTG CCA      102
Lys Tyr Cys Lys Glu Lys Ala Ile Asp Leu Leu Val Gly Phe Val Pro
      10           15           20

AAA ACC TAT TCT ATG GCA CAA GAG TGC AAT ATT TTA GGC TTG TAT GAT      150
Lys Thr Tyr Ser Met Ala Gln Glu Cys Asn Ile Leu Gly Leu Tyr Asp
      25           30           35

GAT GCT TTC ATT ATT ACC AAA CAA GAA AAT CTA GTA GGC ATT ATA TCC      198
Asp Ala Phe Ile Ile Thr Lys Gln Glu Asn Leu Val Gly Ile Ile Ser
      40           45           50

TTA CAA GGA CTA AGC TAT TCT AAT TTA ATG CAA AAA GAC TTA GAG GGC      246
  
```

Leu 55	Gln	Gly	Leu	Ser	Tyr 60	Ser	Asn	Leu	Met	Gln 65	Lys	Asp	Leu	Glu	Gly 70	
TAT Tyr	TTT Phe	GAT Asp	GCT Ala	AGA Arg	CAA Gln	AAT Asn	GTT Val	CTC Leu	AAC Asn	ACC Thr	ATT Ile	AGT Ser	AAA Lys	GAC Asp	ATT Ile	294
				75				80						85		
CAA Gln	TTA Leu	AGA Arg	ATT Ile	GTG Val	GCT Ala	AAA Lys	AGG Arg	CGT Arg	AAG Lys	GAA Glu	TTT Phe	ATC Ile	AAT Asn	CAA Gln	AGT Ser	342
			90					95					100			
CCA Pro	AAT Asn	ATT Ile	GAC Asp	AAT Asn	ATT Ile	TAT Tyr	GCC Ala	AAA Lys	GCT Ala	ATT Ile	ATC Ile	ACA Thr	CAA Gln	TTT Phe	GAA Glu	390
		105					110					115				
AGC Ser	AAG Lys	GGA Gly	ATC Ile	TAT Tyr	AAA Lys	ACA Thr	GAG Glu	TAT Tyr	TTT Phe	TTA Leu	GTG Val	TTT Phe	GAA Glu	ACT Thr	ATC Ile	438
	120				125						130					
ACT Thr	TCT Ser	AAT Asn	GTC Val	AAG Lys	TCT Ser	TTC Phe	TTT Phe	GAA Glu	AAA Lys	AAG Lys	AAA Lys	TTG Leu	GAA Glu	ATG Met	ACT Thr	486
135					140					145					150	
ACT Thr	TCA Ser	ATT Ile	AAT Asn	GAA Glu	GAG Glu	TTA Leu	GAA Glu	GAA Glu	AGC Ser	TCT Ser	AAA Lys	GAA Glu	GAT Asp	AAA Lys	CAA Gln	534
				155					160					165		
GAG Glu	AAT Asn	GAA Glu	AAT Asn	MGC Xaa	TCC Ser	AAT Asn	GAA Glu	ACT Thr	CAT His	TCA Ser	AAC Asn	ACA Thr	AGC Ser	TCT Ser	AAA Lys	582
			170					175					180			
AAA Lys	GAC Asp	AAG Lys	AAA Lys	AAC Asn	AAG Lys	TTC Phe	AAA Lys	AAA Lys	AAG Lys	ATA Ile	ACC Thr	TTT Phe	AGC Ser	ACC Thr	AAA Lys	630
		185					190					195				
AGT Ser	AAA Lys	AGA Arg	GCC Ala	TTA Leu	CTC Leu	ATT Ile	CAA Gln	ACC Thr	ATA Ile	GAA Glu	AGA Arg	GTA Val	AAA Lys	AAC Asn	GCT Ala	678
	200					205					210					
CTT Leu	AAA Lys	GAA Glu	TTT Phe	AAA Lys	CCC Pro	ACT Thr	TTA Leu	CTA Leu	AAT Asn	TCT Ser	AAA Lys	GAA Glu	GTA Val	TTA Leu	AAT Asn	726
215					220					225					230	
TTC Phe	TAC Tyr	GCA Ala	GAA Glu	TAC Tyr	ATC Ile	AAT Asn	GGC Gly	AAA Lys	TAC Tyr	ATC Ile	GCC Ala	TTT Phe	AAT Asn	CCT Pro	AAA Lys	774
				235					240					245		
TTA Leu	AAG Lys	CGA Arg	TTA Leu	AGC Ser	GAT Asp	ACT Thr	ATA Ile	TTG Leu	CAT His	CTA Leu	ATG Met	TGC Cys	ATT Ile	TTA Leu	AGA Arg	822
			250					255					260			
AAG Lys	ATT Ile	ACT Thr	TTG Leu	TCA Ser	TTG Leu	AAT Asn	TTC Phe	AAA Lys	ATC Ile	AAA Lys	ACA Thr	CCT Pro	TTT Phe	GTG Val	CGT Arg	870
		265					270					275				
GTG Val	TGG Trp	GGA Gly	TTA Leu	AGG Arg	CTT Leu	ATG Met	AGA Arg	GCG Ala	AAG Lys	AAA Lys	TTT Phe	CTT Leu	CGC Arg	TCC Ser	CTA Leu	918
	280					285					290					

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 39...1556
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

ATAATTATAT AGAATTAGTG CAAGCCAATC GTTTGAGC ATG CAA GAG TGT GCT TTA	56
Met Gln Glu Cys Ala Leu	
1 5	
AAC TTA GTT ATA AGG GCT AAA AGT AAA GCT AAA TTA GAC AAG TCT TTA	104
Asn Leu Val Ile Arg Ala Lys Ser Lys Ala Lys Leu Asp Lys Ser Leu	
10 15 20	
AAA GAG ATT TTA TCC TTG CTT AAT AAT GCT GGA CTA GGC AGT GTT ACA	152
Lys Glu Ile Leu Ser Leu Leu Asn Asn Ala Gly Leu Gly Ser Val Thr	
25 30 35	
GAA ACT ATA GGG CTA AAA CCA TCT TAT TTT TCA TTC TTC CCA AAT AAC	200
Glu Thr Ile Gly Leu Lys Pro Ser Tyr Phe Ser Phe Phe Pro Asn Asn	
40 45 50	
GCC AAT ATC AAC CCT AGA ATG AGA CAT CAA ACT TCC CAA GTC ATA GCA	248
Ala Asn Ile Asn Pro Arg Met Arg His Gln Thr Ser Gln Val Ile Ala	
55 60 65 70	
TCT TTG ATT TTG TTT GAG AAA AAT AAT ACA GGT TTT AGA GCA AAT TCT	296
Ser Leu Ile Leu Phe Glu Lys Asn Asn Thr Gly Phe Arg Ala Asn Ser	
75 80 85	
TGG GGG GAT ATG CCC TTA TCT GTG TTT AAG AAC CTA GAC CAT AGC CCT	344
Trp Gly Asp Met Pro Leu Ser Val Phe Lys Asn Leu Asp His Ser Pro	
90 95 100	
TAT TTG TTT AAT TTT CAT AAT CAA GAA GTC AAA CAT AAG GGC GTG TTA	392
Tyr Leu Phe Asn Phe His Asn Gln Glu Val Lys His Lys Gly Val Leu	
105 110 115	
GCC CAC AAT GTC GCA CGA GTA GTG GGA CAT ACC ATG ATT ATA GGA GCA	440
Ala His Asn Val Ala Arg Val Val Gly His Thr Met Ile Ile Gly Ala	
120 125 130	
ACA GGT GCT GGT AAA ACC ACA CTC ATT AGC TAT TTG ATG ATG AGT GCC	488
Thr Gly Ala Gly Lys Thr Thr Leu Ile Ser Tyr Leu Met Met Ser Ala	
135 140 145 150	
TTA AAA TAT TCT AAC ATT GAT ATT TTA GCT CTT GAT AGA CTA AAT GGT	536
Leu Lys Tyr Ser Asn Ile Asp Ile Leu Ala Leu Asp Arg Leu Asn Gly	

155					160					165						
TTG	TAT	TCC	TTT	ACC	AAG	TAT	TTT	GAT	GGG	ATT	TAT	AAT	CAA	GGC	GAA	584
Leu	Tyr	Ser	Phe	Thr	Lys	Tyr	Phe	Asp	Gly	Ile	Tyr	Asn	Gln	Gly	Glu	
			170					175					180			
AAC	TTT	CAT	ATT	AAC	CCT	TTT	TCA	TTA	GAA	GAT	AGC	GCA	ACT	AAT	AGA	632
Asn	Phe	His	Ile	Asn	Pro	Phe	Ser	Leu	Glu	Asp	Ser	Ala	Thr	Asn	Arg	
		185					190					195				
GCC	TTT	TTA	TTG	CAT	TTT	TAT	GCC	CAA	ATG	GCA	AAA	GTG	GAT	AGT	TAT	680
Ala	Phe	Leu	Leu	His	Phe	Tyr	Ala	Gln	Met	Ala	Lys	Val	Asp	Ser	Tyr	
	200					205					210					
GAT	GAC	CAT	AAG	GAT	AAA	GTA	GAA	GAT	AGA	ACA	GCC	CTT	TTA	AAT	GCT	728
Asp	Asp	His	Lys	Asp	Lys	Val	Glu	Asp	Arg	Thr	Ala	Leu	Leu	Asn	Ala	
215					220					225					230	
ATT	GAT	ACG	ATG	TAT	AGA	AAT	TAT	AAC	GAT	GAA	GTC	AAA	CAA	GCC	AAA	776
Ile	Asp	Thr	Met	Tyr	Arg	Asn	Tyr	Asn	Asp	Glu	Val	Lys	Gln	Ala	Lys	
				235					240					245		
TTT	AGC	AAC	CAA	GAA	TTA	CCC	CTT	CCT	TTT	GAT	TTA	AAA	GAG	TTT	GTC	824
Phe	Ser	Asn	Gln	Glu	Leu	Pro	Leu	Pro	Phe	Asp	Leu	Lys	Glu	Phe	Val	
			250					255					260			
AAT	GCC	ATT	GCT	AAA	ACC	AAT	ACA	GAC	ATT	TTA	GAT	AGT	AGT	TTT	GAA	872
Asn	Ala	Ile	Ala	Lys	Thr	Asn	Thr	Asp	Ile	Leu	Asp	Ser	Ser	Phe	Glu	
		265					270					275				
GAC	TAT	TTA	AAA	TCT	TCC	TTA	TTT	TCT	AGC	CGA	ATG	GAT	AGT	CTA	GAT	920
Asp	Tyr	Leu	Lys	Ser	Ser	Leu	Phe	Ser	Ser	Arg	Met	Asp	Ser	Leu	Asp	
	280					285					290					
TTT	AAA	ACT	CGT	ATT	AGC	ACC	ATA	AAT	ACC	GAT	AGC	ATT	TTA	CAT	AAT	968
Phe	Lys	Thr	Arg	Ile	Ser	Thr	Ile	Asn	Thr	Asp	Ser	Ile	Leu	His	Asn	
295					300					305					310	
GAT	GAT	GAC	GCT	GGG	CTT	TTA	GCC	TAC	TAT	GTC	TTT	CAT	AAG	ATG	ATT	1016
Asp	Asp	Asp	Ala	Gly	Leu	Leu	Ala	Tyr	Tyr	Val	Phe	His	Lys	Met	Ile	
				315					320					325		
GAC	AGA	GCC	TTA	AAA	ATC	AAT	CGT	GGG	TTT	TTA	TGC	TTT	ATT	GAT	GAG	1064
Asp	Arg	Ala	Leu	Lys	Ile	Asn	Arg	Gly	Phe	Leu	Cys	Phe	Ile	Asp	Glu	
			330					335					340			
TTT	AAG	TCT	TAC	GCT	CAA	AAT	GAA	ATG	ATG	AAT	AAA	AAA	ATC	AAT	GAA	1112
Phe	Lys	Ser	Tyr	Ala	Gln	Asn	Glu	Met	Met	Asn	Lys	Lys	Ile	Asn	Glu	
		345					350					355				
ATC	ATT	ACT	CAA	GCT	AGA	AAG	GCT	AAT	GGG	GTG	ATT	GTT	CTA	GCC	TTA	1160
Ile	Ile	Thr	Gln	Ala	Arg	Lys	Ala	Asn	Gly	Val	Ile	Val	Leu	Ala	Leu	
		360				365					370					
CAA	GAC	ATT	AAC	CAA	CTA	AGC	GAA	GTG	AGA	AAC	GCT	CAA	AGC	TTT	ATA	1208
Gln	Asp	Ile	Asn	Gln	Leu	Ser	Glu	Val	Arg	Asn	Ala	Gln	Ser	Phe	Ile	
375					380					385					390	

			100					105					110			
Lys	His	Lys	Gly	Val	Leu	Ala	His	Asn	Val	Ala	Arg	Val	Val	Gly	His	
		115						120				125				
Thr	Met	Ile	Ile	Gly	Ala	Thr	Gly	Ala	Gly	Lys	Thr	Thr	Leu	Ile	Ser	
	130					135					140					
Tyr	Leu	Met	Met	Ser	Ala	Leu	Lys	Tyr	Ser	Asn	Ile	Asp	Ile	Leu	Ala	
145					150					155					160	
Leu	Asp	Arg	Leu	Asn	Gly	Leu	Tyr	Ser	Phe	Thr	Lys	Tyr	Phe	Asp	Gly	
				165					170					175		
Ile	Tyr	Asn	Gln	Gly	Glu	Asn	Phe	His	Ile	Asn	Pro	Phe	Ser	Leu	Glu	
		180						185						190		
Asp	Ser	Ala	Thr	Asn	Arg	Ala	Phe	Leu	Leu	His	Phe	Tyr	Ala	Gln	Met	
		195					200					205				
Ala	Lys	Val	Asp	Ser	Tyr	Asp	Asp	His	Lys	Asp	Lys	Val	Glu	Asp	Arg	
	210					215					220					
Thr	Ala	Leu	Leu	Asn	Ala	Ile	Asp	Thr	Met	Tyr	Arg	Asn	Tyr	Asn	Asp	
225					230					235					240	
Glu	Val	Lys	Gln	Ala	Lys	Phe	Ser	Asn	Gln	Glu	Leu	Pro	Leu	Pro	Phe	
				245					250					255		
Asp	Leu	Lys	Glu	Phe	Val	Asn	Ala	Ile	Ala	Lys	Thr	Asn	Thr	Asp	Ile	
		260						265						270		
Leu	Asp	Ser	Ser	Phe	Glu	Asp	Tyr	Leu	Lys	Ser	Ser	Leu	Phe	Ser	Ser	
		275					280					285				
Arg	Met	Asp	Ser	Leu	Asp	Phe	Lys	Thr	Arg	Ile	Ser	Thr	Ile	Asn	Thr	
	290					295					300					
Asp	Ser	Ile	Leu	His	Asn	Asp	Asp	Asp	Ala	Gly	Leu	Leu	Ala	Tyr	Tyr	
305					310					315					320	
Val	Phe	His	Lys	Met	Ile	Asp	Arg	Ala	Leu	Lys	Ile	Asn	Arg	Gly	Phe	
				325					330					335		
Leu	Cys	Phe	Ile	Asp	Glu	Phe	Lys	Ser	Tyr	Ala	Gln	Asn	Glu	Met	Met	
			340					345					350			
Asn	Lys	Lys	Ile	Asn	Glu	Ile	Ile	Thr	Gln	Ala	Arg	Lys	Ala	Asn	Gly	
		355					360					365				
Val	Ile	Val	Leu	Ala	Leu	Gln	Asp	Ile	Asn	Gln	Leu	Ser	Glu	Val	Arg	
	370					375					380					
Asn	Ala	Gln	Ser	Phe	Ile	Lys	Asn	Met	Gly	Gln	Leu	Ile	Leu	Tyr	Pro	
385					390					395					400	
Gln	Arg	Asn	Ile	Asp	Thr	Lys	Asp	Leu	Asn	Asp	Lys	Phe	Gly	Ile	Arg	
				405					410					415		
Leu	Ser	Asp	Thr	Glu	Lys	His	Phe	Leu	Glu	Asn	Thr	Ala	Val	Asn	Glu	
			420					425					430			
Tyr	Lys	Val	Leu	Leu	Lys	Asn	Met	Asn	Asp	Gly	Ser	Ser	Asn	Ile	Ile	

```
(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 563 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
```

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 24...509

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

CAACTCTTTT TTAAGGGGGA CAC ATG TCT AAT TTG CAA GAA CTT AGA GAG CAT	53
Met Ser Asn Leu Gln Glu Leu Arg Glu His	
1 5 10	
TTA AAA GAA TTA GAA AAT TCC TTT GAA ATA GGC TCT TTT ACT AAA GAA	101
Leu Lys Glu Leu Glu Asn Ser Phe Glu Ile Gly Ser Phe Thr Lys Glu	
15 20 25	
AAT ATT AAA GAA TAC GCT AAA TGC TTT TTT ATG AGT TTA AGC ATG TTT	149
Asn Ile Lys Glu Tyr Ala Lys Cys Phe Phe Met Ser Leu Ser Met Phe	
30 35 40	
TTA GAA GAA CAA GAA AAA AAC CAA CAA GAA GAG TTT TTA GAA CAA GAT	197
Leu Glu Glu Gln Glu Lys Asn Gln Gln Glu Glu Phe Leu Glu Gln Asp	
45 50 55	
ACC AAA GAA AAT CAA GAA GAG CTC ATT AAA AAC ATT CAA ACA AGC ATT	245
Thr Lys Glu Asn Gln Glu Glu Leu Ile Lys Asn Ile Gln Thr Ser Ile	
60 65 70	
GCT AAA AAC CAA GAG TTA GAA AAA ATC TCT TTT GAA AAA TGG GAG AAT	293
Ala Lys Asn Gln Glu Leu Glu Lys Ile Ser Phe Glu Lys Trp Glu Asn	
75 80 85 90	
AAA ATT CAA GAA AGG GTT TTG CCT AAG TTA AAA CGC ATT GTT ACG CAT	341
Lys Ile Gln Glu Arg Val Leu Pro Lys Leu Lys Arg Ile Val Thr His	
95 100 105	
AAG TTG CAA GAA AGT ATC ACA TCT AGC ATA AAC ACG CAA TTA GAG AGT	389
Lys Leu Gln Glu Ser Ile Thr Ser Ser Ile Asn Thr Gln Leu Glu Ser	
110 115 120	
TTT AAA AAA GAT GAG TTA GAT TTA TCT AGC GTG TTT GAA ATC CAA AGA	437
Phe Lys Lys Asp Glu Leu Asp Leu Ser Ser Val Phe Glu Ile Gln Arg	
125 130 135	
AAG AAC ACT CAA ATA GCG TAT AGA TTA GCT ATA GGG GGG CTT ATA GGT	485
Lys Asn Thr Gln Ile Ala Tyr Arg Leu Ala Ile Gly Gly Leu Ile Gly	
140 145 150	
ATC ATT GCT TTA AGC TCG CAA ATT TGATTATTAA CTCTATACTT CACGCTTTTT	539
Ile Ile Ala Leu Ser Ser Gln Ile	
155 160	
AGCCTTTGTG TGTTCCTTTTG TAAA	563

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

```

Met Ser Asn Leu Gln Glu Leu Arg Glu His Leu Lys Glu Leu Glu Asn
 1           5           10           15
Ser Phe Glu Ile Gly Ser Phe Thr Lys Glu Asn Ile Lys Glu Tyr Ala
      20           25           30
Lys Cys Phe Phe Met Ser Leu Ser Met Phe Leu Glu Glu Gln Glu Lys
      35           40           45
Asn Gln Gln Glu Glu Phe Leu Glu Gln Asp Thr Lys Glu Asn Gln Glu
      50           55           60
Glu Leu Ile Lys Asn Ile Gln Thr Ser Ile Ala Lys Asn Gln Glu Leu
      65           70           75           80
Glu Lys Ile Ser Phe Glu Lys Trp Glu Asn Lys Ile Gln Glu Arg Val
      85           90           95
Leu Pro Lys Leu Lys Arg Ile Val Thr His Lys Leu Gln Glu Ser Ile
      100          105          110
Thr Ser Ser Ile Asn Thr Gln Leu Glu Ser Phe Lys Lys Asp Glu Leu
      115          120          125
Asp Leu Ser Ser Val Phe Glu Ile Gln Arg Lys Asn Thr Gln Ile Ala
      130          135          140
Tyr Arg Leu Ala Ile Gly Leu Ile Gly Ile Ala Leu Ser Ser
      145          150          155          160
Gln Ile

```

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...3186
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

```

CCTTAAATCT AAGGGGTGTG C ATG CCA TAC AAT GAA ATC ACA AGG GTT CAA      51
      Met Pro Tyr Asn Glu Ile Thr Arg Val Gln
      1           5           10
ATC CCT GCC TTA ATG CAT TTA GCC AAG TTG GGC TAT GAT TTT ATC CCC      99

```

Ile	Pro	Ala	Leu	Met	His	Leu	Ala	Lys	Leu	Gly	Tyr	Asp	Phe	Ile	Pro		
				15					20					25			
ACT	AAT	TCT	AAA	GAA	AAT	AAG	CCC	AAC	CTA	GAC	ACC	GCC	ACC	AAC	ATT	147	
Thr	Asn	Ser	Lys	Glu	Asn	Lys	Pro	Asn	Leu	Asp	Thr	Ala	Thr	Asn	Ile		
				30					35					40			
TTA	ACC	AAT	AGT	TTC	ACT	AAA	TCC	TTT	GAG	CGG	TTA	AAC	CCC	ACT	AAA	195	
Leu	Thr	Asn	Ser	Phe	Thr	Lys	Ser	Phe	Glu	Arg	Leu	Asn	Pro	Thr	Lys		
				45					50					55			
AAC	GCA	CAA	GAA	ACG	CTT	GCT	GAA	ATG	AAA	AAA	CGC	TTG	AAT	TGC	GAT	243	
Asn	Ala	Gln	Glu	Thr	Leu	Ala	Glu	Met	Lys	Lys	Arg	Leu	Asn	Cys	Asp		
				60					65					70			
GAT	TTG	GGC	AAA	AGC	TTT	TAT	GAA	TAC	TTG	CTC	AAA	AGC	GAG	AAT	CAA	291	
Asp	Leu	Gly	Lys	Ser	Phe	Tyr	Glu	Tyr	Leu	Leu	Lys	Ser	Glu	Asn	Gln		
				80					85					90			
ATC	ATA	GAC	TTT	GAT	AAC	CCT	AAC	AAC	AAT	CTT	TAT	GAA	ATG	ATG	ACT	339	
Ile	Ile	Asp	Phe	Asp	Asn	Pro	Asn	Asn	Asn	Leu	Tyr	Glu	Met	Met	Thr		
				95					100					105			
GAA	TTA	CCC	TAC	AAA	TCT	TTT	AGG	CCT	GAC	ACC	ACC	CTT	TTT	ATC	AAT	387	
Glu	Leu	Pro	Tyr	Lys	Ser	Phe	Arg	Pro	Asp	Thr	Thr	Leu	Phe	Ile	Asn		
				110					115					120			
GGC	TTG	CCT	TTG	GTG	AAT	ATA	GAA	GTT	AAA	CAG	CCT	TAC	GCC	AAA	AAA	435	
Gly	Leu	Pro	Leu	Val	Asn	Ile	Glu	Val	Lys	Gln	Pro	Tyr	Ala	Lys	Lys		
				125					130					135			
GGC	ATT	AAA	GAA	GAA	AGA	GAT	CGC	CAC	ATC	AAA	CGC	TAT	GAA	AAC	CCT	483	
Gly	Ile	Lys	Glu	Glu	Arg	Asp	Arg	His	Ile	Lys	Arg	Tyr	Glu	Asn	Pro		
				140					145					150			
GAA	AAC	AAA	GTT	TTT	TAT	AAT	CTC	GCG	CAA	ATC	TGG	CTT	TTT	AGC	GAT	531	
Glu	Asn	Lys	Val	Phe	Tyr	Asn	Leu	Ala	Gln	Ile	Trp	Leu	Phe	Ser	Asp		
				155					160					165			
AAC	TTA	CCC	TAT	GAT	GAA	AAC	AAA	CCC	GAT	CAA	GGC	GCG	TTT	TAT	AGC	579	
Asn	Leu	Pro	Tyr	Asp	Glu	Asn	Lys	Pro	Asp	Gln	Gly	Ala	Phe	Tyr	Ser		
				175					180					185			
GCT	TCT	TAT	TCG	CCC	ATT	TTC	CAA	CGC	TTT	GTT	GAA	GCT	CAT	AGG	CTA	627	
Ala	Ser	Tyr	Ser	Pro	Ile	Phe	Gln	Arg	Phe	Val	Glu	Ala	His	Arg	Leu		
				190					195					200			
GAT	ATT	WCC	CCC	SSN	CCC	CSC	CAA	AAA	AAT	GAT	CAA	AAT	CAT	CAA	AAC	675	
Asp	Ile	Xaa	Pro	Xaa	Pro	Xaa	Gln	Lys	Asn	Asp	Gln	Asn	His	Gln	Asn		
				205					210					215			
GAT	CAA	AAT	CAT	CGA	TCG	CTT	GAA	GAA	ATT	CAA	AAA	AGC	GTC	TTA	AAC	723	
Asp	Gln	Asn	His	Arg	Ser	Leu	Glu	Glu	Ile	Gln	Lys	Ser	Val	Leu	Asn		
				220					225					230			
GAA	TTT	AAC	CTT	AAA	GAC	ACC	GAC	ACC	CCA	AAA	AGC	CCT	AAA	GAC	ACC	771	
Glu	Phe	Asn	Leu	Lys	Asp	Thr	Asp	Thr	Pro	Lys	Ser	Pro	Lys	Asp	Thr		
				235					240					245			

CCC Pro	ACA Thr	AAC Asn	TCC Ser	CTT Leu 255	TTA Leu	ACT Thr	TCG Ser	TTT Phe 260	TGC Cys	TCT Ser	CCA Pro	AAA Lys	AGG Arg	CTT Leu 265	TGC Cys	819
TTT Phe	ATC Ile	CTA Leu	AAA Lys 270	TAC Tyr	GGC Gly	ATC Ile	AGT Ser	TTC Phe 275	TTA Leu	AAA Lys	GAA Glu	AAA Lys	TCA Ser 280	GAG Glu	TTT Phe	867
AAA Lys	AAA Lys	CAC His 285	GTT Val	TGG Trp	CGT Arg	TAT Tyr	GCG Ala 290	CAG Gln	ATG Met	TTT Phe	GCG Ala	AGC Ser 295	TTG Leu	AAC Asn	GTT Val	915
TTA Leu	AAA Lys 300	GAA Glu	TTG Leu	CAA Gln	AAG Lys	CAT His 305	TAT Tyr	GGA Gly	ACA Thr	AAC Asn	CAA Gln 310	AAC Asn	CTA Leu	AAA Lys	GAT Asp	963
CCC Pro 315	CTA Leu	AAA Lys	GGC Gly	ATC Ile	ATC Ile 320	TGG Trp	CAC His	ACG Thr	CAA Gln	GGC Gly 325	AGC Ser	GGT Gly	AAA Lys	ACC Thr	GCC Ala 330	1011
TTA Leu	ACC Thr	TAC Tyr	CAC His 335	TTA Leu	ACC Thr	AAA Lys	CTC Leu	ATC Ile 340	AGA Arg	GAC Asp	TTT Phe	TTT Phe	AGC Ser	CGA Arg 345	TCC Ser	1059
AAC Asn	CTA Leu	AAC Asn	AAA Lys 350	AAG Lys	ACT Thr	AAA Lys	TTT Phe	TAT Tyr 355	TTT Phe	ATT Ile	GTG Val	GAC Asp 360	AGG Arg	TTG Leu	GAT Asp	1107
TTA Leu	TTG Leu	GAG Glu 365	CAA Gln	GCC Ala	AAA Lys	AAC Asn	GAG Glu 370	TTT Phe	TTA Leu	AAA Lys	AGA Arg	GGC Gly 375	CTT Leu	TGT Cys	GTG Val	1155
CAT His 380	GAG Glu	GCA Ala	GAA Glu	AAT Asn	AAA Lys	GAG Glu 385	GAT Asp	TTG Leu	AGC Ser	CAA Gln 390	AAA Lys	TTA Leu	AAA Lys	AGC Ser	TCT Ser	1203
AGC Ser 395	GTT Val	TTT Phe	GAA Glu	GGC Gly 400	TCT Ser	CAA Gln	GGG Gly	AAT Asn	GAT Asp	GAA Glu 405	ATC Ile	ATC Ile	GTT Val	GTG Val	AAT Asn 410	1251
ATC Ile	CAA Gln	AAA Lys	TTC Phe	AAA Lys 415	GCC Ala	CCC Pro	AAT Asn	GAA Glu	GAA Glu 420	AAA Lys	TCC Ser	CCC Pro	AAT Asn	GAA Glu 425	GAC Asp	1299
CCC Pro	TCT Ser	AAT Asn	AGC Ser 430	GCT Ala	CCT Pro	AAA Lys	GAA Glu	ATC Ile 435	ATT Ile	TCT Ser	AAA Lys	ACA Thr	GAA Glu 440	TTA Leu	CAA Gln	1347
GAA Glu	TCC Ser	ATT Ile 445	CAA Gln	AAC Asn	AGC Ser	CGC Arg	AAT Asn 450	TTA Leu	CAA Gln	AGG Arg	GTG Val	TTT Phe 455	ATC Ile	ATA Ile	GAT Asp	1395
GAA Glu 460	GCC Ala	CAC His	AGG Arg	AGC Ser	TAC Tyr	GAT Asp 465	CCT Pro	AAA Lys	GGT Gly	TGC Cys	TTT Phe 470	TAC Tyr	GCT Ala	AAT Asn	TTG Leu	1443
ATA Ile	GAA Glu	TGC Cys	GAC Asp	AAG Lys	ACA Thr	GCA Ala	ATT Ile	AAA Lys	ATC Ile	GCC Ala	CTC Leu	ACA Thr	GGC Gly	ACG Thr	CCC Pro	1491

475				480				485				490				
CTA Leu	TTA Leu	GAA Glu	GAC Asp	AAC Asn 495	GCG Ala	CAA Gln	GAT Asp	AAA Lys	GCC Ala 500	ACT Thr	AAA Lys	AAC Asn	ACT Thr	TTT Phe 505	GGC Gly	1539
AAC Asn	TAC Tyr	TTG Leu	CAC His 510	ACC Thr	TAT Tyr	TCT Ser	TAT Tyr	ACA Thr 515	GAA Glu	TCC Ser	ATT Ile	AAA Lys	GAC Asp 520	AGA Arg	CAC His	1587
ACC Thr	CTA Leu	AAA Lys 525	CTC Leu	CAG Gln	TTA Leu	GAA Glu	AGC Ser 530	ATT Ile	GAA Glu	ACG Thr	AGC Ser	TAT Tyr 535	AAA Lys	GAA Glu	AAA Lys	1635
TTA Leu	CAA Gln 540	GAA Glu	ATC Ile	TAT Tyr	CGC Arg	CTT Leu 545	TTA Leu	CAA Gln	GAA Glu	AGC Ser	ATC Ile 550	ACT Thr	ATT Ile	GAA Glu	GAC Asp	1683
ACA Thr 555	GAA Glu	GTT Val	AAA Lys	AAA Lys	GAA Glu 560	ACG Thr	ATT Ile	TTT Phe	AAC Asn 565	GAT Asp	GAA Glu	AAA Lys	TAC Tyr	ATT Ile	AAC Asn 570	1731
GCC Ala	ATG Met	CTC Leu	TAT Tyr	TAT Tyr 575	ATC Ile	ATT Ile	AGA Arg	GAT Asp	TTA Leu 580	TTG Leu	GAT Asp	TTT Phe	AGG Arg	CGT Arg 585	TTG Leu	1779
AAT Asn	GAT Asp	AAT Asn	GAA Glu 590	CGC Arg	TTA Leu	AAG Lys	GCT Ala	ATG Met 595	GTG Val	GTT Val	TGT Cys	TTT Phe	TCT Ser 600	AGC Ser	AAG Lys	1827
CAA Gln	GCC Ala	AGA Arg 605	TTA Leu	GCT Ala	GAT Asp	TGT Cys	CTT Leu 610	TTT Phe	AAT Asn	GAA Glu	GTC Val	CAA Gln 615	GAA Glu	AAA Lys	GTC Val	1875
TTA Leu	CAA Gln 620	GAA Glu	AAC Asn	CCC Pro	AAC Asn	CTA Leu 625	AGG Arg	ATT Ile	TTA Leu	AAC Asn	AAA Lys 630	CTC Leu	AAA Lys	TCC Ser	AGC Ser	1923
CTG Leu 635	ATT Ile	TTG Leu	CAT His	GAT Asp 640	GAA Glu	CAA Gln	GAA Glu	GTC Val	AAA Lys	GAA Glu 645	AAG Lys	GTT Val	CAT His	TCT Ser	TTC Phe 650	1971
AAA Lys	CAT His	GAA Glu	GAT Asp	ACC Thr 655	GAT Asp	ATA Ile	GTC Val	TTT Phe	GTG Val 660	TTT Phe	AAC Asn	ATG Met	CTT Leu	TTA Leu 665	ACC Thr	2019
GGC Gly	TTT Phe	GAT Asp	TTA Leu 670	CCC Pro	AGT Ser	CTC Leu	AAA Lys	CGC Arg 675	CTT Leu	TAT Tyr	ATC Ile	CAC His	AGA Arg 680	GAA Glu	TTA Leu	2067
AAA Lys	GAT Asp	CAC His 685	AAT Asn	TTG Leu	CTC Leu	CAA Gln	GCC Ala 690	CTA Leu	GCC Ala	AGA Arg	GTG Val	AAT Asn 695	CGC Arg	TCC Ser	TAT Tyr	2115
AAA Lys	AAC Asn 700	ATG Met	TCT Ser	TTT Phe	GGC Gly	TAC Tyr 705	CTT Leu	ATA Ile	GAT Asp	TTT Phe 710	GTA Val	GGC Gly	ATT Ile	CAA Gln	GAA Glu	2163

AAT Asn 715	TTT Phe 715	GAC Asp 715	AAA Lys 715	ACG Thr 720	ACT Thr 720	GAT Asp 720	GAT Asp 720	TAC Tyr 720	TTG Leu 725	AAA Lys 725	GAA Glu 725	TTA Leu 725	AAC Asn 730	CGA Arg 730	TTC Phe 730	2211
AAT Asn 735	CAA Gln 735	AGC Ser 735	GGT Gly 735	GCC Ala 735	AAT Asn 740	AGC Ser 740	GAT Asp 740	TCT Ser 740	CAT His 740	ATC Ile 745	AAA Lys 745	GAC Asp 745	ATG Met 745	TTT Phe 745	GCG Ala 745	2259
GAT Asp 750	CGT Arg 750	AAG Lys 750	ACT Thr 750	TTA Leu 750	GAA Glu 755	GAA Glu 755	GAC Asp 755	ATT Ile 755	AAA Lys 755	AAC Asn 760	GCC Ala 760	TAT Tyr 760	GAT Asp 760	GAT Asp 760	CTT Leu 760	2307
TTT Phe 765	GAT Asp 765	TAC Tyr 765	CCC Pro 770	ATT Ile 770	GAC Asp 770	GAT Asp 770	ATA Ile 770	GAG Glu 775	GGC Gly 775	ATG Met 775	ACT Thr 775	AGC Ser 775	GCC Ala 775	ATT Ile 775	GTC Val 775	2355
AGC Ser 780	ATG Met 780	AGC Ser 785	GCA Ala 785	ATG Met 785	AAC Asn 790	GAG Glu 790	CTT Leu 790	GTA Val 790	AAA Lys 790	GTC Val 795	TCA Ser 795	CGC Arg 795	GCC Ala 795	ATT Ile 795	AAC Asn 795	2403
ACG Thr 795	CTC Leu 795	AAA Lys 800	GAG Glu 800	CGC Arg 800	TAC Tyr 800	AAT Asn 805	TTA Leu 805	ATC Ile 805	CGC Arg 805	ACT Thr 805	TCT Ser 810	AAT Asn 810	GAT Asp 810	AAA Lys 810	AAA Lys 810	2451
ATC Ile 815	CTT Leu 815	TCA Ser 820	CTA Leu 820	AAA Lys 825	GAA Glu 825	AAA Lys 825	ATT Ile 825	GAT Asp 825	ATT Ile 830	GAA Glu 830	AAG Lys 830	ATC Ile 835	CAT His 835	AAA Lys 835	ATC Ile 835	2499
TCT Ser 830	TCA Ser 830	ATG Met 835	CTT Leu 835	CAT His 840	CAA Gln 840	AAA Lys 845	GCC Ala 845	AAA Lys 850	CAC His 850	CTC Leu 855	CAT His 855	GCG Ala 860	TTA Leu 860	AAG Lys 860	AAT Asn 860	2547
ATC Ile 845	AAT Asn 845	GAG Glu 850	CCT Pro 850	AAA Lys 855	AAC Asn 855	CCA Pro 860	AAC Asn 860	GAT Asp 865	TTA Leu 865	ATG Met 870	ATT Ile 870	TTA Leu 875	GAA Glu 875	GAC Asp 875	CTC Leu 875	2595
ATC Ile 860	GCT Ala 860	CTT Leu 865	TTA Leu 865	GAC Asp 870	TTT Phe 870	AAA Lys 875	ATA Ile 875	GAG Glu 880	TTT Phe 880	AAA Lys 885	GAA Glu 885	CGC Arg 890	AAA Lys 890	GAA Glu 890	TTA Leu 890	2643
CGC Arg 875	TTT Phe 875	AAA Lys 880	GAA Glu 880	CAA Gln 885	GAA Glu 885	GAG Glu 890	ATT Ile 890	ACC Thr 895	ACC Thr 895	AAA Lys 900	CAA Gln 900	AAG Lys 905	CAA Gln 905	GCT Ala 910	AAA Lys 910	2691
GAG Glu 895	ATT Ile 895	TTA Leu 900	GAA Glu 900	AAA Lys 905	ATC Ile 905	CCG Pro 910	GAT Asp 910	CAA Gln 915	CAA Gln 915	GAT Asp 920	AAA Lys 920	GAA Glu 925	ATC Ile 925	CAA Gln 930	AAG Lys 930	2739
TTT Phe 910	TAC Tyr 910	AAA Lys 915	GAC Asp 920	TTT Phe 920	TCA Ser 925	AAA Lys 925	TTA Leu 930	CTC Leu 930	CAA Gln 935	ACG Thr 935	CCC Pro 940	ACA Thr 940	ACA Thr 940	AGC Ser 945	CAG Gln 945	2787
AAT Asn 925	TTT Phe 925	GAG Glu 930	GAA Glu 930	ATT Ile 935	TCT Ser 935	CAT His 940	TCC Ser 940	TAT Tyr 945	GAT Asp 945	GCG Ala 950	ATC Ile 950	ATT Ile 955	TCA Ser 955	CAA Gln 960	CTC Leu 960	2835
AAA Lys 955	CAA Gln 955	CAC His 960	AAA Lys 965	GAA Glu 965	CAA Gln 970	ACC Thr 970	ACC Thr 970	CAC His 975	TTA Leu 975	TTA Leu 975	AAC Asn 980	AAA Lys 980	TAC Tyr 985	GAT Asp 985	AAT Asn 985	2883

Ile	Glu	Val	Lys	Gln	Pro	Tyr	Ala	Lys	Lys	Gly	Ile	Lys	Glu	Glu	Arg
	130					135					140				
Asp	Arg	His	Ile	Lys	Arg	Tyr	Glu	Asn	Pro	Glu	Asn	Lys	Val	Phe	Tyr
145					150					155					160
Asn	Leu	Ala	Gln	Ile	Trp	Leu	Phe	Ser	Asp	Asn	Leu	Pro	Tyr	Asp	Glu
				165					170					175	
Asn	Lys	Pro	Asp	Gln	Gly	Ala	Phe	Tyr	Ser	Ala	Ser	Tyr	Ser	Pro	Ile
			180					185					190		
Phe	Gln	Arg	Phe	Val	Glu	Ala	His	Arg	Leu	Asp	Ile	Xaa	Pro	Xaa	Pro
		195					200					205			
Xaa	Gln	Lys	Asn	Asp	Gln	Asn	His	Gln	Asn	Asp	Gln	Asn	His	Arg	Ser
	210					215					220				
Leu	Glu	Glu	Ile	Gln	Lys	Ser	Val	Leu	Asn	Glu	Phe	Asn	Leu	Lys	Asp
225					230					235					240
Thr	Asp	Thr	Pro	Lys	Ser	Pro	Lys	Asp	Thr	Pro	Thr	Asn	Ser	Leu	Leu
				245					250					255	
Thr	Ser	Phe	Cys	Ser	Pro	Lys	Arg	Leu	Cys	Phe	Ile	Leu	Lys	Tyr	Gly
			260					265					270		
Ile	Ser	Phe	Leu	Lys	Glu	Lys	Ser	Glu	Phe	Lys	Lys	His	Val	Trp	Arg
		275					280					285			
Tyr	Ala	Gln	Met	Phe	Ala	Ser	Leu	Asn	Val	Leu	Lys	Glu	Leu	Gln	Lys
	290					295					300				
His	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	Lys	Asp	Pro	Leu	Lys	Gly	Ile	Ile
305					310					315					320
Trp	His	Thr	Gln	Gly	Ser	Gly	Lys	Thr	Ala	Leu	Thr	Tyr	His	Leu	Thr
			325						330					335	
Lys	Leu	Ile	Arg	Asp	Phe	Phe	Ser	Arg	Ser	Asn	Leu	Asn	Lys	Lys	Thr
			340					345					350		
Lys	Phe	Tyr	Phe	Ile	Val	Asp	Arg	Leu	Asp	Leu	Leu	Glu	Gln	Ala	Lys
	355					360						365			
Asn	Glu	Phe	Leu	Lys	Arg	Gly	Leu	Cys	Val	His	Glu	Ala	Glu	Asn	Lys
	370					375					380				
Glu	Asp	Leu	Ser	Gln	Lys	Leu	Lys	Ser	Ser	Ser	Val	Phe	Glu	Gly	Ser
385				390						395					400
Gln	Gly	Asn	Asp	Glu	Ile	Ile	Val	Val	Asn	Ile	Gln	Lys	Phe	Lys	Ala
				405					410					415	
Pro	Asn	Glu	Glu	Lys	Ser	Pro	Asn	Glu	Asp	Pro	Ser	Asn	Ser	Ala	Pro
			420					425					430		
Lys	Glu	Ile	Ile	Ser	Lys	Thr	Glu	Leu	Gln	Glu	Ser	Ile	Gln	Asn	Ser
	435					440						445			
Arg	Asn	Leu	Gln	Arg	Val	Phe	Ile	Ile	Asp	Glu	Ala	His	Arg	Ser	Tyr
	450					455					460				
Asp	Pro	Lys	Gly	Cys	Phe	Tyr	Ala	Asn	Leu	Ile	Glu	Cys	Asp	Lys	Thr
465				470											

			580					585					590		
Lys	Ala	Met	Val	Val	Cys	Phe	Ser	Ser	Lys	Gln	Ala	Arg	Leu	Ala	Asp
		595					600					605			
Cys	Leu	Phe	Asn	Glu	Val	Gln	Glu	Lys	Val	Leu	Gln	Glu	Asn	Pro	Asn
	610					615					620				
Leu	Arg	Ile	Leu	Asn	Lys	Leu	Lys	Ser	Ser	Leu	Ile	Leu	His	Asp	Glu
625					630					635					640
Gln	Glu	Val	Lys	Glu	Lys	Val	His	Ser	Phe	Lys	His	Glu	Asp	Thr	Asp
				645					650					655	
Ile	Val	Phe	Val	Phe	Asn	Met	Leu	Leu	Thr	Gly	Phe	Asp	Leu	Pro	Ser
			660					665					670		
Leu	Lys	Arg	Leu	Tyr	Ile	His	Arg	Glu	Leu	Lys	Asp	His	Asn	Leu	Leu
		675					680					685			
Gln	Ala	Leu	Ala	Arg	Val	Asn	Arg	Ser	Tyr	Lys	Asn	Met	Ser	Phe	Gly
	690					695					700				
Tyr	Leu	Ile	Asp	Phe	Val	Gly	Ile	Gln	Glu	Asn	Phe	Asp	Lys	Thr	Thr
705					710					715					720
Asp	Asp	Tyr	Leu	Lys	Glu	Leu	Asn	Arg	Phe	Asn	Gln	Ser	Gly	Ala	Asn
				725					730					735	
Ser	Asp	Ser	His	Ile	Lys	Asp	Met	Phe	Ala	Asp	Arg	Lys	Thr	Leu	Glu
			740					745					750		
Glu	Asp	Ile	Lys	Asn	Ala	Tyr	Asp	Asp	Leu	Phe	Asp	Tyr	Pro	Ile	Asp
		755					760					765			
Asp	Ile	Glu	Gly	Met	Thr	Ser	Ala	Ile	Val	Ser	Met	Ser	Ala	Met	Asn
	770					775					780				
Glu	Leu	Val	Lys	Val	Ser	Arg	Ala	Ile	Asn	Thr	Leu	Lys	Glu	Arg	Tyr
785					790					795					800
Asn	Leu	Ile	Arg	Thr	Ser	Asn	Asp	Lys	Lys	Ile	Leu	Ser	Leu	Lys	Glu
				805					810					815	
Lys	Ile	Asp	Ile	Glu	Lys	Ile	His	Lys	Ile	Ser	Ser	Met	Leu	His	Gln
			820					825					830		
Lys	Ala	Lys	His	Leu	His	Ala	Leu	Lys	Asn	Ile	Asn	Glu	Pro	Lys	Asn
		835					840					845			
Pro	Asn	Asp	Leu	Met	Ile	Leu	Glu	Asp	Leu	Ile	Ala	Leu	Leu	Asp	Phe
	850					855					860				
Lys	Ile	Glu	Phe	Lys	Glu	Arg	Lys	Glu	Leu	Arg	Phe	Lys	Glu	Gln	Glu
865					870					875					880
Glu	Ile	Thr	Thr	Lys	Gln	Lys	Gln	Ala	Lys	Glu	Ile	Leu	Glu	Lys	Ile
				885					890					895	
Pro	Asp	Gln	Gln	Asp	Lys	Glu	Ile	Gln	Lys	Phe	Tyr	Lys	Asp	Phe	Ser
			900					905					910		
Lys	Leu	Leu	Gln	Thr	Pro	Thr	Thr	Ser	Gln	Asn	Phe	Glu	Glu	Ile	Ser
		915					920					925			
His	Ser	Tyr	Asp	Ala	Ile	Ile	Ser	Gln	Leu	Lys	Gln	His	Lys	Glu	Gln
	930</														

1055

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 26...511
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

TAGAAGAAATT TGAAAGGTTG CTCGC ATG CAA AGA GAA TTA AGG CTT TTA AAT																52
Met Gln Arg Glu Leu Arg Leu Leu Asn																
1 5																
AAC	AAG	CAT	TGC	ATG	GAA	TAC	TTG	CAA	TTT	CTG	TCC	AAA	AAC	CAT	TTG	100
Asn	Lys	His	Cys	Met	Glu	Tyr	Leu	Gln	Phe	Leu	Ser	Lys	Asn	His	Leu	
10 15 20 25																
AGT	TTT	AAC	CTT	TTG	TGC	GAA	AGA	GAT	GCG	ATT	GAT	TTT	TCC	CCC	AAG	148
Ser	Phe	Asn	Leu	Leu	Cys	Glu	Arg	Asp	Ala	Ile	Asp	Phe	Ser	Pro	Lys	
30 35 40																
CTC	CCT	AAA	GAA	ATT	CAT	GAA	AAA	TTC	GGC	GCG	TTA	GTG	CTA	TTT	GTT	196
Leu	Pro	Lys	Glu	Ile	His	Glu	Lys	Phe	Gly	Ala	Leu	Val	Leu	Phe	Val	
45 50 55																
TTA	GCC	GGA	TAC	ACC	TTA	GAA	AGC	TTG	ATA	ATT	GAT	ACA	AAA	AGC	GTG	244
Leu	Ala	Gly	Tyr	Thr	Leu	Glu	Ser	Leu	Ile	Ile	Asp	Thr	Lys	Ser	Val	
60 65 70																
CAA	TTT	GAA	GCC	GGG	TTT	GGC	CCT	AAT	AAC	ATT	GGC	AGT	GTG	GTT	CAA	292
Gln	Phe	Glu	Ala	Gly	Phe	Gly	Pro	Asn	Asn	Ile	Gly	Ser	Val	Val	Gln	
75 80 85																
GTA	AAA	CTT	CCT	GGC	ATC	ATT	CAA	ATC	CTT	ATC	AAA	GAA	AAA	AAT	GAA	340
Val	Lys	Leu	Pro	Gly	Ile	Ile	Gln	Ile	Leu	Ile	Lys	Glu	Lys	Asn	Glu	
90 95 100 105																
AAT	GCC	GTT	TTA	TTC	AAT	CGT	TGC	GAT	TCG	CTT	GAA	TTG	TTT	CAA	AAA	388
Asn	Ala	Val	Leu	Phe	Asn	Arg	Cys	Asp	Ser	Leu	Glu	Leu	Phe	Gln	Lys	
110 115 120																
GAA	GAT	TCA	ATC	GCG	CAA	GAG	CCA	AAA	AAA	GAC	GAG	CGG	GAG	TCT	AAA	436
Glu	Asp	Ser	Ile	Ala	Gln	Glu	Pro	Lys	Lys	Asp	Glu	Arg	Glu	Ser	Lys	
125 130 135																
GAA	TGG	CTG	GAT	TCT	AAA	GAG	GCT	CTT	TTT	TCC	AAT	TCC	AAA	AAC	CGC	484
Glu	Trp	Leu	Asp	Ser	Lys	Glu	Ala	Leu	Phe	Ser	Asn	Ser	Lys	Asn	Arg	

140

145

150

GCG ATT TTA GAA AAT CTG CAC AAA AGC TAAAGGAATC ATTGATGAGC GTTTTGA 538
Ala Ile Leu Glu Asn Leu His Lys Ser
155 160

AATTGCATGT AAAAGTCTTT CGTTTTGAAA CCAATA 574

(2) INFORMATION FOR SEQ ID NO:598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

Met	Gln	Arg	Glu	Leu	Arg	Leu	Leu	Asn	Asn	Lys	His	Cys	Met	Glu	Tyr
1				5					10					15	
Leu	Gln	Phe	Leu	Ser	Lys	Asn	His	Leu	Ser	Phe	Asn	Leu	Leu	Cys	Glu
			20					25					30		
Arg	Asp	Ala	Ile	Asp	Phe	Ser	Pro	Lys	Leu	Pro	Lys	Glu	Ile	His	Glu
		35					40					45			
Lys	Phe	Gly	Ala	Leu	Val	Leu	Phe	Val	Leu	Ala	Gly	Tyr	Thr	Leu	Glu
	50					55					60				
Ser	Leu	Ile	Ile	Asp	Thr	Lys	Ser	Val	Gln	Phe	Glu	Ala	Gly	Phe	Gly
65					70					75				80	
Pro	Asn	Asn	Ile	Gly	Ser	Val	Val	Gln	Val	Lys	Leu	Pro	Gly	Ile	Ile
			85						90					95	
Gln	Ile	Leu	Ile	Lys	Glu	Lys	Asn	Glu	Asn	Ala	Val	Leu	Phe	Asn	Arg
			100					105					110		
Cys	Asp	Ser	Leu	Glu	Leu	Phe	Gln	Lys	Glu	Asp	Ser	Ile	Ala	Gln	Glu
		115					120					125			
Pro	Lys	Lys	Asp	Glu	Arg	Glu	Ser	Lys	Glu	Trp	Leu	Asp	Ser	Lys	Glu
	130					135					140				
Ala	Leu	Phe	Ser	Asn	Ser	Lys	Asn	Arg	Ala	Ile	Leu	Glu	Asn	Leu	His
145					150					155				160	
Lys	Ser														

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1697 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 14...1648
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

TTTAGGGGGG	TAA	ATG	CCT	TCA	AAC	GCT	CTT	TTG	ATT	GAA	GAA	ATC	ACT	49
	Met	Pro	Ser	Asn	Ala	Leu	Leu	Ile	Glu	Glu	Ile	Thr		
	1				5					10				
CAT	TTA	ATC	AAT	GTT	TCT	CAT	AGT	AGC	GTG	CAT	AAT	TGG	ATC	97
His	Leu	Ile	Asn	Val	Ser	His	Ser	Ser	Val	His	Asn	Trp	Ile	
	15					20					25			
AAT	CTT	TTA	GAG	AAA	CTA	GAA	ATT	GAT	CAT	AAA	ATT	TAT	GTG	145
Asn	Leu	Leu	Glu	Lys	Leu	Glu	Ile	Asp	His	Lys	Ile	Tyr	Val	
	30					35				40				
AGT	TCT	TTT	TTA	GAT	TTT	TGC	CGC	AAC	CAT	TTA	GGG	AAA	AAC	193
Ser	Ser	Phe	Leu	Asp	Phe	Cys	Arg	Asn	His	Leu	Gly	Lys	Asn	
45					50					55			Lys	
													Leu	
													60	
AAC	AAA	TAC	GCT	AAC	AAA	TCC	TTA	AAA	GGC	GTG	CAT	AAC	CAT	241
Asn	Lys	Tyr	Ala	Asn	Lys	Ser	Leu	Lys	Gly	Val	His	Asn	His	
				65					70				Gln	
													Glu	
													75	
TTG	ATT	TTA	AAA	TAC	CTA	GAA	ATA	TTA	GAA	AAT	AGC	TCT	GAT	289
Leu	Ile	Leu	Lys	Tyr	Leu	Glu	Ile	Leu	Glu	Asn	Ser	Ser	Asp	
			80					85					Leu	
													Glu	
													90	
AAG	TTG	GGT	TCT	TAT	TAT	GAA	GAA	GAG	CTT	TCT	AAC	GCC	ACC	337
Lys	Leu	Gly	Ser	Tyr	Tyr	Glu	Glu	Glu	Leu	Ser	Asn	Ala	Thr	
		95					100					105	Arg	
													Asn	
TTA	GAA	GGC	ATT	TAC	TAC	ACT	CCT	AAC	AGG	ATA	GTA	GAA	CAA	385
Leu	Glu	Gly	Ile	Tyr	Tyr	Thr	Pro	Asn	Arg	Ile	Val	Glu	Gln	
	110					115					120		Leu	
													Phe	
ACC	CTC	CCT	AAA	GAT	TTT	GAT	GTC	TCT	CAA	GCG	ATT	TTT	TGC	433
Thr	Leu	Pro	Lys	Asp	Phe	Asp	Val	Ser	Gln	Ala	Ile	Phe	Cys	
125					130					135			Asp	
													Pro	
													140	
GCT	GTG	GGG	AGT	GGG	AAT	TTT	ATC	ATG	CAT	GCT	TTA	AAA	CTG	481
Ala	Val	Gly	Ser	Gly	Asn	Phe	Ile	Met	His	Ala	Leu	Lys	Leu	
				145					150				Gly	
													Phe	
													155	
AAG	GTT	GAA	AAC	ATT	TAT	GGC	TAT	GAT	ACG	GAC	GCT	TTT	GCT	529
Lys	Val	Glu	Asn	Ile	Tyr	Gly	Tyr	Asp	Thr	Asp	Ala	Phe	Ala	
			160					165				170	Val	
													Ala	
TTG	ACT	AAA	AAG	CGT	ATT	AAA	GAG	CGT	TAT	CAT	TTA	GAT	TGC	577
Leu	Thr	Lys	Lys	Arg	Ile	Lys	Glu	Arg	Tyr	His	Leu	Asp	Cys	
		175					180					185	Leu	
													Asn	
ATT	GTG	CAA	AAA	GAT	TTT	TTA	AAT	TTA	AAA	CAC	ACC	CCG	CAA	625
Ile	Val	Gln	Lys	Asp	Phe	Leu	Asn	Leu	Lys	His	Thr	Pro	Gln	
	190					195					200		Phe	
													Asp	
TGC	ATT	TTC	ACT	AAC	CCG	CCA	TGG	GGC	AAG	AAA	TAC	AAT	CAA	673
Cys	Ile	Phe	Thr	Asn	Pro	Pro	Trp	Gly	Lys	Lys	Tyr	Asn	Gln	
205					210					215			Asn	
													Gln	
													220	

AAA Lys	GAA Glu	AAT Asn	TTT Phe	AAA Lys 225	CAG Gln	CAA Gln	TTC Phe	AAC Asn	CTC Leu 230	TCT Ser	CAA Gln	AGC Ser	CTA Leu	GAT Asp 235	AGC Ser	721
GCG Ala	TCG Ser	CTC Leu	TTT Phe 240	TTT Phe	ATA Ile	GCG Ala	AGT Ser	TTG Leu	AAT Asn 245	TGT Cys	TTA Leu	AAA Lys	GAA Glu 250	AAC Asn	GCT Ala	769
CAT His	TTG Leu	GGG Gly 255	TTA Leu	TTA Leu	TTA Leu	CCC Pro	GAA Glu 260	AGT Ser	TGT Cys	TTG Leu	AAT Asn	ATT Ile 265	GAT Asp	GCG Ala	TTT Phe	817
AAA Lys	AAA Lys 270	ATG Met	CGA Arg	GAA Glu	ATG Met	GCT Ala 275	TTA Leu	AAG Lys	TTT Phe	CAC His	ATT Ile 280	AGA Arg	AGC Ser	CTG Leu	ATT Ile	865
GAT Asp 285	TTT Phe	GAC Asp	AAA Lys	CCT Pro	TTT Phe 290	AAA Lys	AAT Asn	CTA Leu	ATG Met	ACT Thr 295	AAG Lys	GCT Ala	GTG Val	GGT Gly	TTG Leu 300	913
GCG Ala	CTT Leu	AAA Lys	AAA Lys	ACC Thr 305	CCT Pro	AAT Asn	AAG Lys	GAT Asp	CAA Gln 310	AAA Lys	ATC Ile	TCA Ser	TGC Cys	TTT Phe 315	TAT Tyr	961
CAA Gln	AAT Asn	AGC Ser	AAG Lys 320	TTC Phe	AAA Lys	CGC Arg	TCG Ser	CCC Pro 325	TCT Ser	TCT Ser	TTT Phe	TTT Phe	AAC Asn 330	AAC Asn	CCT Pro	1009
AAA Lys	AAG Lys	ATT Ile 335	TTT Phe	AAT Asn	ATC Ile	CAT His	TGC Cys 340	TCT Ser	AGC Ser	AAA Lys	GAA Glu	AAT Asn 345	AAA Lys	ATT Ile	TTA Leu	1057
GAC Asp	CAC His 350	CTT Leu	TTT Phe	TCC Ser	CTC Leu	CCT Pro 355	CAT His	ATG Met	ACT Thr	TTA Leu	AAA Lys 360	AAT Asn	AAC Asn	GCT Ala	CAT His	1105
TTT Phe 365	GCT Ala	TTA Leu	GGG Gly	ATT Ile	GTT Val 370	ACA Thr	GGC Gly	AAC Asn	AAT Asn	AAA Lys 375	GAA Glu	AAA Lys	TTA Leu	CAC His	CCC Pro 380	1153
AAA Lys	CAA Gln	GAA Glu	AAA Lys	AAT Asn 385	ACC Thr	ATT Ile	CCC Pro	ATT Ile	TTT Phe 390	AGG Arg	GGT Gly	TCA Ser	GAT Asp	ATT Ile 395	TTA Leu	1201
AAA Lys	GAC Asp	GGA Gly	TTA Leu 400	AAA Lys	GCC Ala	CCT Pro	AGC Ser	CAA Gln 405	TTC Phe	ATT Ile	AAC Asn	GCT Ala	GGT Gly 410	TTA Leu	AAA Lys	1249
GAC Asp	TGC Cys	CAG Gln 415	CAA Gln	GTC Val	GCC Ala	CCC Pro	TTA Leu 420	AGC Ser	CTT Leu	TAT Tyr	CAA Gln	GCT Ala 425	AGA Arg	GAA Glu	AAA Lys	1297
ATC Ile	GTG Val 430	TAT Tyr	AAA Lys	TTC Phe	ATT Ile	TCT Ser 435	TCA Ser	AAG Lys	CTT Leu	GTC Val	TTT Phe 440	TTT Phe	TAT Tyr	GAC Asp	AAT Asn	1345
AAG Lys	CAA Gln	CGC Arg	CTT Leu	TTT Phe	TTA Leu	AAC Asn	AGC Ser	GCG Ala	AAC Asn	ATG Met	TTT Phe	GTT Val	TTA Leu	AAA Lys	GAA Glu	1393

445	450	455	460	
AAT TTC CCT ATC AAC GCT CAT GCA TTA AAA GAA TTG TTA AAC AGC GAT				1441
Asn Phe Pro Ile Asn Ala His Ala Leu Lys Glu Leu Leu Asn Ser Asp	465	470	475	
TTA ATG CAA TTC ATT TTT GAA TCG CTT TTT AAA ACG CAT AAA ATC TTA				1489
Leu Met Gln Phe Ile Phe Glu Ser Leu Phe Lys Thr His Lys Ile Leu	480	485	490	
AGA AAA GAT TTG GAA TGT TTG CCC CTA TTT GTG CAA TTT ATT AAC GAT				1537
Arg Lys Asp Leu Glu Cys Leu Pro Leu Phe Val Gln Phe Ile Asn Asp	495	500	505	
AAT TTT GAT GAA AAA TTT TAT TTA AAA AAT TTA GGG ATA GAA AAA AAA				1585
Asn Phe Asp Glu Lys Phe Tyr Leu Lys Asn Leu Gly Ile Glu Lys Lys	510	515	520	
GAC CCT AAA CAT TTC ACC ATC AGG AAA AAT CAT GCA TGT TGC TTG TCT				1633
Asp Pro Lys His Phe Thr Ile Arg Lys Asn His Ala Cys Cys Leu Ser	525	530	535	540
TTT GGC TTT AGG GGA TAATCTCATC ACGCTTAGCC TTTTAAAAGA AATCGCTTTC A				1689
Phe Gly Phe Arg Gly	545			
AACAGCAA				1697

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

Met	Pro	Ser	Asn	Ala	Leu	Leu	Ile	Glu	Glu	Ile	Thr	His	Leu	Ile	Asn
1				5				10					15		
Val	Ser	His	Ser	Ser	Val	His	Asn	Trp	Ile	Lys	Thr	Asn	Leu	Leu	Glu
			20					25					30		
Lys	Leu	Glu	Ile	Asp	His	Lys	Ile	Tyr	Val	Lys	Thr	Ser	Ser	Phe	Leu
		35					40					45			
Asp	Phe	Cys	Arg	Asn	His	Leu	Gly	Lys	Asn	Lys	Leu	Asn	Lys	Tyr	Ala
	50				55					60					
Asn	Lys	Ser	Leu	Lys	Gly	Val	His	Asn	His	Gln	Glu	Leu	Ile	Leu	Lys
65				70						75				80	
Tyr	Leu	Glu	Ile	Leu	Glu	Asn	Ser	Ser	Asp	Leu	Glu	Lys	Leu	Gly	Ser
			85					90					95		
Tyr	Tyr	Glu	Glu	Glu	Leu	Ser	Asn	Ala	Thr	Arg	Asn	Leu	Glu	Gly	Ile
		100					105					110			
Tyr	Tyr	Thr	Pro	Asn	Arg	Ile	Val	Glu	Gln	Leu	Phe	Thr	Leu	Pro	Lys
	115				120							125			
Asp	Phe	Asp	Val	Ser	Gln	Ala	Ile	Phe	Cys	Asp	Pro	Ala	Val	Gly	Ser
	130				135					140					

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 46...1842
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

TATTGTGTTA TACTTCTAAT TTCAATTTTG CTTGTTAGGA CATTT	ATG AAA AAT ATT	57
	Met Lys Asn Ile	
	1	
AGA AAT ATC GCT GTA ATC GCG CAT GTT GAT CAT GGG AAA ACC ACT CTA		105
Arg Asn Ile Ala Val Ile Ala His Val Asp His Gly Lys Thr Thr Leu		
5 10 15 20		
GTA GAT GGC TTA CTT TCT CAA TCT GGC ACA TTT AGT GAG AGG GAA AAA		153
Val Asp Gly Leu Leu Ser Gln Ser Gly Thr Phe Ser Glu Arg Glu Lys		
25 30 35		
GTG GAT GAA AGG GTG ATG GAT AGC AAT GAT TTG GAA AGA GAA AGA GGG		201
Val Asp Glu Arg Val Met Asp Ser Asn Asp Leu Glu Arg Glu Arg Gly		
40 45 50		
ATT ACT ATC CTG TCT AAA AAC ACC GCT ATT TAT TAC AAA GAC ACT AAA		249
Ile Thr Ile Leu Ser Lys Asn Thr Ala Ile Tyr Tyr Lys Asp Thr Lys		
55 60 65		
ATC AAT ATC ATT GAC ACT CCC GGG CAT GCT GAT TTT GGG GGC GAA GTG		297
Ile Asn Ile Ile Asp Thr Pro Gly His Ala Asp Phe Gly Gly Glu Val		
70 75 80		
GAG CGC GTT TTA AAA ATG GTG GAT GGG GTG TTG CTT TTA GTG GAC GCT		345
Glu Arg Val Leu Lys Met Val Asp Gly Val Leu Leu Leu Val Asp Ala		
85 90 95 100		
CAA GAA GGG GTC ATG CCT CAA ACT AAA TTC GTG GTT AAA AAG GCT TTG		393
Gln Glu Gly Val Met Pro Gln Thr Lys Phe Val Val Lys Lys Ala Leu		
105 110 115		
AGT TTT GGG ATT TGC CCT ATT GTG GTG GTG AAT AAA ATT GAT AAG CCT		441
Ser Phe Gly Ile Cys Pro Ile Val Val Val Asn Lys Ile Asp Lys Pro		
120 125 130		
GCC GCT GAA CCG GAC AGA GTG GTG GAT GAA GTT TTT GAC TTG TTC GTA		489
Ala Ala Glu Pro Asp Arg Val Val Asp Glu Val Phe Asp Leu Phe Val		
135 140 145		
GCC ATG GGG GCT AGC GAT AAG CAA TTG GAT TTC CCT GTG GTG TAT GCC		537
Ala Met Gly Ala Ser Asp Lys Gln Leu Asp Phe Pro Val Val Tyr Ala		
150 155 160		
GCC GCA CGA GAT GGC TAT GCG ATG AAA AGT TTA GAC GAT GAA AAG AAA		585

Ala 165	Ala	Arg	Asp	Gly	Tyr 170	Ala	Met	Lys	Ser	Leu 175	Asp	Asp	Glu	Lys	Lys 180	
AAT Asn	TTA Leu	GAG Glu	CCT Pro	TTG Leu	TTT Phe	GAA Glu	ACG Thr	ATT Ile	TTA Leu	GAG Glu	CAT His	GTG Val	CCA Pro	AGC Ser	CCT Pro	633
AGC Ser	GGG Gly	AGC Ser	GTT Val	GAT Asp	GAG Glu	CCT Pro	TTG Leu	CAA Gln	ATG Met	CAA Gln	ATT Ile	TTC Phe	ACG Thr	CTT Leu	GAT Asp	681
TAT Tyr	GAC Asp	AAT Asn	TAT Tyr	GTG Val	GGC Gly	AAA Lys	ATC Ile	GGT Gly	ATC Ile	GCT Ala	AGG Arg	GTG Val	TTT Phe	AAT Asn	GGC Gly	729
TCG Ser	GTT Val	AAA Lys	AAG Lys	AAT Asn	GAA Glu	AGC Ser	GTG Val	CTG Leu	TTG Leu	ATG Met	AAA Lys	AGC Ser	GAT Asp	GGG Gly	AGT Ser	777
AAA Lys	GAA Glu	AAT Asn	GGC Gly	CGT Arg	ATC Ile	ACT Thr	AAG Lys	CTT Leu	ATA Ile	GGT Gly	TTT Phe	TTA Leu	GGG Gly	CTG Leu	GCT Ala	825
AGG Arg	ACT Thr	GAG Glu	ATT Ile	GAA Glu	AAC Asn	GCT Ala	TAT Tyr	GCG Ala	GGC Gly	GAT Asp	ATT Ile	GTA Val	GCG Ala	ATT Ile	GCC Ala	873
GGG Gly	TTT Phe	AAT Asn	GCA Ala	ATG Met	GAT Asp	GTG Val	GGC Gly	GAT Asp	AGC Ser	GTC Val	GTT Val	GAT Asp	CCT Pro	GCT Ala	AAC Asn	921
CCC Pro	ATG Met	CCT Pro	TTA Leu	GAT Asp	CCC Pro	ATG Met	CAT His	TTA Leu	GAA Glu	GAG Glu	CCT Pro	ACG Thr	ATG Met	AGC Ser	GTG Val	969
TAT Tyr	TTT Phe	GCT Ala	GTC Val	AAT Asn	GAT Asp	TCA Ser	CCC Pro	TTA Leu	GCC Ala	GGG Gly	TTA Leu	GAA Glu	GGA Gly	AAG Lys	CAT His	1017
GTT Val	ACT Thr	GCT Ala	AAT Asn	AAA Lys	TTG Leu	AAA Lys	GAC Asp	AGG Arg	CTC Leu	TTA Leu	AAA Lys	GAA Glu	ATG Met	CAA Gln	ACC Thr	1065
AAT Asn	ATC Ile	GCT Ala	ATG Met	AAA Lys	TGC Cys	GAA Glu	GAA Glu	ATG Met	GGC Gly	GAG Glu	GGC Gly	AAG Lys	TTT Phe	AAA Lys	GTG Val	1113
AGT Ser	GGG Gly	CGT Arg	GGG Gly	GAA Glu	TTG Leu	CAA Gln	ATC Ile	ACT Thr	ATT Ile	TTA Leu	GCT Ala	GAA Glu	AAC Asn	TTG Leu	CGC Arg	1161
CGT Arg	GAA Glu	GGG Gly	TTT Phe	GAA Glu	TTT Phe	AGC Ser	ATT Ile	TCA Ser	CGC Arg	CCT Pro	GAA Glu	GTC Val	ATC Ile	ATT Ile	AAA Lys	1209
GAA Glu	GAA Glu	AAT Asn	GGC Gly	GTT Val	AAA Lys	TGC Cys	GAG Glu	CCT Pro	TTT Phe	GAG Glu	CAT His	TTA Leu	GTG Val	ATT Ile	GAC Asp	1257

ACG CCC CAA GAT TTT AGT GGG GCT ATC ATT GAG AGA TTG GGC AAA AGA Thr Pro Gln Asp Phe Ser Gly Ala Ile Ile Glu Arg Leu Gly Lys Arg 405 410 415 420	1305
AAA GCT GAG ATG AAA GCG ATG AAT CCC ATG AGT GAT GGC TAT ACA AGA Lys Ala Glu Met Lys Ala Met Asn Pro Met Ser Asp Gly Tyr Thr Arg 425 430 435	1353
TTA GAA TTT GAA ATT CCT GCA AGA GGG CTT ATC GGT TAT AGG AGC GAG Leu Glu Phe Glu Ile Pro Ala Arg Gly Leu Ile Gly Tyr Arg Ser Glu 440 445 450	1401
TTT TTA ACC GAC ACC AAG GGC GAA GGC GTG ATG AAT CAT AGC TTT TTA Phe Leu Thr Asp Thr Lys Gly Glu Gly Val Met Asn His Ser Phe Leu 455 460 465	1449
GAA TTC CGC CCT TTC AGC GGG AGC GTG GAA TCG CGC AAA AAT GGG GCG Glu Phe Arg Pro Phe Ser Gly Ser Val Glu Ser Arg Lys Asn Gly Ala 470 475 480	1497
CTA ATC AGC ATG GAA AAT GGC GAA GCG ACC GCT TTT TCC CTT TTC AAT Leu Ile Ser Met Glu Asn Gly Glu Ala Thr Ala Phe Ser Leu Phe Asn 485 490 495 500	1545
ATC CAA GAA AGA GGC ACG CTT TTT ATC AAC CCC CAA ACG AAG GTT TAT Ile Gln Glu Arg Gly Thr Leu Phe Ile Asn Pro Gln Thr Lys Val Tyr 505 510 515	1593
GTG GGC ATG GTC ATT GGC GAG CAC AGC CGG GAT AAT GAT TTA GAT GTC Val Gly Met Val Ile Gly Glu His Ser Arg Asp Asn Asp Leu Asp Val 520 525 530	1641
AAT CCT ATT AAA TCC AAG CAT TTA ACC AAC ATG AGA GCG AGC GGG AGC Asn Pro Ile Lys Ser Lys His Leu Thr Asn Met Arg Ala Ser Gly Ser 535 540 545	1689
GAT GAT GCG ATC AAA CTC ACC CCG CCT AGG ACT ATG GTG TTA GAA AGA Asp Asp Ala Ile Lys Leu Thr Pro Pro Arg Thr Met Val Leu Glu Arg 550 555 560	1737
GCG TTA GAA TGG ATT GAA GAA GAT GAG ATT TTG GAA GTT ACC CCC TTG Ala Leu Glu Trp Ile Glu Glu Asp Glu Ile Leu Glu Val Thr Pro Leu 565 570 575 580	1785
AAT TTA AGG ATC AGG AAA AAG ATT TTA GAC CCT AAC ATG AGG AAA AGG Asn Leu Arg Ile Arg Lys Lys Ile Leu Asp Pro Asn Met Arg Lys Arg 585 590 595	1833
GCG AAA AAA TAAATAGAAT TTTTGTGAAT GCATGCCAAT TTATTCAACC AA Ala Lys Lys	1884

(2) INFORMATION FOR SEQ ID NO:602:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 599 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

Met	Lys	Asn	Ile	Arg	Asn	Ile	Ala	Val	Ile	Ala	His	Val	Asp	His	Gly
1				5					10					15	
Lys	Thr	Thr	Leu	Val	Asp	Gly	Leu	Leu	Ser	Gln	Ser	Gly	Thr	Phe	Ser
			20					25					30		
Glu	Arg	Glu	Lys	Val	Asp	Glu	Arg	Val	Met	Asp	Ser	Asn	Asp	Leu	Glu
		35					40					45			
Arg	Glu	Arg	Gly	Ile	Thr	Ile	Leu	Ser	Lys	Asn	Thr	Ala	Ile	Tyr	Tyr
	50					55					60				
Lys	Asp	Thr	Lys	Ile	Asn	Ile	Ile	Asp	Thr	Pro	Gly	His	Ala	Asp	Phe
65					70					75					80
Gly	Gly	Glu	Val	Glu	Arg	Val	Leu	Lys	Met	Val	Asp	Gly	Val	Leu	Leu
			85						90					95	
Leu	Val	Asp	Ala	Gln	Glu	Gly	Val	Met	Pro	Gln	Thr	Lys	Phe	Val	Val
			100					105					110		
Lys	Lys	Ala	Leu	Ser	Phe	Gly	Ile	Cys	Pro	Ile	Val	Val	Val	Asn	Lys
		115					120					125			
Ile	Asp	Lys	Pro	Ala	Ala	Glu	Pro	Asp	Arg	Val	Val	Asp	Glu	Val	Phe
	130					135					140				
Asp	Leu	Phe	Val	Ala	Met	Gly	Ala	Ser	Asp	Lys	Gln	Leu	Asp	Phe	Pro
145					150					155					160
Val	Val	Tyr	Ala	Ala	Ala	Arg	Asp	Gly	Tyr	Ala	Met	Lys	Ser	Leu	Asp
				165					170					175	
Asp	Glu	Lys	Lys	Asn	Leu	Glu	Pro	Leu	Phe	Glu	Thr	Ile	Leu	Glu	His
			180					185					190		
Val	Pro	Ser	Pro	Ser	Gly	Ser	Val	Asp	Glu	Pro	Leu	Gln	Met	Gln	Ile
		195					200					205			
Phe	Thr	Leu	Asp	Tyr	Asp	Asn	Tyr	Val	Gly	Lys	Ile	Gly	Ile	Ala	Arg
	210					215					220				
Val	Phe	Asn	Gly	Ser	Val	Lys	Lys	Asn	Glu	Ser	Val	Leu	Leu	Met	Lys
225					230					235					240
Ser	Asp	Gly	Ser	Lys	Glu	Asn	Gly	Arg	Ile	Thr	Lys	Leu	Ile	Gly	Phe
				245					250					255	
Leu	Gly	Leu	Ala	Arg	Thr	Glu	Ile	Glu	Asn	Ala	Tyr	Ala	Gly	Asp	Ile
			260					265					270		
Val	Ala	Ile	Ala	Gly	Phe	Asn	Ala	Met	Asp	Val	Gly	Asp	Ser	Val	Val
		275					280					285			
Asp	Pro	Ala	Asn	Pro	Met	Pro	Leu	Asp	Pro	Met	His	Leu	Glu	Glu	Pro
	290					295					300				
Thr	Met	Ser	Val	Tyr	Phe	Ala	Val	Asn	Asp	Ser	Pro	Leu	Ala	Gly	Leu
305					310					315					320
Glu	Gly	Lys	His	Val	Thr	Ala	Asn	Lys	Leu	Lys	Asp	Arg	Leu	Leu	Lys
				325					330					335	
Glu	Met	Gln	Thr	Asn	Ile	Ala	Met	Lys	Cys	Glu	Glu	Met	Gly	Glu	Gly
			340					345					350		
Lys	Phe	Lys	Val	Ser	Gly	Arg	Gly	Glu	Leu	Gln	Ile	Thr	Ile	Leu	Ala
		355					360					365			
Glu	Asn	Leu	Arg	Arg	Glu	Gly	Phe	Glu	Phe	Ser	Ile	Ser	Arg	Pro	Glu
	370					375					380				
Val	Ile	Ile	Lys	Glu	Glu	Asn	Gly	Val	Lys	Cys	Glu	Pro	Phe	Glu	His
385					390					395					400
Leu	Val	Ile	Asp	Thr	Pro	Gln	Asp	Phe	Ser	Gly	Ala	Ile	Ile	Glu	Arg

35				40				45								
AGA Arg 50	GAT Asp	TAT Tyr	ATT Ile	TTA Leu	GAG Glu 55	CAT His	GCC Ala	ATT Ile	TTG Leu	AAC Asn 60	GCC Ala	CTA Leu	GAT Asp	TAT Tyr	GGT Gly 65	248
GTG Val	CCT Pro	CAA Gln	ATG Met	AGA Arg 70	GAA Glu	CGA Arg	GTG Val	ATT Ile	TTA Leu 75	GTG Val	GGC Gly	GTG Val	CTT Leu	AAA Lys 80	AGC Ser	296
TTT Phe	AAA Lys	CAA Gln	AAA Lys 85	TTT Phe	TAC Tyr	TTC Phe	CCT Pro	AAA Lys 90	CCC Pro	ATA Ile	AAA Lys	ACG Thr	CAT His 95	TTT Phe	TCT Ser	344
CTG Leu	AAA Lys	GAC Asp 100	GCT Ala	TTA Leu	GGG Gly	GAT Asp	TTA Leu 105	CCA Pro	CCC Pro	ATT Ile	CAA Gln	AGC Ser 110	GGT Gly	GAA Glu	AAT Asn	392
GGT Gly 115	GAT Asp	GCT Ala	TTA Leu	GGT Gly	TAT Tyr	CTT Leu 120	AAA Lys	AAT Asn	GCG Ala	GAT Asp	AAT Asn	GTT Val	TTT Phe	TTG Leu	GAA Glu	440
TTT Phe 130	GTG Val	CGA Arg	AAT Asn	TCT Ser	AAA Lys 135	GAA Glu	TTA Leu	AGC Ser	GAA Glu	CAT His 140	AGC Ser	AGT Ser	CCT Pro	AAA Lys	AAC Asn 145	488
AAT Asn	GAA Glu	AAA Lys	CTG Leu	ATA Ile 150	AAA Lys	ATC Ile	ATG Met	CAA Gln	ACG Thr 155	CTA Leu	AAA Lys	GAC Asp	GGA Gly	CAG Gln 160	AGT Ser	536
AAA Lys	GAT Asp	GAT Asp	TTG Leu 165	CCA Pro	GAA Glu	AGT Ser	CTG Leu	CGT Arg 170	CCC Pro	AAA Lys	AGT Ser	GGT Gly 175	TAT Tyr	ATT Ile	AAT Asn	584
ACC Thr	TAT Tyr	GCC Ala 180	AAA Lys	ATG Met	TGG Trp	TGG Trp	GAA Glu 185	AAA Lys	CCA Pro	GCC Ala	CCC Pro	ACC Thr 190	ATT Ile	ACA Thr	AGA Arg	632
AAT Asn 195	TTT Phe	TCT Ser	ACC Thr	CCA Pro	AGC Ser	AGT Ser 200	TCT Ser	AGG Arg	TGT Cys	ATC Ile	CAT His 205	CCA Pro	AGA Arg	GAC Asp	TCT Ser	680
AGA Arg 210	GCG Ala	TTA Leu	AGC Ser	ATT Ile	AGA Arg 215	GAG Glu	GGG Gly	GCA Ala	AGA Arg	TTG Leu 220	CAA Gln	AGC Ser	TTT Phe	CCT Pro	GAT Asp 225	728
AAT Asn	TAT Tyr	AAA Lys	TTC Phe	TGT Cys 230	GGG Gly	AGT Ser	GGT Gly	AGC Ser	GCT Ala 235	AAA Lys	AGA Arg	TTG Leu	CAA Gln	ATT Ile 240	GGC Gly	776
AAT Asn	GCC Ala	GTG Val	CCG Pro 245	CCT Pro	TTA Leu	TTG Leu	AGT Ser	GTA Val 250	GCG Ala	CTC Leu	GCG Ala	CAG Gln	GCG Ala 255	GTC Val	TTT Phe	824
GAC Asp	TTT Phe	TTA Leu 260	AAG Lys	GGG Gly	TAAGATGTTTT AACAAATAATG ACTTTAAGGA TTACAGAAAA T											880

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 13...1338
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

TGGTAGTTAA	GA	ATG	GGT	AAT	CAT	TTT	TCT	AAA	TTA	GGA	TTT	GTT	TTA	GCC	51	
	Met	Gly	Asn	His	Phe	Ser	Lys	Leu	Gly	Phe	Val	Leu	Ala			
	1				5					10						
GCA	TTA	GGA	AGC	GCG	ATA	GGT	TTA	GGG	CAT	ATC	TGG	CGT	TTC	CCC	TAC	99
Ala	Leu	Gly	Ser	Ala	Ile	Gly	Leu	Gly	His	Ile	Trp	Arg	Phe	Pro	Tyr	
	15					20				25						
ATG	ACT	GGG	GTG	AGT	GGT	GGG	GCT	TTT	GTT	TTA	TTG	TTT	TTA	TTT		147
Met	Thr	Gly	Val	Ser	Gly	Gly	Gly	Ala	Phe	Val	Leu	Leu	Phe	Leu	Phe	
	30				35				40					45		
TTA	TCT	TTA	AGC	GTT	GGC	GCG	GCG	ATG	TTT	ATC	GCT	GAA	ATG	CTA	TTA	195
Leu	Ser	Leu	Ser	Val	Gly	Ala	Ala	Met	Phe	Ile	Ala	Glu	Met	Leu	Leu	
				50					55					60		
GGA	CAA	AGC	ACT	CAA	AAA	AAT	GTA	ACA	GAA	GCT	TTT	AAA	GAG	CTT	GAC	243
Gly	Gln	Ser	Thr	Gln	Lys	Asn	Val	Thr	Glu	Ala	Phe	Lys	Glu	Leu	Asp	
			65				70					75				
ATT	AAC	CCC	AAA	AAA	CGC	TGG	AAA	TAC	GCA	GGG	CTT	TTG	CTT	GTT	TCT	291
Ile	Asn	Pro	Lys	Lys	Arg	Trp	Lys	Tyr	Ala	Gly	Leu	Leu	Leu	Val	Ser	
		80					85					90				
GGG	CCA	TTA	ATA	CTG	ACT	TTT	TAC	GGC	ACG	ATT	TTA	GGT	TGG	GTG	CTT	339
Gly	Pro	Leu	Ile	Leu	Thr	Phe	Tyr	Gly	Thr	Ile	Leu	Gly	Trp	Val	Leu	
	95					100					105					
TAT	TAT	TTG	GTG	AGT	GTT	AGT	TTT	AAT	TTG	CCT	AAC	AAT	ATC	CAA	GAA	387
Tyr	Tyr	Leu	Val	Ser	Val	Ser	Phe	Asn	Leu	Pro	Asn	Asn	Ile	Gln	Glu	
	110				115					120				125		
TCT	GAA	CAA	ATT	TTT	ACT	CAA	ACT	TTG	CAG	TCT	ATA	GGG	CTA	CAA	TCC	435
Ser	Glu	Gln	Ile	Phe	Thr	Gln	Thr	Leu	Gln	Ser	Ile	Gly	Leu	Gln	Ser	
				130					135					140		
ATA	GGG	CTT	TTT	AGC	GTT	TTA	TTG	ATA	ACC	GGA	TGG	ATT	GTT	TCT	AGG	483
Ile	Gly	Leu	Phe	Ser	Val	Leu	Leu	Ile	Thr	Gly	Trp	Ile	Val	Ser	Arg	
		145						150					155			
GGG	ATT	AAA	GAA	GGC	ATT	GAA	AAG	CTC	AAT	TTG	GTT	TTA	ATG	CCC	TTA	531
Gly	Ile	Lys	Glu	Gly	Ile	Glu	Lys	Leu	Asn	Leu	Val	Leu	Met	Pro	Leu	
		160					165					170				
CTC	TTT	GCT	ACT	TTT	TTT	GGT	TTG	CTT	TTC	TAT	GCG	ATG	AGC	ATG	GAT	579
Leu	Phe	Ala	Thr	Phe	Phe	Gly	Leu	Leu	Phe	Tyr	Ala	Met	Ser	Met	Asp	
	175					180					185					
TCT	TTT	TCT	AAA	GCT	TTT	CAT	TTC	ATG	TTT	GAT	TTC	AAA	CCA	AAA	GAT	627

Ser 190	Phe	Ser	Lys	Ala	Phe 195	His	Phe	Met	Phe	Asp 200	Phe	Lys	Pro	Lys	Asp 205	
TTG Leu	ACC Thr	TCT Ser	CAA Gln	GTG Val 210	TTC Phe	ACT Thr	TAT Tyr	TCC Ser	TTG Leu 215	GGG Gly	CAG Gln	GTT Val	TTC Phe	TTT Phe 220	TCC Ser	675
TTA Leu	AGC Ser	ATC Ile	GGT Gly 225	TTA Leu	GGG Gly	ATC Ile	AAT Asn 230	ATC Ile	ACT Thr	TAC Tyr	GCT Ala	GCG Ala	GTT Val 235	ACG Thr	GAT Asp	723
AAA Lys	ACG Thr	CAG Gln 240	AAT Asn	TTG Leu	CTT Leu	AAA Lys	AGC Ser 245	ACT Thr	ATT Ile	TGG Trp	GTG Val 250	GTT Val	TTA Leu	TCA Ser	GGA Gly	771
ATT Ile 255	CTA Leu	ATT Ile	TCT Ser	CTT Leu	GTG Val 260	GCA Ala	GGA Gly	CTT Leu	ATG Met	ATT Ile 265	TTC Phe	ACT Thr	TTT Phe	GTG Val	TTT Phe	819
GAA Glu 270	TAT Tyr	GGG Gly	GCG Ala	AAT Asn 275	GTC Val	TCA Ser	CAA Gln	GGC Gly	ACA Thr 280	GGG Gly	TTA Leu	ATC Ile	TTC Phe	ACT Thr	TCT Ser 285	867
TTA Leu	CCG Pro	GTG Val	GTT Val	TTT Phe 290	GGC Gly	CAA Gln	ATG Met	GGA Gly	GCG Ala 295	ATA Ile	GGC Gly	ATT Ile	CTT Leu	GTT Val 300	TCG Ser	915
ATT Ile	CTT Leu	TTC Phe 305	TTG Leu	CTC Ala	GCG Ala	CTC Leu	GCT Ala 310	TTT Phe	GCT Ala	GGC Gly	ATC Ile	ACT Thr	TCT Ser 315	ACG Thr	GTG Val	963
GCT Ala	TTA Leu	TTG Leu 320	GAG Glu	CCA Pro	AGC Ser	GTG Val	ATG Met 325	TAT Tyr	CTT Leu	ACC Thr	GAA Glu 330	AGG Arg	TAT Tyr	CAA Gln	TAC Tyr	1011
TCT Ser 335	CGT Arg	TTT Phe	AAG Lys	GTT Val	ACT Thr	TGG Trp 340	GGT Gly	CTT Leu	GTA Val	GCA Ala 345	CTA Leu	ATT Ile	TTT Phe	GTG Val	GTA Val	1059
GGC Gly 350	GTG Val	GTG Val	TTG Leu	ATT Ile 355	TTC Phe	TCG Ser	CTC Leu	CAT His	AAG Lys 360	GAT Asp	TAT Tyr	AAA Lys	GAT Asp	TAT Tyr	CTC Leu 365	1107
ACT Thr	TTC Phe	TTT Phe	GAA Glu 370	AAA Lys	AGT Ser	CTT Leu	TTT Phe	GAT Asp 375	TGG Trp	TTG Leu	GAT Asp	TTT Phe	GCA Ala 380	TCA Ser	AGC Ser	1155
ACC Thr	ATT Ile	ATC Ile	ATG Met 385	CCT Pro	TTA Leu	GGC Gly	GGG Gly	ATG Met 390	GCA Ala	ACC Thr	TTT Phe	ATT Ile	TTT Phe 395	ATG Met	GGT Gly	1203
TGG Trp	GTT Val	TTG Leu 400	AAA Lys	AAA Lys	GAA Glu	AAA Lys	TTG Leu 405	CGT Arg	CTT Leu	TTG Leu	AGC Ser 410	GTG Val	CAC His	TTT Phe	TTA Leu	1251
GGC Gly 415	CCT Pro	AAA Lys	TTG Leu	TTT Phe	GCA Ala 420	ACT Thr	TGG Trp 425	TAT Tyr	TTC Phe	TTG Leu 425	CTT Leu	AAA Lys	TAT Tyr	ATC Ile	ACC Thr	1299

CCT TTA ATT GTG TTT TCC ATT TGG TTG AGC AAG ATT TAT TAAAATATTT GG 1350
 Pro Leu Ile Val Phe Ser Ile Trp Leu Ser Lys Ile Tyr
 430 435 440

CATGGGAAAA TTTTCTAAAT TAGGCT

1376

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

Met	Gly	Asn	His	Phe	Ser	Lys	Leu	Gly	Phe	Val	Leu	Ala	Ala	Leu	Gly
1				5					10					15	
Ser	Ala	Ile	Gly	Leu	Gly	His	Ile	Trp	Arg	Phe	Pro	Tyr	Met	Thr	Gly
			20					25					30		
Val	Ser	Gly	Gly	Gly	Ala	Phe	Val	Leu	Leu	Phe	Leu	Phe	Leu	Ser	Leu
		35					40					45			
Ser	Val	Gly	Ala	Ala	Met	Phe	Ile	Ala	Glu	Met	Leu	Leu	Gly	Gln	Ser
	50					55					60				
Thr	Gln	Lys	Asn	Val	Thr	Glu	Ala	Phe	Lys	Glu	Leu	Asp	Ile	Asn	Pro
65					70					75				80	
Lys	Lys	Arg	Trp	Lys	Tyr	Ala	Gly	Leu	Leu	Val	Ser	Gly	Pro	Leu	
				85				90					95		
Ile	Leu	Thr	Phe	Tyr	Gly	Thr	Ile	Leu	Gly	Trp	Val	Leu	Tyr	Tyr	Leu
			100					105					110		
Val	Ser	Val	Ser	Phe	Asn	Leu	Pro	Asn	Asn	Ile	Gln	Glu	Ser	Glu	Gln
		115					120					125			
Ile	Phe	Thr	Gln	Thr	Leu	Gln	Ser	Ile	Gly	Leu	Gln	Ser	Ile	Gly	Leu
	130					135					140				
Phe	Ser	Val	Leu	Leu	Ile	Thr	Gly	Trp	Ile	Val	Ser	Arg	Gly	Ile	Lys
145					150					155				160	
Glu	Gly	Ile	Glu	Lys	Leu	Asn	Leu	Val	Leu	Met	Pro	Leu	Leu	Phe	Ala
				165					170					175	
Thr	Phe	Phe	Gly	Leu	Leu	Phe	Tyr	Ala	Met	Ser	Met	Asp	Ser	Phe	Ser
			180					185					190		
Lys	Ala	Phe	His	Phe	Met	Phe	Asp	Phe	Lys	Pro	Lys	Asp	Leu	Thr	Ser
		195					200					205			
Gln	Val	Phe	Thr	Tyr	Ser	Leu	Gly	Gln	Val	Phe	Phe	Ser	Leu	Ser	Ile
	210					215					220				
Gly	Leu	Gly	Ile	Asn	Ile	Thr	Tyr	Ala	Ala	Val	Thr	Asp	Lys	Thr	Gln
225					230					235				240	
Asn	Leu	Leu	Lys	Ser	Thr	Ile	Trp	Val	Val	Leu	Ser	Gly	Ile	Leu	Ile
				245					250					255	
Ser	Leu	Val	Ala	Gly	Leu	Met	Ile	Phe	Thr	Phe	Val	Phe	Glu	Tyr	Gly
			260					265					270		
Ala	Asn	Val	Ser	Gln	Gly	Thr	Gly	Leu	Ile	Phe	Thr	Ser	Leu	Pro	Val
		275					280					285			
Val	Phe	Gly	Gln	Met	Gly	Ala	Ile	Gly	Ile	Leu	Val	Ser	Ile	Leu	Phe
	290					295					300				
Leu	Leu	Ala	Leu	Ala	Phe	Ala	Gly	Ile	Thr	Ser	Thr	Val	Ala	Leu	Leu
305					310					315				320	

Glu	Pro	Ser	Val	Met	Tyr	Leu	Thr	Glu	Arg	Tyr	Gln	Tyr	Ser	Arg	Phe	
				325					330					335		
Lys	Val	Thr	Trp	Gly	Leu	Val	Ala	Leu	Ile	Phe	Val	Val	Gly	Val	Val	
			340					345					350			
Leu	Ile	Phe	Ser	Leu	His	Lys	Asp	Tyr	Lys	Asp	Tyr	Leu	Thr	Phe	Phe	
		355					360					365				
Glu	Lys	Ser	Leu	Phe	Asp	Trp	Leu	Asp	Phe	Ala	Ser	Ser	Thr	Ile	Ile	
	370					375					380					
Met	Pro	Leu	Gly	Gly	Met	Ala	Thr	Phe	Ile	Phe	Met	Gly	Trp	Val	Leu	
385					390					395					400	
Lys	Lys	Glu	Lys	Leu	Arg	Leu	Leu	Ser	Val	His	Phe	Leu	Gly	Pro	Lys	
			405					410						415		
Leu	Phe	Ala	Thr	Trp	Tyr	Phe	Leu	Leu	Lys	Tyr	Ile	Thr	Pro	Leu	Ile	
		420					425						430			
Val	Phe	Ser	Ile	Trp	Leu	Ser	Lys	Ile	Tyr							
	435						440									

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 17...1081
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

GAAATAAGGA	TGCTTG	ATG	AAA	AGC	ATT	TTG	CTC	TTT	ATG	ATT	TTT	GTA	GTT		52	
		Met	Lys	Ser	Ile	Leu	Leu	Phe	Met	Ile	Phe	Val	Val			
		1				5					10					
TGT	CAG	TTA	GAA	GGC	AAA	AAA	TTT	TCA	CAA	GAT	AAT	TTT	AAG	GTG	GAT	100
Cys	Gln	Leu	Glu	Gly	Lys	Lys	Phe	Ser	Gln	Asp	Asn	Phe	Lys	Val	Asp	
	15					20					25					
TAT	AAC	TAC	TAT	TTG	CGC	AAA	CAG	GAT	TTG	CAC	ATC	ATT	AAA	ACG	CAA	148
Tyr	Asn	Tyr	Tyr	Leu	Arg	Lys	Gln	Asp	Leu	His	Ile	Ile	Lys	Thr	Gln	
	30					35				40						
AAC	GAT	TTG	TCC	AAT	TCT	TGG	TAT	CTC	CCT	CCA	CAA	AAA	GCC	CCC	AAA	196
Asn	Asp	Leu	Ser	Asn	Ser	Trp	Tyr	Leu	Pro	Pro	Gln	Lys	Ala	Pro	Lys	
45					50					55				60		
GAA	CAT	TCT	TGG	GTG	GAT	TTT	GCT	AAA	AAA	TAT	TTA	AAC	ATG	ATG	GAT	244
Glu	His	Ser	Trp	Val	Asp	Phe	Ala	Lys	Lys	Tyr	Leu	Asn	Met	Met	Asp	
			65					70						75		
TAT	CTA	GGC	ACT	TAT	TTT	CTG	CCT	TTT	TAT	CAT	AGT	TTC	ACC	CCC	ATT	292
Tyr	Leu	Gly	Thr	Tyr	Phe	Leu	Pro	Phe	Tyr	His	Ser	Phe	Thr	Pro	Ile	
			80					85						90		

TTT	CAA	TGG	TAC	CAC	CCC	AAT	ATC	AAC	CCG	TAT	CAA	CGC	AAT	GAG	TTT	340
Phe	Gln	Trp	Tyr	His	Pro	Asn	Ile	Asn	Pro	Tyr	Gln	Arg	Asn	Glu	Phe	
		95														
AAG	TTC	CAA	ATT	AGT	TTT	AGA	GTG	CCT	GTA	TTT	AGG	CAT	ATT	CTT	TGG	388
Lys	Phe	Gln	Ile	Ser	Phe	Arg	Val	Pro	Val	Phe	Arg	His	Ile	Leu	Trp	
		110														
ACT	AAA	GGC	ACG	CTG	TAT	TTA	GCT	TAT	ACC	CAA	ACT	GAC	TGG	TTT	CAA	436
Thr	Lys	Gly	Thr	Leu	Tyr	Leu	Ala	Tyr	Thr	Gln	Thr	Asp	Trp	Phe	Gln	
		125														
ATT	TAC	AAT	GAC	CCC	CAA	TCC	GCT	CCC	ATG	CGA	ATG	ATG	AAT	TTC	ATG	484
Ile	Tyr	Asn	Asp	Pro	Gln	Ser	Ala	Pro	Met	Arg	Met	Met	Asn	Phe	Met	
			145													
CCT	GAA	CTC	ATT	TAT	GTT	TAT	CCT	ATC	AAT	TTT	AAA	CCT	TTT	GGG	GGT	532
Pro	Glu	Leu	Ile	Tyr	Val	Tyr	Pro	Ile	Asn	Phe	Lys	Pro	Phe	Gly	Gly	
			160													
AAA	ATA	GGG	AAT	TTT	TCT	GAA	ATT	TGG	ATA	GGT	TGG	CAG	CAC	ATT	TCT	580
Lys	Ile	Gly	Asn	Phe	Ser	Glu	Ile	Trp	Ile	Gly	Trp	Gln	His	Ile	Ser	
			175													
AAT	GGC	GTG	GGG	GGC	GCG	CAA	TGT	TAC	CAA	CCT	TTT	AAT	AAA	GAA	GGC	628
Asn	Gly	Val	Gly	Gly	Ala	Gln	Cys	Tyr	Gln	Pro	Phe	Asn	Lys	Glu	Gly	
			190													
AAT	CCT	GAA	AAC	CAG	TTT	CCA	GGA	CAA	CCT	GTA	ATC	GTT	AAA	GAT	TAT	676
Asn	Pro	Glu	Asn	Gln	Phe	Pro	Gly	Gln	Pro	Val	Ile	Val	Lys	Asp	Tyr	
			205													
AAT	GGG	CAA	AAA	GAT	GTG	CGC	TGG	GGG	GGG	TGT	CGT	TCG	GTG	AGC	GCG	724
Asn	Gly	Gln	Lys	Asp	Val	Arg	Trp	Gly	Gly	Cys	Arg	Ser	Val	Ser	Ala	
			225													
GGG	CAA	CGC	CCT	GTG	TTT	CGT	TTG	GTG	TGG	GAA	AAG	GGA	GGC	CTA	AAA	772
Gly	Gln	Arg	Pro	Val	Phe	Arg	Leu	Val	Trp	Glu	Lys	Gly	Gly	Leu	Lys	
			240													
ATC	ATG	GTC	GCT	TAT	TGG	CCC	TAT	GTC	CCT	TAT	GAT	CAA	TCC	AAT	CCT	820
Ile	Met	Val	Ala	Tyr	Trp	Pro	Tyr	Val	Pro	Tyr	Asp	Gln	Ser	Asn	Pro	
			255													
AAT	TTG	ATT	GAT	TAC	ATG	GGG	TAT	GGT	AAC	GCT	AAA	ATT	GAT	TAC	AGG	868
Asn	Leu	Ile	Asp	Tyr	Met	Gly	Tyr	Gly	Asn	Ala	Lys	Ile	Asp	Tyr	Arg	
			270													
AGA	GGG	CGC	CAC	CAT	TTT	GAA	TTG	CAG	CTT	TAT	GAT	ATT	TTC	ACG	CAA	916
Arg	Gly	Arg	His	His	Phe	Glu	Leu	Gln	Leu	Tyr	Asp	Ile	Phe	Thr	Gln	
			285													
TAC	TGG	CGT	TAT	GAT	CGC	TGG	CAT	GGA	GCT	TTC	CGC	TTA	GGC	TAT	ACC	964
Tyr	Trp	Arg	Tyr	Asp	Arg	Trp	His	Gly	Ala	Phe	Arg	Leu	Gly	Tyr	Thr	
			305													
TAT	CGC	ATT	AAC	CCT	TTT	GTG	GGG	ATT	TAT	GCG	CAG	TGG	TTT	AAC	GGC	1012
Tyr	Arg	Ile	Asn	Pro	Phe	Val	Gly	Ile	Tyr	Ala	Gln	Trp	Phe	Asn	Gly	

320 325 330
 TAT GGC GAT GGC TTG TAT GAA TAC GAT GTT TTT TCC AAT CGT ATA GGG 1060
 Tyr Gly Asp Gly Leu Tyr Glu Tyr Asp Val Phe Ser Asn Arg Ile Gly
 335 340 345
 GTA GGA ATA CGC TTA AAC CCT TAAAAAAGCG TTCTTTTAYG CTATAATTAA GACC 1115
 Val Gly Ile Arg Leu Asn Pro
 350 355
 AAAAAA 1120

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

Met	Lys	Ser	Ile	Leu	Leu	Phe	Met	Ile	Phe	Val	Val	Cys	Gln	Leu	Glu
1				5					10					15	
Gly	Lys	Lys	Phe	Ser	Gln	Asp	Asn	Phe	Lys	Val	Asp	Tyr	Asn	Tyr	Tyr
			20					25					30		
Leu	Arg	Lys	Gln	Asp	Leu	His	Ile	Ile	Lys	Thr	Gln	Asn	Asp	Leu	Ser
		35					40					45			
Asn	Ser	Trp	Tyr	Leu	Pro	Pro	Gln	Lys	Ala	Pro	Lys	Glu	His	Ser	Trp
	50					55				60					
Val	Asp	Phe	Ala	Lys	Lys	Tyr	Leu	Asn	Met	Met	Asp	Tyr	Leu	Gly	Thr
65				70					75					80	
Tyr	Phe	Leu	Pro	Phe	Tyr	His	Ser	Phe	Thr	Pro	Ile	Phe	Gln	Trp	Tyr
			85					90					95		
His	Pro	Asn	Ile	Asn	Pro	Tyr	Gln	Arg	Asn	Glu	Phe	Lys	Phe	Gln	Ile
		100					105						110		
Ser	Phe	Arg	Val	Pro	Val	Phe	Arg	His	Ile	Leu	Trp	Thr	Lys	Gly	Thr
		115					120					125			
Leu	Tyr	Leu	Ala	Tyr	Thr	Gln	Thr	Asp	Trp	Phe	Gln	Ile	Tyr	Asn	Asp
	130					135				140					
Pro	Gln	Ser	Ala	Pro	Met	Arg	Met	Met	Asn	Phe	Met	Pro	Glu	Leu	Ile
145				150					155					160	
Tyr	Val	Tyr	Pro	Ile	Asn	Phe	Lys	Pro	Phe	Gly	Gly	Lys	Ile	Gly	Asn
			165					170					175		
Phe	Ser	Glu	Ile	Trp	Ile	Gly	Trp	Gln	His	Ile	Ser	Asn	Gly	Val	Gly
		180					185					190			
Gly	Ala	Gln	Cys	Tyr	Gln	Pro	Phe	Asn	Lys	Glu	Gly	Asn	Pro	Glu	Asn
	195						200					205			
Gln	Phe	Pro	Gly	Gln	Pro	Val	Ile	Val	Lys	Asp	Tyr	Asn	Gly	Gln	Lys
	210					215					220				
Asp	Val	Arg	Trp	Gly	Gly	Cys	Arg	Ser	Val	Ser	Ala	Gly	Gln	Arg	Pro
225				230					235					240	
Val	Phe	Arg	Leu	Val	Trp	Glu	Lys	Gly	Gly	Leu	Lys	Ile	Met	Val	Ala
			245					250					255		
Tyr	Trp	Pro	Tyr	Val	Pro	Tyr	Asp	Gln	Ser	Asn	Pro	Asn	Leu	Ile	Asp
			260				265						270		

GTG GAT AAA GCT AAT AAG AGT TTA GAA GAA ATC GCT TGC GAA GAA GCG	390
Val Asp Lys Ala Asn Lys Ser Leu Glu Glu Ile Ala Cys Glu Glu Ala	
105 110 115	
CTA GAA GAA TGC GGT TAT CAA ATT AGC CCT AAA AAT TTA GAA ACC ATA	438
Leu Glu Glu Cys Gly Tyr Gln Ile Ser Pro Lys Asn Leu Glu Thr Ile	
120 125 130 135	
GGC CAA TTT TAT AGC GCG ACT GGG TTG AGT GGG AGT TTG CAA ACG CTC	486
Gly Gln Phe Tyr Ser Ala Thr Gly Leu Ser Gly Ser Leu Gln Thr Leu	
140 145 150	
TAT TAC GCT GAA GTG CAT AAG AAT TTG AAA GTT TCA AAG GGT GGG GGG	534
Tyr Tyr Ala Glu Val His Lys Asn Leu Lys Val Ser Lys Gly Gly Gly	
155 160 165	
ATT GAT ACC GAA AGG ATT GAA GTG CTG TTT TTA GAG CGA TCA AAA GCT	582
Ile Asp Thr Glu Arg Ile Glu Val Leu Phe Leu Glu Arg Ser Lys Ala	
170 175 180	
CTT GAT TTT ATA ATG GAT TTT CAA TAC GCT AAA ACC ACC GGA TTG TCT	630
Leu Asp Phe Ile Met Asp Phe Gln Tyr Ala Lys Thr Thr Gly Leu Ser	
185 190 195	
TTA GCC ATT TTA TGG CAT TTA AAA AAG TTT AAA AAT GTT TAAAAGGAAT TT	681
Leu Ala Ile Leu Trp His Leu Lys Lys Phe Lys Asn Val	
200 205 210	
TATGTTAAGG CTTTTG	697

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

Met Ser Tyr Phe Lys Asn Ala Phe Asn Gln Lys Ser Leu Ile Asp Asp	
1 5 10 15	
Ser Ser Val Tyr Leu Glu Pro Cys Ser Ser Ser Asn Phe Ile Glu Leu	
20 25 30	
Lys Arg Met His Tyr Asn Glu Glu Asn Thr Lys Lys Thr Trp Asp Ile	
35 40 45	
Ile Lys Ser Leu Asp Ser Val Ala Val Leu Leu Tyr Glu Lys Glu Ser	
50 55 60	
Asp Cys Phe Val Ile Val Lys Gln Phe Arg Pro Ala Ile Tyr Ala Arg	
65 70 75 80	
Arg Phe His Phe Lys Cys Asp Gln Asp Gln Thr Ile Asp Gly Tyr Thr	
85 90 95	
Tyr Glu Leu Cys Ala Gly Leu Val Asp Lys Ala Asn Lys Ser Leu Glu	
100 105 110	
Glu Ile Ala Cys Glu Glu Ala Leu Glu Glu Cys Gly Tyr Gln Ile Ser	
115 120 125	

Pro Lys Asn Leu Glu Thr Ile Gly Gln Phe Tyr Ser Ala Thr Gly Leu
130 135 140
Ser Gly Ser Leu Gln Thr Leu Tyr Tyr Ala Glu Val His Lys Asn Leu
145 150 155 160
Lys Val Ser Lys Gly Gly Ile Asp Thr Glu Arg Ile Glu Val Leu
165 170 175
Phe Leu Glu Arg Ser Lys Ala Leu Asp Phe Ile Met Asp Phe Gln Tyr
180 185 190
Ala Lys Thr Thr Gly Leu Ser Leu Ala Ile Leu Trp His Leu Lys Lys
195 200 205
Phe Lys Asn Val
210

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2071 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...2022
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

TGCGAACAAAT TATGGGATGA TATTATAAAAA ATTGGTGGGA ATGATAAG ATG AAC GGA	57
Met Asn Gly	
1	
CAT TTT ATC GGT TCT ATT TTG TAT GTG CTA GAT AGT AAT ACG CAC TCT	105
His Phe Ile Gly Ser Ile Leu Tyr Val Leu Asp Ser Asn Thr His Ser	
5 10 15	
AAC AAT ACA TTA CTC ATC ATT GAC GGC CAA CAA AGG CTC ACC ACT ATC	153
Asn Asn Thr Leu Leu Ile Ile Asp Gly Gln Gln Arg Leu Thr Thr Ile	
20 25 30 35	
ACG CTT TTA CTC ATC GCT TTA AGG AAT CAT CTA AGC GAA GAA GTT GAA	201
Thr Leu Leu Leu Ile Ala Leu Arg Asn His Leu Ser Glu Glu Val Glu	
40 45 50	
ATT TTG GAG AAA TTT TCG CGT AAA GAA ATA GAG AGC TAT CTT ATC AAC	249
Ile Leu Glu Lys Phe Ser Arg Lys Glu Ile Glu Ser Tyr Leu Ile Asn	
55 60 65	
AGC AAT AAG GAC GGC GAT AAG AAA TTC AGG CTC ATT CTT TCA GAG TCC	297
Ser Asn Lys Asp Gly Asp Lys Lys Phe Arg Leu Ile Leu Ser Glu Ser	
70 75 80	
GAT AAA GAC ACC TTG CTG TCT TTG ATT GAT AAA AAC AAA AGA AAG CCG	345
Asp Lys Asp Thr Leu Leu Ser Leu Ile Asp Lys Asn Lys Arg Lys Pro	
85 90 95	

AGC Ser 100	GAG Glu 100	CCT Pro 100	TCG Ser 100	GTA Val 100	AAA Lys 105	ATA Ile 105	GTG Val 105	GAA Glu 105	AAT Asn 110	TTT Phe 110	GAA Glu 110	TTG Leu 110	TTT Phe 110	GAA Glu 115	AAA Lys 115	393
TGG Trp 120	ATC Ile 120	AGT Ser 120	GAA Glu 120	AAC Asn 120	ACC Thr 120	GAC Asp 120	AAA Lys 125	CTA Leu 125	GAA Glu 125	ACG Thr 125	ATT Ile 125	TTT Phe 130	AAA Lys 130	GGA Gly 130	TTA Leu 130	441
AAA Lys 135	AAA Lys 135	CTC Leu 135	ATG Met 135	ATA Ile 135	GTT Val 140	TGG Trp 140	ATT Ile 140	TCT Ser 140	TTA Leu 140	GAT Asp 145	AAA Lys 145	GGA Gly 145	AAA Lys 145	GAT Asp 145	GAT Asp 145	489
CCT Pro 150	CAA Gln 150	CTT Leu 150	ATT Ile 150	TTT Phe 150	GAG Glu 155	AGC Ser 155	ATG Met 155	AAC Asn 155	TCA Ser 160	AAA Lys 160	GAT Asp 160	ATC Ile 160	GAA Glu 160	CTC Leu 160	ACG Thr 160	537
CAA Gln 165	ACG Thr 165	GAT Asp 165	TTG Leu 165	ATC Ile 165	AGA Arg 170	AAT Asn 170	TAT Tyr 170	ATC Ile 170	GTA Val 175	ATG Met 175	GAA Glu 175	ACG Thr 175	GAG Glu 175	GTT Val 175	GAA Glu 175	585
AAA Lys 180	CAG Gln 180	GAA Glu 180	GAC Asp 180	TTT Phe 185	TAT Tyr 185	AAT Asn 185	CAA Gln 185	TAT Tyr 190	TGG Trp 190	AGG Arg 190	GCT Ala 190	ATG Met 190	GAG Glu 195	GAG Glu 195	AGA Arg 195	633
TTT Phe 200	GAA Glu 200	CAA Gln 200	AAT Asn 200	GAA Glu 200	ACA Thr 200	TTG Leu 205	TTT Phe 205	AAT Asn 205	CGG Arg 205	TTT Phe 205	GTC Val 210	CGG Arg 210	CAT His 210	TAT Tyr 210	CTC Leu 210	681
ACG Thr 215	ATC Ile 215	AAA Lys 215	ATA Ile 215	GGA Gly 215	AAG Lys 215	ATT Ile 220	CCC Pro 220	AAT Asn 220	GAG Glu 225	AAA Lys 225	AGA Arg 225	GTT Val 225	TAT Tyr 225	GAA Glu 225	GCT Ala 225	729
TTC Phe 230	AAG Lys 230	GAT Asp 230	TAC Tyr 230	CGG Arg 235	CAA Gln 235	AAA Lys 235	AAG Lys 235	GGG Gly 235	ATA Ile 240	GAA Glu 240	ATA Ile 240	GAG Glu 240	GAT Asp 240	TTA Leu 240	TTA Leu 240	777
AAA Lys 245	GAT Asp 245	TTA Leu 245	CAA Gln 245	AAA Lys 245	TAC Tyr 250	TGC Cys 250	GGG Gly 250	TAT Tyr 250	TTT Phe 255	TGC Cys 255	CAG Gln 255	ATT Ile 255	GCA Ala 255	TTC Phe 255	AAA Lys 255	825
AAA Lys 260	GAA Glu 260	GAC Asp 260	GAT Asp 265	AAA Lys 265	GAT Asp 265	TTA Leu 270	AAC Asn 270	AAG Lys 270	GCT Ala 270	TTA Leu 275	AGT Ser 275	TTT Phe 275	TTG Leu 275	GTG Val 275	AAT Asn 275	873
TTA Leu 280	GAG Glu 280	ATG Met 280	GAT Asp 280	GTG Val 280	ATC Ile 280	TAT Tyr 285	CCG Pro 285	CTA Leu 285	CTA Leu 285	CTA Leu 285	GAG Glu 290	CTT Leu 290	TAT Tyr 290	AGC Ser 290	GAT Asp 290	921
TAT Tyr 295	AAG Lys 295	GAT Asp 295	GGC Gly 295	GTT Val 300	TTA Leu 300	TCC Ser 300	AAG Lys 300	CAG Gln 300	GAT Asp 305	TTT Phe 305	ATC Ile 305	CCT Pro 305	ATT Ile 305	ATC Ile 305	TAT Tyr 305	969
TTA Leu 310	ATA Ile 310	GAG Glu 310	AGC Ser 310	TAT Tyr 315	ATT Ile 315	TGC Cys 315	AGA Arg 315	AGG Arg 320	GCG Ala 320	GTG Val 320	TGT Cys 320	GGG Gly 320	CTT Leu 320	GGC Gly 320	ACA Thr 320	1017
AAT Asn 1065	AGT Ser 1065	CTC Leu 1065	AAT Asn 1065	AAA Lys 1065	GTT Val 1065	TTT Phe 1065	CCC Pro 1065	TCT Ser 1065	TTT Phe 1065	ACA Thr 1065	AAG Lys 1065	CAC His 1065	ATC Ile 1065	CAA Gln 1065	AAA Lys 1065	1065

325				330				335								
GAT Asp 340	GAA Glu	TAT Tyr	TTT Phe	AAA Lys	AGC Ser	CTA Leu	AAG Lys	GCG Ala	CAT His	TTT Phe	GTC Val	TGT Cys	CTG Leu	ACA Thr	GAA Glu 355	1113
AAA Lys	CAA Gln	AGA Arg	TTT Phe	CCA Pro 360	AAC Asn	AAT Asn	GAC Asp	GAG Glu	TTT Phe 365	AAA Lys	AAG Lys	CTT Leu	TTT Phe	ATT Ile 370	ACG Thr	1161
ATA Ile	GAT Asp	TTT Phe	TAT Tyr 375	AAG Lys	TTT Phe	AAA Lys	AAA Lys	AAT Asn 380	AAA Lys	TAC Tyr	TTT Phe	CTT Leu	GAA Glu 385	AGG Arg	TTA Leu	1209
GAA Glu	AAT Asn	TTT Phe 390	GAC Asp	ACA Thr	AAA Lys	GAA Glu	CCG Pro 395	GTC Val	GAT Asp	ACT Thr	CAA Gln	AAA Lys 400	TGC Cys	AAT Asn	ATA Ile	1257
GAA Glu	CAT His 405	ATA Ile	ATG Met	CCT Pro	CAA Gln	ACC Thr 410	CTT Leu	ACT Thr	CCA Pro	GAA Glu	TGG Trp 415	CAA Gln	AGG Arg	GAT Asp	TTG Leu	1305
GGT Gly 420	GAA Glu	AAT Asn	TTT Phe	CAA Gln 425	GCA Ala	ATA Ile	CAC His	GAG Glu	AAA Lys	TAC Tyr 430	CTC Leu	CAC His	ACA Thr	ATA Ile	GGG Gly 435	1353
AAT Asn	CTC Leu	ACT Thr	CTA Leu	ACC Thr 440	GGT Gly	TAT Tyr	AAC Asn	TCT Ser	AAG Lys 445	TAT Tyr	AGC Ser	AAC Asn	AAT Asn	TCT Ser 450	TTC Phe	1401
CAA Gln	GAA Glu	AAA Lys	AGA Arg 455	GAT Asp	ATG Met	GAG Glu	AAG Lys	GGC Gly 460	TTT Phe	AAA Lys	CAA Gln	AGC Ser	TCA Ser 465	TTA Leu	AAA Lys	1449
CTC Leu	AAT Asn	CAA Gln 470	AGT Ser	TTG Leu	AAA Lys	GAT Asp	TTG Leu 475	GAA Glu	TCT Ser	TTT Phe	GGC Gly 480	GAA Glu	AAA Lys	GAG Glu	ATT Ile	1497
GAA Glu	AAA Lys 485	AGG Arg	GCT Ala	AGT Ser	GAT Asp	TTA Leu 490	GCG Ala	GAT Asp	TGG Trp	GCT Ala 495	TTA Leu	AAG Lys	ATT Ile	TGG Trp	ACT Thr	1545
TAC Tyr 500	CCA Pro	ATT Ile	CTA Leu	GAG Glu	GCA Ala 505	GAA Glu	ACA Thr	TTA Leu	GAG Glu	GAA Glu 510	TAT Tyr	AAA Lys	CCC Pro	AAA Lys	AAA Lys 515	1593
GAA Glu	AAG Lys	AAA Lys	GAA Glu 520	AAG Lys	AAA Lys	GAA Glu	AAA Lys	GAG Glu 525	GAG Glu	TAT Tyr	AAA Lys	CTC Leu	AAG Lys	AAA Lys 530	GAA Glu	1641
AAA Lys	AAG Lys	GTT Val 535	TAT Tyr	GAT Asp	TTA Leu	AGC Ser	TCT Ser	TAT Tyr 540	AAG Lys	TTT Phe	AGC Ser	TCT Ser	GAT Asp 545	TCA Ser	AGG Arg	1689
GAA Glu	TTG Leu	TTT Phe 550	GAT Asp	ATT Ile	TTA Leu	AGA Arg	GAA Glu 555	AAG Lys	ATT Ile	AAA Lys	GCT Ala 560	CTT Leu	GAT Asp	GAA Glu	AGG Arg	1737

Glu	Leu	Thr	Gln	Thr 165	Asp	Leu	Ile	Arg	Asn 170	Tyr	Ile	Val	Met	Glu 175	Thr
Glu	Val	Glu	Lys 180	Gln	Glu	Asp	Phe	Tyr 185	Asn	Gln	Tyr	Trp	Arg 190	Ala	Met
Glu	Glu	Arg 195	Phe	Glu	Gln	Asn	Glu 200	Thr	Leu	Phe	Asn	Arg 205	Phe	Val	Arg
His	Tyr 210	Leu	Thr	Ile	Lys	Ile 215	Gly	Lys	Ile	Pro	Asn 220	Glu	Lys	Arg	Val
Tyr 225	Glu	Ala	Phe	Lys	Asp 230	Tyr	Arg	Gln	Lys	Lys 235	Gly	Ile	Glu	Ile	Glu 240
Asp	Leu	Leu	Lys 245	Asp	Leu	Gln	Lys	Tyr	Cys 250	Gly	Tyr	Phe	Cys 255	Gln	Ile
Ala	Phe	Lys	Lys 260	Glu	Asp	Asp	Lys	Asp 265	Leu	Asn	Lys	Ala	Leu 270	Ser	Phe
Leu	Val	Asn 275	Leu	Glu	Met	Asp	Val 280	Ile	Tyr	Pro	Leu	Leu 285	Leu	Glu	Leu
Tyr	Ser 290	Asp	Tyr	Lys	Asp	Gly 295	Val	Leu	Ser	Lys	Gln 300	Asp	Phe	Ile	Pro
Ile 305	Ile	Tyr	Leu	Ile	Glu 310	Ser	Tyr	Ile	Cys	Arg 315	Arg	Ala	Val	Cys	Gly 320
Leu	Gly	Thr	Asn 325	Ser	Leu	Asn	Lys	Val	Phe 330	Pro	Ser	Phe	Thr 335	Lys	His
Ile	Gln	Lys	Asp 340	Glu	Tyr	Phe	Lys	Ser 345	Leu	Lys	Ala	His	Phe 350	Val	Cys
Leu	Thr	Glu 355	Lys	Gln	Arg	Phe	Pro 360	Asn	Asn	Asp	Glu	Phe 365	Lys	Lys	Leu
Phe	Ile 370	Thr	Ile	Asp	Phe	Tyr 375	Lys	Phe	Lys	Lys	Asn 380	Lys	Tyr	Phe	Leu
Glu 385	Arg	Leu	Glu	Asn 390	Phe	Asp	Thr	Lys	Glu	Pro 395	Val	Asp	Thr	Gln	Lys 400
Cys	Asn	Ile	Glu	His 405	Ile	Met	Pro	Gln	Thr 410	Leu	Thr	Pro	Glu	Trp 415	Gln
Arg	Asp	Leu	Gly 420	Glu	Asn	Phe	Gln	Ala 425	Ile	His	Glu	Lys	Tyr 430	Leu	His
Thr	Ile	Gly 435	Asn	Leu	Thr	Leu	Thr 440	Gly	Tyr	Asn	Ser	Lys 445	Tyr	Ser	Asn
Asn	Ser 450	Phe	Gln	Glu	Lys	Arg 455	Asp	Met	Glu	Lys	Gly 460	Phe	Lys	Gln	Ser
Ser 465	Leu	Lys	Leu	Asn 470	Gln	Ser	Leu	Lys	Asp	Leu 475	Glu	Ser	Phe	Gly	Glu 480
Lys	Glu	Ile	Glu	Lys 485	Arg	Ala	Ser	Asp	Leu 490	Ala	Asp	Trp	Ala	Leu 495	Lys
Ile	Trp	Thr	Tyr 500	Pro	Ile	Leu	Glu	Ala 505	Glu	Thr	Leu	Glu	Glu 510	Tyr	Lys
Pro	Lys 515	Lys	Glu	Lys	Lys	Glu	Lys 520	Lys	Glu	Lys	Glu	Glu 525	Tyr	Lys	Leu
Lys	Lys 530	Glu	Lys	Lys	Val	Tyr 535	Asp	Leu	Ser	Ser	Tyr 540	Lys	Phe	Ser	Ser
Asp 545	Ser	Arg	Glu	Leu	Phe 550	Asp	Ile	Leu	Arg	Glu 555	Lys	Ile	Lys	Ala	Leu 560
Asp	Glu	Arg	Ile	Thr 565	Glu	Lys	Phe	Asn	Gln 570	Lys	Tyr	Ile	Ala	Tyr 575	Lys
Phe	Cys	Lys	Ile 580	Ser	Phe	Val	Asp	Ile 585	Val	Val	Gln	Glu	Lys 590	Gly	Leu
Lys	Leu	Tyr 595	Leu	Lys	Met	Asn	Leu 600	Asn	Glu	Leu	Gln	Asp 605	Glu	Ile	Lys
Glu	Lys 610	Leu	Lys	Ile	Arg	Asp 615	Val	Ser	Asn	Ile	Gly 620	Arg	Pro	Cys	Val

Gly	Asn	Met	Glu	Val	Glu	Leu	Glu	Thr	Lys	Glu	Asn	Ile	Pro	Tyr	Cys
625					630					635					640
Leu	Gly	Leu	Ile	Lys	Gln	Ala	Leu	Glu	Lys	Gln	Met	Gly	Gly	Arg	Asn
				645					650					655	
Arg	Gln														

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...558
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

GTGGTGGCTG	AGTAGAAA	ATG	TTT	GAA	GCG	ACG	ACG	ATT	TTA	GGC	TAT	AGA	51
		Met	Phe	Glu	Ala	Thr	Thr	Ile	Leu	Gly	Tyr	Arg	
		1				5					10		
GGG GAA TTG AAT CAT AAA AAG TTC GCG CTC ATT GGA GGC GAT GGG CAG	99												
Gly Glu Leu Asn His Lys Lys Phe Ala Leu Ile Gly Gly Asp Gly Gln													
	15					20					25		
GTA ACT TTG GGT AAT TGC GTG GTC AAA GCC AAT GCG ACA AAA ATC AGA	147												
Val Thr Leu Gly Asn Cys Val Val Lys Ala Asn Ala Thr Lys Ile Arg													
	30					35					40		
AGC TTG TAT CAC AAC CAG GTT TTA AGC GGG TTT GCC GGA AGC ACC GCG	195												
Ser Leu Tyr His Asn Gln Val Leu Ser Gly Phe Ala Gly Ser Thr Ala													
	45					50					55		
GAC GCT TTT AGT TTG TTT GAT ATG TTT GAA CGC ATT TTA GAG AGC AAA	243												
Asp Ala Phe Ser Leu Phe Asp Met Phe Glu Arg Ile Leu Glu Ser Lys													
	60					65					70		75
AAG GGG GAT TTG TTT AAA AGC GTG GTG GAT TTC AGT AAA GAA TGG CGC	291												
Lys Gly Asp Leu Phe Lys Ser Val Val Asp Phe Ser Lys Glu Trp Arg													
	80										85		90
AAA GAT AAG TAT TTA CGC CGA CTG GAA GCG ATG ATG ATC GTT TTA AAC	339												
Lys Asp Lys Tyr Leu Arg Arg Leu Glu Ala Met Met Ile Val Leu Asn													
	95										100		105
TTC GAT CAC ATT TTC ATT TTG AGC GGC ATG GGC GAT GTT TTA GAA GCT	387												
Phe Asp His Ile Phe Ile Leu Ser Gly Met Gly Asp Val Leu Glu Ala													
	110										115		120
GAA GAC AAT AAG ATC GCT GCT ATT GGG AGT GGG GGG AAT TAC GCT TTA	435												

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 34...396
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

TGTTTCATAG TAACAAATTG AAAATATACC ATT ATG TAT GGA GGT AAT GCT ATG	54
Met Tyr Gly Gly Asn Ala Met	
1 5	
GCT GAC ACA ATC AAT ACA ACT GAA GCA ACT CAT GAA ACA AAA AAA CCA	102
Ala Asp Thr Ile Asn Thr Thr Glu Ala Thr His Glu Thr Lys Lys Pro	
10 15 20	
AAC GCT TTT GTA AAT TTT TTC AAA AAC AAT TTG ACT GAT AAG CGT TAT	150
Asn Ala Phe Val Asn Phe Phe Lys Asn Asn Leu Thr Asp Lys Arg Tyr	
25 30 35	
GAT TCA TTA GGT CTC ATT GGA GCA GGG GTT TTA TGT TGT GTC TTG AGC	198
Asp Ser Leu Gly Leu Ile Gly Ala Gly Val Leu Cys Cys Val Leu Ser	
40 45 50 55	
GGT GCT ATG GGG ATT GTT GGG ATA ATC TTT GTC GCA ATA GGA ATC TTT	246
Gly Ala Met Gly Ile Val Gly Ile Ile Phe Val Ala Ile Gly Ile Phe	
60 65 70	
TTG TCT TTT TCT AAT ATC AAC TTA GTG AAA TTA GTT GAA AAA TTG TCC	294
Leu Ser Phe Ser Asn Ile Asn Leu Val Lys Leu Val Glu Lys Leu Ser	
75 80 85	
AAA AAA CAA TCT AAA GTG CCA ACA ACT GTC AAT AAC GAA ACT CAA AAA	342
Lys Lys Gln Ser Lys Val Pro Thr Val Asn Asn Glu Thr Gln Lys	
90 95 100	
TCT CAA GCA ACA AGC GTT ACC AAC GAA CCA ACT GAA GCC AAA GAG ACT	390
Ser Gln Ala Thr Ser Val Thr Asn Glu Pro Thr Glu Ala Lys Glu Thr	
105 110 115	
AAA GAT TGAGGCAAAA CAACGATTTT GACTGAAGAA AGAATGAGAG AAAATTTCAA AA	448
Lys Asp	
120	
AT	450

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

Met Tyr Gly Gly Asn Ala Met Ala Asp Thr Ile Asn Thr Thr Glu Ala
1 5 10 15
Thr His Glu Thr Lys Lys Pro Asn Ala Phe Val Asn Phe Phe Lys Asn
20 25 30
Asn Leu Thr Asp Lys Arg Tyr Asp Ser Leu Gly Leu Ile Gly Ala Gly
35 40 45
Val Leu Cys Cys Val Leu Ser Gly Ala Met Gly Ile Val Gly Ile Ile
50 55 60
Phe Val Ala Ile Gly Ile Phe Leu Ser Phe Ser Asn Ile Asn Leu Val
65 70 75 80
Lys Leu Val Glu Lys Leu Ser Lys Lys Gln Ser Lys Val Pro Thr Thr
85 90 95
Val Asn Asn Glu Thr Gln Lys Ser Gln Ala Thr Ser Val Thr Asn Glu
100 105 110
Pro Thr Glu Ala Lys Glu Thr Lys Asp
115 120

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 69...443
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

TAACCATTAG TTTCAAGCAG TATGAAAATC TTCTCCATAT CCATCAAAAAA GGTTGCGACA 60
ATGAAGTG ATG TGC AGA ACG CTC ATC TCT ATC GCT TTG TTA GAA AGC TCT 110
Met Cys Arg Thr Leu Ile Ser Ile Ala Leu Leu Glu Ser Ser
1 5 10
CTA GGG TTG AAC AAC AGG CGA GAA AAA TCC CTT AAA GAC ACT TCT TAT 158
Leu Gly Leu Asn Asn Arg Arg Glu Lys Ser Leu Lys Asp Thr Ser Tyr 30
15 20 25 30
TCC ATG TTT CAT ATC ACC CTA AAC ACC GCT AAA AAA TTC TAC CCT ACC 206
Ser Met Phe His Ile Thr Leu Asn Thr Ala Lys Lys Phe Tyr Pro Thr 45
35 40 45
TAC TCT AAA ACG CTC CTC AAA TTC AAA TTG CTA AAC GAT GTG GGT TTT 254
Tyr Ser Lys Thr Leu Leu Lys Phe Lys Leu Leu Asn Asp Val Gly Phe 60
50 55 60

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 31...2274
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

ATTTTATATC AAACACAGGT AGTAGGCACA	ATG GAA GAC TTT TTG TAT AAC ACC	54
	Met Glu Asp Phe Leu Tyr Asn Thr	
	1 5	
TTA TAT TTC ATA GAG GAT TAT AAG TTG GTT GTT ATT TTT AGT TTC ATA		102
Leu Tyr Phe Ile Glu Asp Tyr Lys Leu Val Val Ile Phe Ser Phe Ile		
10 15 20		
GGG TTA ATA GCG TTA TTT TTT CTT TAC AAA TTC ATA AAA GCT CAA AAA		150
Gly Leu Ile Ala Leu Phe Phe Leu Tyr Lys Phe Ile Lys Ala Gln Lys		
25 30 35 40		
AAG GCT TTT AAA GAT AAA GCT AAC CAG CCT CAA AAG AAA AAA AGC TTT		198
Lys Ala Phe Lys Asp Lys Ala Asn Gln Pro Gln Lys Lys Lys Ser Phe		
45 50 55		
AAA GAA ATC ATT ATA GAT GGG CTG AAA GAA AGG GTT AAA ACC TTT GGC		246
Lys Glu Ile Ile Ile Asp Gly Leu Lys Glu Arg Val Lys Thr Phe Gly		
60 65 70		
TTT TGG TTG CAA GCT ATA CTA TTA CTA TCC TAT TCT TTT ATC ACA TCA		294
Phe Trp Leu Gln Ala Ile Leu Leu Leu Ser Tyr Ser Phe Ile Thr Ser		
75 80 85		
GGA TTA TTT TTC TTG ATT CTC TTA GGT AAT TTT TAT GAT GAT AAT CGA		342
Gly Leu Phe Phe Leu Ile Leu Leu Gly Asn Phe Tyr Asp Asp Asn Arg		
90 95 100		
TCG CCT GAG AGC GAT GAT GAT CTT TTT GAT ATA TGG ATC TAT GCG ATA		390
Ser Pro Glu Ser Asp Asp Asp Leu Phe Asp Ile Trp Ile Tyr Ala Ile		
105 110 115 120		
CAA GAT TTT CCT AAT TAC TAT TTT AAA GCG CTT GGT TTT AGT TCA CTC		438
Gln Asp Phe Pro Asn Tyr Tyr Phe Lys Ala Leu Gly Phe Ser Ser Leu		
125 130 135		
AAG ATT TAT GGG TTC AAT ATA TCC TTA GTC GTA TAT GGT TCT ATT TTA		486
Lys Ile Tyr Gly Phe Asn Ile Ser Leu Val Val Tyr Gly Ser Ile Leu		
140 145 150		
TGC TCT TAT ATC TTC ATT ACC TTT TTT GTG TGG TTC TTA AAA TAC TTA		534
Cys Ser Tyr Ile Phe Ile Thr Phe Phe Val Trp Phe Leu Lys Tyr Leu		
155 160 165		
ACT CGG ACT AGA GAT ATA GGA GCG AAT AAA AAA GTT GAT GAT CTC TTT		582
Thr Arg Thr Arg Asp Ile Gly Ala Asn Lys Lys Val Asp Asp Leu Phe		
170 175 180		
GGT AGC GCG AGT TGG GAA ACT GAA GAG AAA ATG ATC AAA GCC AAA CTC		630
Gly Ser Ala Ser Trp Glu Thr Glu Glu Lys Met Ile Lys Ala Lys Leu		
185 190 195 200		

ATC Ile	ACG Thr	CCC Pro	AAC Asn	AAT Asn 205	AAA Lys	AAA Lys	CGC Arg	GCC Ala	TTT Phe 210	GAC Asp	AAA Lys	CGA Arg	GAG Glu	GTG Val 215	ATT Ile	678
GTA Val	GGC Gly	AGG Arg	CGT Arg 220	GGC Gly	TTG Leu	GGG Gly	GAT Asp	TTT Phe 225	ATC Ile	GCT Ala	TAC Tyr	GCA Ala	GGG Gly 230	CAG Gln	GCG Ala	726
TTC Phe	ATT Ile	GGC Gly 235	TTG Leu	ATT Ile	GCT Ala	CCT Pro	ACT Thr 240	AGA Arg	AGC Ser	GGT Gly	AAG Lys	GGG Gly 245	GTG Val	GGT Gly	TTC Phe	774
ATC Ile 250	ATG Met	CCC Pro	AAT Asn	ATG Met	ATC Ile	AAT Asn 255	TAT Tyr	CCT Pro	CAA Gln	AAT Asn	ATC Ile 260	GTT Val	GTG Val	TTT Phe	GAC Asp	822
CCT Pro 265	AAA Lys	GCT Ala	GAC Asp	ACT Thr	ATG Met 270	GAG Glu	ACT Thr	TGC Cys	GGA Gly	AAA Lys 275	ATC Ile	AGA Arg	GAA Glu	AAA Lys	CGC Arg 280	870
TTC Phe	AAC Asn	CAA Gln	AAA Lys 285	GTG Val	TTC Phe	ATC Ile	TAT Tyr	GAA Glu	CCT Pro 290	TTC Phe	TCC Ser	TTA Leu	AAA Lys	ACA Thr 295	CAC His	918
CGA Arg	TTT Phe	AAT Asn	CCT Pro 300	TTC Phe	GCT Ala	TAT Tyr	GTG Val	GAT Asp 305	TTT Phe	GGT Gly	AAT Asn	GAT Asp	GTG Val 310	GTT Val	TTG Leu	966
ACC Thr	GAA Glu	GAC Asp 315	ATA Ile	CTC Leu	TCT Ser	CAA Gln	ATT Ile 320	GAC Asp	ACA Thr	CGC Arg	CTA Leu	AAA Lys 325	GGG Gly	CAT His	GGC Gly	1014
ATG Met 330	GTG Val	GCT Ala	AGT Ser	GGA Gly	GGG Gly	GAT Asp 335	TTT Phe	TCC Ser	ACT Thr	CAA Gln	ATC Ile 340	TTT Phe	GGA Gly	TTA Leu	GCA Ala	1062
AAG Lys 345	CTC Leu	GTG Val	TTC Phe	CCT Pro	GAA Glu 350	AGA Arg	CCT Pro	AAT Asn	GAA Glu	AAA Lys 355	GAT Asp	CCT Pro	TTC Phe	TTT Phe	AGC Ser 360	1110
AAT Asn	CAA Gln	GCG Ala	CGA Arg 365	AAT Asn	CTT Leu	TTT Phe	GTC Val	ATC Ile	AAT Asn 370	TGC Cys	AAT Asn	ATT Ile	TAC Tyr	AGG Arg 375	GAT Asp	1158
CTC Leu	ATG Met	TGG Trp	ACT Thr 380	AAA Lys	AAG Lys	GGG Gly	CTT Leu	GAG Glu 385	TTT Phe	GTC Val	AAA Lys	AGA Arg	AAA Lys 390	AAA Lys	ATC Ile	1206
ATC Ile	ATG Met	CCT Pro 395	GAA Glu	ACA Thr	CCC Pro	ACG Thr	ATG Met 400	TTT Phe	TTC Phe	ATA Ile	GGT Gly	TCT Ser 405	ATG Met	GCA Ala	AGC Ser	1254
GGG Gly 410	ATC Ile	AAC Asn	TTG Leu	ATT Ile	GAT Asp	GAA Glu 415	GAC Asp	ACA Thr	AAC Asn	ATG Met	GAA Glu 420	AAA Lys	GTC Val	GTG Val	TCT Ser	1302
TTA Leu	ATG Met	GAA Glu	TTT Phe	TTT Phe	GGA Gly	GGT Gly	GAA Glu	GAA Glu	GAT Asp	AAG Lys	AGT Ser	GGC Gly	GAT Asp	AAT Asn	CTA Leu	1350

425				430				435				440				
AGA Arg	GTG Val	CTT Leu	AGT Ser	CCT Pro 445	GCC Ala	ACT Thr	AGA Arg	AAC Asn	ATG Met 450	TGG Trp	AAT Asn	AGC Ser	TTC Phe	AAG Lys 455	ACA Thr	1398
ATG Met	GGC Gly	GGC Gly	GCT Ala 460	AGA Arg	GAA Glu	ACT Thr	TAT Tyr	AGC Ser 465	TCG Ser	GTT Val	CAA Gln	GGG Gly	GTA Val 470	TAC Tyr	ACT Thr	1446
TCA Ser	GCC Ala	TTT Phe 475	GCG Ala	CCT Pro	TAT Tyr	AAT Asn	AAC Asn 480	GCA Ala	ATG Met	ATT Ile	AGA Arg	AAT Asn 485	TTC Phe	ACG Thr	AGC Ser	1494
GCC Ala	AAT Asn 490	GAT Asp	TTT Phe	GAT Asp	TTC Phe	AGG Arg 495	CGT Arg	TTA Leu	AGG Arg	ATC Ile	GAT Asp 500	GAA Glu	GTG Val	AGT Ser	ATT Ile	1542
GGT Gly 505	GTG Val	ATC Ile	GCT Ala	AAT Asn	CCT Pro 510	AAA Lys	GAA Glu	AGC Ser	ACT Thr	ATT Ile 515	GTT Val	GGA Gly	CCG Pro	ATA Ile	TTA Leu 520	1590
GAG Glu	CTG Leu	TTT Phe	TTC Phe	AAT Asn 525	GTG Val	ATG Met	ATT Ile	TAT Tyr	AGC Ser 530	AAT Asn	TTG Leu	ATT Ile	CTG Leu	CCA Pro 535	ATC Ile	1638
CAT His	GAT Asp	CCA Pro	CAG Gln 540	TGC Cys	AAA Lys	AGA Arg	AGT Ser	TGC Cys 545	TTG Leu	ATG Met	CTC Leu	ATG Met	GAC Asp 550	GAA Glu	TTC Phe	1686
ACT Thr	TTA Leu	TGT Cys 555	GGC Gly	TAT Tyr	TTA Leu	GAG Glu	ACC Thr 560	TTT Phe	GTT Val	AAA Lys	GCG Ala	GTA Val 565	GGG Gly	ATT Ile	ATG Met	1734
GCA Ala	GAA Glu 570	TAC Tyr	AAC Asn	ATG Met	CGC Arg	CCC Pro 575	GCT Ala	TTT Phe	GTG Val	TTT Phe	CAA Gln 580	AGT Ser	AAG Lys	GCG Ala	CAA Gln	1782
CTA Leu 585	GAG Glu	AAT Asn	GAC Asp	CCC Pro	CCA Pro 590	CTT Leu	GGT Gly	TAT Tyr	GGT Gly 595	AGG Arg	AAT Asn	GGC Gly	GCT Ala	AAG Lys	ACT Thr 600	1830
ATT Ile	TTA Leu	GAC Asp	AAC Asn 605	CTT Leu	TCT Ser	TTG Leu	AAT Asn	ATG Met	TAT Tyr 610	TAT Tyr	GGG Gly	ATT Ile	AAC Asn 615	AAC Asn	GAT Asp	1878
AAC Asn	TAC Tyr	TAT Tyr	GAA Glu 620	CAT His	TTT Phe	GAA Glu	AAA Lys 625	CTT Leu	TCT Ser	AAG Lys	GTA Val	TTA Leu	GGG Gly 630	AAA Lys	TAC Tyr	1926
ACA Thr	AGG Arg	CAA Gln 635	GAC Asp	GTG Val	AGC Ser	CGA Arg	AGC Ser 640	ATT Ile	GAT Asp	GAT Asp	AAT Asn	ACA Thr 645	GGT Gly	AAG Lys	ACC Thr	1974
AAC Asn	ACT Thr 650	TCT Ser	ATC Ile	AGC Ser	AAC Asn	AAA Lys 655	GAG Glu	CGG Arg	TTT Phe	TTG Leu	ATG Met 660	ACC Thr	CCT Pro	GAT Asp	GAA Glu	2022

TTG ATG ACT ATG GGC GAT GAG CTT ATC ATT CTA GAG AAT ACG CTC AAA	2070
Leu Met Thr Met Gly Asp Glu Leu Ile Ile Leu Glu Asn Thr Leu Lys	
665 670 675 680	
CCT ATC AAG TGC CAC AAG GCG CTT TAC TAT GAT GAT CCA TTC TTC ACC	2118
Pro Ile Lys Cys His Lys Ala Leu Tyr Tyr Asp Asp Pro Phe Phe Thr	
685 690 695	
GAT GAA CTC ATT AAG GTA AGT CCA AGC TTG AGC AAG AAA TAC AAA TTG	2166
Asp Glu Leu Ile Lys Val Ser Pro Ser Leu Ser Lys Lys Tyr Lys Leu	
700 705 710	
GGG AAA GTG CCT AAT CAA GCA ACT TTC TAT GAT GAT TTG CAA GCC GCT	2214
Gly Lys Val Pro Asn Gln Ala Thr Phe Tyr Asp Asp Leu Gln Ala Ala	
715 720 725	
AAA ACT AGA GGT GAA TTG AGT TAT GAT AAA TCT TTA GTG CCT GTG GGT	2262
Lys Thr Arg Gly Glu Leu Ser Tyr Asp Lys Ser Leu Val Pro Val Gly	
730 735 740	
TCA AGT GAA CTG TGATTAAGAC AAAATATCTT AACAAAAAGA AAATTAAAAG ATAAT	2319
Ser Ser Glu Leu	
745	
GATATAAATA	2329

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

Met Glu Asp Phe Leu Tyr Asn Thr Leu Tyr Phe Ile Glu Asp Tyr Lys	
1 5 10 15	
Leu Val Val Ile Phe Ser Phe Ile Gly Leu Ile Ala Leu Phe Phe Leu	
20 25 30	
Tyr Lys Phe Ile Lys Ala Gln Lys Lys Ala Phe Lys Asp Lys Ala Asn	
35 40 45	
Gln Pro Gln Lys Lys Lys Ser Phe Lys Glu Ile Ile Ile Asp Gly Leu	
50 55 60	
Lys Glu Arg Val Lys Thr Phe Gly Phe Trp Leu Gln Ala Ile Leu Leu	
65 70 75 80	
Leu Ser Tyr Ser Phe Ile Thr Ser Gly Leu Phe Phe Leu Ile Leu Leu	
85 90 95	
Gly Asn Phe Tyr Asp Asp Asn Arg Ser Pro Glu Ser Asp Asp Asp Leu	
100 105 110	
Phe Asp Ile Trp Ile Tyr Ala Ile Gln Asp Phe Pro Asn Tyr Tyr Phe	
115 120 125	
Lys Ala Leu Gly Phe Ser Ser Leu Lys Ile Tyr Gly Phe Asn Ile Ser	
130 135 140	
Leu Val Val Tyr Gly Ser Ile Leu Cys Ser Tyr Ile Phe Ile Thr Phe	
145 150 155 160	

Phe	Val	Trp	Phe	Leu	Lys	Tyr	Leu	Thr	Arg	Thr	Arg	Asp	Ile	Gly	Ala	
				165					170					175		
Asn	Lys	Lys	Val	Asp	Asp	Leu	Phe	Gly	Ser	Ala	Ser	Trp	Glu	Thr	Glu	
			180					185					190			
Glu	Lys	Met	Ile	Lys	Ala	Lys	Leu	Ile	Thr	Pro	Asn	Asn	Lys	Lys	Arg	
		195					200					205				
Ala	Phe	Asp	Lys	Arg	Glu	Val	Ile	Val	Gly	Arg	Arg	Gly	Leu	Gly	Asp	
	210					215						220				
Phe	Ile	Ala	Tyr	Ala	Gly	Gln	Ala	Phe	Ile	Gly	Leu	Ile	Ala	Pro	Thr	
225					230					235					240	
Arg	Ser	Gly	Lys	Gly	Val	Gly	Phe	Ile	Met	Pro	Asn	Met	Ile	Asn	Tyr	
				245					250					255		
Pro	Gln	Asn	Ile	Val	Val	Phe	Asp	Pro	Lys	Ala	Asp	Thr	Met	Glu	Thr	
			260					265					270			
Cys	Gly	Lys	Ile	Arg	Glu	Lys	Arg	Phe	Asn	Gln	Lys	Val	Phe	Ile	Tyr	
		275					280					285				
Glu	Pro	Phe	Ser	Leu	Lys	Thr	His	Arg	Phe	Asn	Pro	Phe	Ala	Tyr	Val	
	290					295					300					
Asp	Phe	Gly	Asn	Asp	Val	Val	Leu	Thr	Glu	Asp	Ile	Leu	Ser	Gln	Ile	
305					310					315					320	
Asp	Thr	Arg	Leu	Lys	Gly	His	Gly	Met	Val	Ala	Ser	Gly	Gly	Asp	Phe	
				325					330					335		
Ser	Thr	Gln	Ile	Phe	Gly	Leu	Ala	Lys	Leu	Val	Phe	Pro	Glu	Arg	Pro	
			340					345					350			
Asn	Glu	Lys	Asp	Pro	Phe	Phe	Ser	Asn	Gln	Ala	Arg	Asn	Leu	Phe	Val	
		355					360					365				
Ile	Asn	Cys	Asn	Ile	Tyr	Arg	Asp	Leu	Met	Trp	Thr	Lys	Lys	Gly	Leu	
	370					375					380					
Glu	Phe	Val	Lys	Arg	Lys	Lys	Ile	Ile	Met	Pro	Glu	Thr	Pro	Thr	Met	
385					390					395					400	
Phe	Phe	Ile	Gly	Ser	Met	Ala	Ser	Gly	Ile	Asn	Leu	Ile	Asp	Glu	Asp	
				405					410					415		
Thr	Asn	Met	Glu	Lys	Val	Val	Ser	Leu	Met	Glu	Phe	Phe	Gly	Gly	Glu	
		420						425					430			
Glu	Asp	Lys	Ser	Gly	Asp	Asn	Leu	Arg	Val	Leu	Ser	Pro	Ala	Thr	Arg	
		435					440					445				
Asn	Met	Trp	Asn	Ser	Phe	Lys	Thr	Met	Gly	Gly	Ala	Arg	Glu	Thr	Tyr	
	450					455					460					
Ser	Ser	Val	Gln	Gly	Val	Tyr	Thr	Ser	Ala	Phe	Ala	Pro	Tyr	Asn	Asn	
465					470					475					480	
Ala	Met	Ile	Arg	Asn	Phe	Thr	Ser	Ala	Asn	Asp	Phe	Asp	Phe	Arg	Arg	
				485					490					495		
Leu	Arg	Ile	Asp	Glu	Val	Ser	Ile	Gly	Val	Ile	Ala	Asn	Pro	Lys	Glu	
		500						505					510			
Ser	Thr	Ile	Val	Gly	Pro	Ile	Leu	Glu	Leu	Phe	Phe	Asn	Val	Met	Ile	
		515					520					525				
Tyr	Ser	Asn	Leu	Ile	Leu	Pro	Ile	His	Asp	Pro	Gln	Cys	Lys	Arg	Ser	
	530					535						540				
Cys	Leu	Met	Leu	Met	Asp	Glu	Phe	Thr	Leu	Cys	Gly	Tyr	Leu	Glu	Thr	
545					550					555					560	
Phe	Val	Lys	Ala	Val	Gly	Ile	Met	Ala	Glu	Tyr	Asn	Met	Arg	Pro	Ala	
			565						570					575		
Phe	Val	Phe	Gln	Ser	Lys	Ala	Gln	Leu	Glu	Asn	Asp	Pro	Pro	Leu	Gly	
		580						585					590			
Tyr	Gly	Arg	Asn	Gly	Ala	Lys	Thr	Ile	Leu	Asp	Asn	Leu	Ser	Leu	Asn	
		595					600					605				
Met	Tyr	Tyr	Gly	Ile	Asn	Asn	Asp	Asn	Tyr	Tyr	Glu	His	Phe	Glu	Lys	
	610					615					620					

Leu Ser Lys Val Leu Gly Lys Tyr Thr Arg Gln Asp Val Ser Arg Ser
 625 630 635 640
 Ile Asp Asp Asn Thr Gly Lys Thr Asn Thr Ser Ile Ser Asn Lys Glu
 645 650 655
 Arg Phe Leu Met Thr Pro Asp Glu Leu Met Thr Met Gly Asp Glu Leu
 660 665 670
 Ile Ile Leu Glu Asn Thr Leu Lys Pro Ile Lys Cys His Lys Ala Leu
 675 680 685
 Tyr Tyr Asp Asp Pro Phe Phe Thr Asp Glu Leu Ile Lys Val Ser Pro
 690 695 700
 Ser Leu Ser Lys Lys Tyr Lys Leu Gly Lys Val Pro Asn Gln Ala Thr
 705 710 715 720
 Phe Tyr Asp Asp Leu Gln Ala Ala Lys Thr Arg Gly Glu Leu Ser Tyr
 725 730 735
 Asp Lys Ser Leu Val Pro Val Gly Ser Ser Glu Leu
 740 745

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1037 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 19...1008
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

TAAATTTGGA ATAAGAAC ATG ACT GAA GAC AGA TTG AGT GCA GAA GAT AAA	51
Met Thr Glu Asp Arg Leu Ser Ala Glu Asp Lys	
1 5 10	
AAG TTT CTA GAA GTA GAA AGA GCT TTA AAA GAA GCG GCA TTA AAT CCT	99
Lys Phe Leu Glu Val Glu Arg Ala Leu Lys Glu Ala Ala Leu Asn Pro	
15 20 25	
CTA AGG CAT GCT ACT GAA GAA CTT TTT GGT GAT TTT TTA AAA ATG GAA	147
Leu Arg His Ala Thr Glu Glu Leu Phe Gly Asp Phe Leu Lys Met Glu	
30 35 40	
AAT ATC ACT GAG ATT TGT TAC AAT GGG AAC AAG GTT GTA TGG GTT TTA	195
Asn Ile Thr Glu Ile Cys Tyr Asn Gly Asn Lys Val Val Trp Val Leu	
45 50 55	
AAA AAT AAT GGC GAA TGG CAA CCA TTT GAT GTG AGA GAC AGG AAA GCC	243
Lys Asn Asn Gly Glu Trp Gln Pro Phe Asp Val Arg Asp Arg Lys Ala	
60 65 70 75	
TTT AGC CTG TCT CGT TTA ATG CAT TTT GCT CGG TGT TGT GCA AGT TTT	291
Phe Ser Leu Ser Arg Leu Met His Phe Ala Arg Cys Cys Ala Ser Phe	
80 85 90	

AAG AAA AAA ACA ATA GAC AAC TAT GAA AAT CCT ATT TTG AGC AGC AAT	339
Lys Lys Lys Thr Ile Asp Asn Tyr Glu Asn Pro Ile Leu Ser Ser Asn	
95 100 105	
TTA GCG AAT GGT GAA AGG GTG CAG ATT GTC CTT TCC CCT GTT ACA GTT	387
Leu Ala Asn Gly Glu Arg Val Gln Ile Val Leu Ser Pro Val Thr Val	
110 115 120	
AAT GAT GAA ACC ATT TCC ATA TCC ATA AGG ATA CCT AGC AAA ACA ACC	435
Asn Asp Glu Thr Ile Ser Ile Ser Ile Arg Ile Pro Ser Lys Thr Thr	
125 130 135	
TAT CCT CAT AGC TTC TTT GAA GAG CAA GGT TTT TAT AAT CTA CTA GAC	483
Tyr Pro His Ser Phe Phe Glu Glu Gln Gly Phe Tyr Asn Leu Leu Asp	
140 145 150 155	
AAC AAA GAA CAA GCG ATC AGC GCG ATT AAA GAT GGT ATT GCT ATT GGT	531
Asn Lys Glu Gln Ala Ile Ser Ala Ile Lys Asp Gly Ile Ala Ile Gly	
160 165 170	
AAA AAT GTG ATT GTT TGT GGT GGC ACA GGA AGC GGT AAA ACG ACT TAT	579
Lys Asn Val Ile Val Cys Gly Gly Thr Gly Ser Gly Lys Thr Thr Tyr	
175 180 185	
ATC AAA AGC ATC ATG GAG TTT ATC CCT AAA GAA GAA AGG ATC ATA TCC	627
Ile Lys Ser Ile Met Glu Phe Ile Pro Lys Glu Glu Arg Ile Ile Ser	
190 195 200	
ATT GAA GAC ACC GAA GAG ATT GTA TTC AAA CAC CAC AAA AAC TAC ACA	675
Ile Glu Asp Thr Glu Glu Ile Val Phe Lys His His Lys Asn Tyr Thr	
205 210 215	
CAG CTT TTT TTT GGT GGG AAT ATC ACC TCT GCT GAT TGC TTA AAG TCA	723
Gln Leu Phe Phe Gly Gly Asn Ile Thr Ser Ala Asp Cys Leu Lys Ser	
220 225 230 235	
TGT CTG AGA ATG CGG CCT GAT AGA ATC ATT TTA GGG GAA CTC AGA AGC	771
Cys Leu Arg Met Arg Pro Asp Arg Ile Ile Leu Gly Glu Leu Arg Ser	
240 245 250	
AGT GAG GCA TAC GAT TTT TAT AAT GTG CTT TGT AGC GGT CAT AAA GGC	819
Ser Glu Ala Tyr Asp Phe Tyr Asn Val Leu Cys Ser Gly His Lys Gly	
255 260 265	
ACA CTA ACC ACT CTG CAT GCA GGG AGC AGT GAA GAA GCG TTT ATC CGT	867
Thr Leu Thr Thr Leu His Ala Gly Ser Ser Glu Glu Ala Phe Ile Arg	
270 275 280	
TTG GCC AAC ATG AGT TCA TCT AAT AGC GCA GCA AGG AAT ATC AAG TTT	915
Leu Ala Asn Met Ser Ser Ser Asn Ser Ala Ala Arg Asn Ile Lys Phe	
285 290 295	
GAA AGT CTT ATT GAG GGC TTT AAA GAT TTG ATT GAT ATG ATT GTC CAT	963
Glu Ser Leu Ile Glu Gly Phe Lys Asp Leu Ile Asp Met Ile Val His	
300 305 310 315	
ATC AAC CAC CAC AAA CAG TGT GAT GAA TTT TAT ATC AAA CAC AGG TAGTA	1013
Ile Asn His His Lys Gln Cys Asp Glu Phe Tyr Ile Lys His Arg	

330

1037

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

Met 1	Thr	Glu	Asp	Arg	Leu	Ser	Ala	Glu	Asp	Lys	Lys	Phe	Leu	Glu	Val
Glu	Arg	Ala	Leu	Lys	Glu	Ala	Ala	Leu	Asn	Pro	Leu	Arg	His	Ala	Thr
Glu	Glu	Leu	Phe	Gly	Asp	Phe	Leu	Lys	Met	Glu	Asn	Ile	Thr	Glu	Ile
Cys	Tyr	Asn	Gly	Asn	Lys	Val	Val	Trp	Val	Leu	Lys	Asn	Asn	Gly	Glu
Trp	Gln	Pro	Phe	Asp	Val	Arg	Asp	Arg	Lys	Ala	Phe	Ser	Leu	Ser	Arg
Leu	Met	His	Phe	Ala	Arg	Cys	Cys	Ala	Ser	Phe	Lys	Lys	Lys	Thr	Ile
Asp	Asn	Tyr	Glu	Asn	Pro	Ile	Leu	Ser	Ser	Asn	Leu	Ala	Asn	Gly	Glu
Arg	Val	Gln	Ile	Val	Leu	Ser	Pro	Val	Thr	Val	Asn	Asp	Glu	Thr	Ile
Ser	Ile	Ser	Ile	Arg	Ile	Pro	Ser	Lys	Thr	Thr	Tyr	Pro	His	Ser	Phe
Phe	Glu	Glu	Gln	Gly	Phe	Tyr	Asn	Leu	Leu	Asp	Asn	Lys	Glu	Gln	Ala
Ile	Ser	Ala	Ile	Lys	Asp	Gly	Ile	Ala	Ile	Gly	Lys	Asn	Val	Ile	Val
Cys	Gly	Gly	Thr	Gly	Ser	Gly	Lys	Thr	Thr	Tyr	Ile	Lys	Ser	Ile	Met
Glu	Phe	Ile	Pro	Lys	Glu	Glu	Arg	Ile	Ile	Ser	Ile	Glu	Asp	Thr	Glu
Glu	Ile	Val	Phe	Lys	His	His	Lys	Asn	Tyr	Thr	Gln	Leu	Phe	Phe	Gly
Gly	Asn	Ile	Thr	Ser	Ala	Asp	Cys	Leu	Lys	Ser	Cys	Leu	Arg	Met	Arg
Pro	Asp	Arg	Ile	Ile	Leu	Gly	Glu	Leu	Arg	Ser	Ser	Glu	Ala	Tyr	Asp
Phe	Tyr	Asn	Val	Leu	Cys	Ser	Gly	His	Lys	Gly	Thr	Leu	Thr	Thr	Leu
His	Ala	Gly	Ser	Ser	Glu	Glu	Ala	Phe	Ile	Arg	Leu	Ala	Asn	Met	Ser
Ser	Ser	Asn	Ser	Ala	Ala	Arg	Asn	Ile	Lys	Phe	Glu	Ser	Leu	Ile	Glu
Gly	Phe	Lys	Asp	Leu	Ile	Asp	Met	Ile	Val	His	Ile	Asn	His	His	Lys
Gln	Cys	Asp	Glu	Phe	Tyr	Ile	Lys	His	Arg						

Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	Male			
Female				
Marital status	Married			
Single				
Divorced				
Widowed				
Education	High school			
College				
Postgraduate				
Occupation	Manager			
Teacher				
Engineer				
Other				
Income	Low			
Medium				
High				
Health status	Good			
Fair				
Poor				
Stress level	Low			
Medium				
High				
Life satisfaction	High			
Medium				
Low				

(2) INFORMATION FOR SEQ ID NO:623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...5250
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

TAAATAAAAA	GCGGTTAAGA	C	ATG	AAT	GAA	GAA	AAC	GAT	AAA	CTT	GAA	ACT	51
			Met	Asn	Glu	Glu	Asn	Asp	Lys	Leu	Glu	Thr	
			1				5					10	
TCT AAA AAA	GCC CAA CAA	GAT TCA	CCC CAA	GAT TTA	TCC AAT	GAA GAA							99
Ser Lys Lys	Ala Gln Gln	Asp Ser	Pro Gln	Asp Leu	Ser Asn	Glu Glu							
	15		20			25							
GCA ACA GAA	GCC AAT CAT	TTT GAA	AAT CTT	TTA AAA	GAA TCC	AAA GAA							147
Ala Thr Glu	Ala Asn His	Phe Glu	Asn Leu	Leu Lys	Glu Ser	Lys Glu							
	30		35			40							
AGC TCA GAT	CAT CAT CTT	GAC AAC	CCC ACA	GAA ACT	CAA ACC	CAT TTT							195
Ser Ser Asp	His His Leu	Asp Asn	Pro Thr	Glu Thr	Gln Thr	His Phe							
	45		50			55							
GAT GGA GAC	AAG TCA GAA	GAA ACC	CAA ACT	CAA ATG	GAT TCT	GAA GGT							243
Asp Gly Asp	Lys Ser Glu	Glu Thr	Gln Thr	Gln Met	Asp Ser	Glu Gly							
	60		65			70							
AAT GAA ACT	TCA GAA TCT	AGC AAT	GGC AGT	CTA GCA	GAC AAG	TTA TTC							291
Asn Glu Thr	Ser Glu Ser	Ser Asn	Gly Ser	Leu Ala	Asp Lys	Leu Phe							
	75		80			85							
AAA AAA GCC	AGA AAA TTA	GTT GAT	AAT AAA	AAA CCT	TTC ACT	CAG CAA							339
Lys Lys Ala	Arg Lys Leu	Val Asp	Asn Lys	Lys Lys	Pro Phe	Thr Gln							
	95		100			105							
AAG AAT TTA	GAT GAA GAA	ACC CAA	GAA CTG	AAC GAA	GAA GAC	GAT CAA							387
Lys Asn Leu	Asp Glu Glu	Thr Gln	Glu Leu	Asn Glu	Glu Asp	Asp Gln							
	110		115			120							
GAA AAT AAT	GAG TAT CAA	GAA GAA	ACT CAA	ACG GAC	TTA ATT	GAT GAT							435
Glu Asn Asn	Glu Tyr Gln	Glu Glu	Thr Gln	Thr Asp	Leu Ile	Asp Asp							
	125		130			135							
GAA ACT TCT	AAA AAA ACC	CAA CAA	CAT TCA	CCC CAA	GAT TTA	TCC AAT							483
Glu Thr Ser	Lys Lys Thr	Gln Gln	His Ser	Pro Gln	Asp Leu	Ser Asn							
	140		145			150							

GAA GAA GCA ACA GAA GCC AAT CAT TTT GAA AAT CTT TTA AAA GAA TCC Glu Glu Ala Thr Glu Ala Asn His Phe Glu Asn Leu Leu Lys Glu Ser 155 160 165 170	531
AAA GAA AGC TCA GAT CAT CAT CTT GAC AAC CCC ACA GAA ACT CAA ACC Lys Glu Ser Ser Asp His His Leu Asp Asn Pro Thr Glu Thr Gln Thr 175 180 185	579
AAT TTT GAT GGA GAC AAG TCA GAA GAA ACC CAA ACT CAA ATG GAT TCT Asn Phe Asp Gly Asp Lys Ser Glu Glu Thr Gln Thr Gln Met Asp Ser 190 195 200	627
GAA GGT AAT GAA ACT TCA GAA TCT AGC AAT GGC AGT CTA GCA GAC AAG Glu Gly Asn Glu Thr Ser Glu Ser Ser Asn Gly Ser Leu Ala Asp Lys 205 210 215	675
TTA TTC AAA AAA GCC AGA AAA TTA GTT GAT AAT AAA AAA CCT TTC ACT Leu Phe Lys Lys Ala Arg Lys Leu Val Asp Asn Lys Lys Pro Phe Thr 220 225 230	723
CAG CAA AAG AAT TTA GAT GAA GAA ACC CAA GAA CTG AAC GAA GAA GAC Gln Gln Lys Asn Leu Asp Glu Glu Thr Gln Glu Leu Asn Glu Glu Asp 235 240 245 250	771
GAT CAA GAA AAT AAT GAG TAT CAA GAA GAA ACT CAA ACG GAC TTA ATT Asp Gln Glu Asn Asn Glu Tyr Gln Glu Glu Thr Gln Thr Asp Leu Ile 255 260 265	819
GAT GAT GAA ACT TCT AAA AAA ACC CAA CAA CAT TCA CCC CAA GAT TTA Asp Asp Glu Thr Ser Lys Lys Thr Gln Gln His Ser Pro Gln Asp Leu 270 275 280	867
TCC AAT GAA GAA GCA ACA GAA GCC AAT CAT TTT GAA AAT CTT TTA AAA Ser Asn Glu Glu Ala Thr Glu Ala Asn His Phe Glu Asn Leu Leu Lys 285 290 295	915
GAA TCC AAA GAA AGC TCA GAT CAT CAT CTT GAC AAC CCC ACA GAA ACT Glu Ser Lys Glu Ser Ser Asp His His Leu Asp Asn Pro Thr Glu Thr 300 305 310	963
CAA ACC AAT TTT GAT GGA GAC AAG TCA GAA GAA ATA ACT GAC GAC TCT Gln Thr Asn Phe Asp Gly Asp Lys Ser Glu Glu Ile Thr Asp Asp Ser 315 320 325 330	1011
AAC GAT CAA GAG ATT ATC AAA GGA AGC AAA AAG AAA TAT ATT ATT GGT Asn Asp Gln Glu Ile Ile Lys Gly Ser Lys Lys Lys Tyr Ile Ile Gly 335 340 345	1059
GGC ATT GTA GTC GCT GTT CTT ATC GTG ATT ATT TTA TTT TCT AGA AGC Gly Ile Val Val Ala Val Leu Ile Val Ile Ile Leu Phe Ser Arg Ser 350 355 360	1107
ATT TTT CAC TAC TTC ATG CCT TTG GAA GAT AAA AGC TCT CGT TTT AGC Ile Phe His Tyr Phe Met Pro Leu Glu Asp Lys Ser Ser Arg Phe Ser 365 370 375	1155
AAA GAC AGG AAT CTT TAT GTC AAT GAT GAA ATC CAA ATA AGG CAA GAG Lys Asp Arg Asn Leu Tyr Val Asn Asp Glu Ile Gln Ile Arg Gln Glu	1203

380					385					390						
TAT	AAC	CGA	TTG	CTG	AAA	GAA	CGG	AAT	GAA	AAA	GGC	AAT	ATG	ATC	GAT	1251
Tyr	Asn	Arg	Leu	Leu	Lys	Glu	Arg	Asn	Glu	Lys	Gly	Asn	Met	Ile	Asp	
395					400					405					410	
AAG	AAT	CTT	TTC	TTC	AAT	GAC	GAT	CCC	AAT	AGA	ACC	TTA	TAC	AAC	TAT	1299
Lys	Asn	Leu	Phe	Phe	Asn	Asp	Asp	Pro	Asn	Arg	Thr	Leu	Tyr	Asn	Tyr	
				415					420					425		
TTG	AAT	ATT	GCA	GAA	ATT	GAG	GAC	AAA	AAC	CCG	TTG	AGA	GCC	TTT	TAT	1347
Leu	Asn	Ile	Ala	Glu	Ile	Glu	Asp	Lys	Asn	Pro	Leu	Arg	Ala	Phe	Tyr	
			430					435					440			
GAA	TGT	ATT	AGT	AAT	GGT	GGC	AAC	TAT	GAA	GAA	TGT	TTG	AAG	CTT	ATC	1395
Glu	Cys	Ile	Ser	Asn	Gly	Gly	Asn	Tyr	Glu	Glu	Cys	Leu	Lys	Leu	Ile	
		445					450					455				
AAA	GAC	AAA	AAA	CTT	CAA	GAT	CAG	ATG	AAA	AAG	ACT	CTA	GAG	GCT	TAT	1443
Lys	Asp	Lys	Lys	Leu	Gln	Asp	Gln	Met	Lys	Lys	Thr	Leu	Glu	Ala	Tyr	
	460					465					470					
AAC	GAC	TGC	ATC	AAA	AAT	GCC	AAA	ACT	GAA	GAA	GAA	AGG	ATC	AAG	TGT	1491
Asn	Asp	Cys	Ile	Lys	Asn	Ala	Lys	Thr	Glu	Glu	Glu	Arg	Ile	Lys	Cys	
	475					480					485				490	
TTA	GAT	TTA	ATC	AAA	GAT	GAA	AAC	CTA	AAA	AAA	AGC	TTA	CTG	AAC	CAA	1539
Leu	Asp	Leu	Ile	Lys	Asp	Glu	Asn	Leu	Lys	Lys	Ser	Leu	Leu	Asn	Gln	
				495					500					505		
CAA	AAA	GTT	CAA	GTG	GCG	CTA	GAT	TGT	TTG	AAA	AAC	GCT	AAA	ACC	GAT	1587
Gln	Lys	Val	Gln	Val	Ala	Leu	Asp	Cys	Leu	Lys	Asn	Ala	Lys	Thr	Asp	
			510					515					520			
GAA	GAA	CGA	AAC	GAG	TGC	CTA	AAA	CTC	ATA	AAT	GAC	CCT	GAG	ATT	AGA	1635
Glu	Glu	Arg	Asn	Glu	Cys	Leu	Lys	Leu	Ile	Asn	Asp	Pro	Glu	Ile	Arg	
		525					530					535				
GAG	AAA	TTC	CGT	AAG	GAA	TTA	GAG	CTT	CAA	AAA	GAG	CTT	CAA	GAG	TAT	1683
Glu	Lys	Phe	Arg	Lys	Glu	Leu	Glu	Leu	Gln	Lys	Glu	Leu	Gln	Glu	Tyr	
	540					545					550					
AAG	GAT	TGT	ATC	AAA	AAC	GCC	AAA	ACA	GAA	GCT	GAG	AAA	AAC	AAA	TGC	1731
Lys	Asp	Cys	Ile	Lys	Asn	Ala	Lys	Thr	Glu	Ala	Glu	Lys	Asn	Lys	Cys	
	555					560					565				570	
TTG	AAA	GGC	TTG	TCT	AAA	GAA	GCT	ATA	GAG	AGA	TTG	AAA	CAG	CAA	GCG	1779
Leu	Lys	Gly	Leu	Ser	Lys	Glu	Ala	Ile	Glu	Arg	Leu	Lys	Gln	Gln	Ala	
				575					580					585		
CTA	GAT	TGT	TTG	AAA	AAC	GCT	AAA	ACC	GAT	GAA	GAA	CGA	AAC	GAG	TGC	1827
Leu	Asp	Cys	Leu	Lys	Asn	Ala	Lys	Thr	Asp	Glu	Glu	Arg	Asn	Glu	Cys	
			590					595					600			
TTG	AAA	AAT	ATT	CCC	CAA	GAC	TTG	CAA	AAA	GAA	CTA	TTA	GCT	GAT	ATG	1875
Leu	Lys	Asn	Ile	Pro	Gln	Asp	Leu	Gln	Lys	Glu	Leu	Ala	Asp	Met		
		605					610					615				

AGC Ser	GTC Val	AAG Lys	GCT Ala	TAC Tyr	AAG Lys	GAT Asp	TGC Cys	GTA Val	TCA Ser	AAA Lys	GCT Ala	AGA Arg	AAT Asn	GAA Glu	AAA Lys	1923
GAG Glu	AAA Lys	CAA Gln	GAA Glu	TGC Cys	GAG Glu	AAA Lys	TTG Leu	CTC Leu	ACG Thr	CCT Pro	GAA Glu	GCG Ala	AGG Arg	AAA Lys	AAG Lys	1971
TTA Leu	GAA Glu	CAA Gln	CAG Gln	GTT Val	CTA Leu	GAT Asp	TGT Cys	TTG Leu	AAA Lys	AAC Asn	GCT Ala	AAA Lys	ACC Thr	GAT Asp	GAA Glu	2019
GAA Glu	CGA Arg	AAA Lys	AAG Lys	TGT Cys	TTG Leu	AAA Lys	GAT Asp	CTC Leu	CCT Pro	AAA Lys	GAC Asp	TTA Leu	CAA Gln	AGC Ser	GAT Asp	2067
ATT Ile	CTA Leu	GCC Ala	AAA Lys	GAG Glu	AGC Ser	CTG Leu	AAA Lys	GCT Ala	TAT Tyr	AAA Lys	GAC Asp	TGC Cys	GTA Val	TCT Ser	CAA Gln	2115
GCC Ala	AAA Lys	ACC Thr	GAA Glu	GCT Ala	GAG Glu	AAA Lys	AAA Lys	GAA Glu	TGC Cys	GAG Glu	AAA Lys	TTA Leu	CTC Leu	ACC Thr	CCT Pro	2163
GAA Glu	GCG Ala	AAA Lys	AAA Lys	CTT Leu	TTA Leu	GAA Glu	GAA Glu	GAA Glu	GCC Ala	AAA Lys	GAG Glu	AGC Ser	GTT Val	AAG Lys	GCT Ala	2211
TAT Tyr	TTG Leu	GAT Asp	TGC Cys	GTA Val	TCT Ser	CAA Gln	GCC Ala	AAA Lys	ACC Thr	GAA Glu	GCT Ala	GAG Glu	AAA Lys	AAA Lys	GAA Glu	2259
TGC Cys	GAG Glu	AAA Lys	TTG Leu	CTC Leu	ACC Thr	CCT Pro	GAA Glu	GCG Ala	AAA Lys	AAA Lys	AAG Lys	TTA Leu	GAA Glu	GAA Glu	GCT Ala	2307
AAA Lys	AAA Lys	AGC Ser	GTT Val	AAA Lys	GCT Ala	TAC Tyr	TTG Leu	GAT Asp	TGC Cys	GTA Val	TCA Ser	AGA Arg	GCT Ala	AGG Arg	AAT Asn	2355
GAA Glu	AAA Lys	GAG Glu	AAA Lys	AAA Lys	GAA Glu	TGC Cys	GAG Glu	AAA Lys	TTG Leu	CTC Leu	ACC Thr	CCT Pro	GAA Glu	GCG Ala	AAA Lys	2403
AAA Lys	CTT Leu	TTA Leu	GAG Glu	CAA Gln	CAA Gln	GCA Ala	CTA Leu	GAT Asp	TGT Cys	TTG Leu	AAA Lys	AAC Asn	GCT Ala	AAA Lys	ACC Thr	2451
GAT Asp	AAA Lys	GAA Glu	CGA Arg	AAA Lys	AAG Lys	TGT Cys	TTG Leu	AAA Lys	GAT Asp	CTC Leu	CCT Pro	AAA Lys	GAC Asp	TTG Leu	CAG Gln	2499
AAA Lys	AAG Lys	GTT Val	TTA Leu	GCT Ala	AAA Lys	GAA Glu	AGC Ser	GTT Val	AAA Lys	GCT Ala	TAC Tyr	TTG Leu	GAT Asp	TGC Cys	GTA Val	2547
TCT Ser	CAA Gln	GCC Ala	AAA Lys	ACT Thr	GAA Glu	GCT Ala	GAG Glu	AAA Lys	AAA Lys	GAA Glu	TGC Cys	GAG Glu	AAA Lys	TTA Leu	CTC Leu	2595

845	850	855	
ACC CCT GAA GCG AGA AAA CTT TTA GAA GAA GCT AAA AAA AGC GTT AAG Thr Pro Glu Ala Arg Lys Leu Leu Glu Glu Ala Lys Lys Ser Val Lys 860 865 870			2643
GCT TAY TTG GAT TGC GTA TCT CAA GCC AAA ACT GAA GCT GAG AAA AAA Ala Xaa Leu Asp Cys Val Ser Gln Ala Lys Thr Glu Ala Glu Lys Lys 875 880 885 890			2691
GAA TGC GAG AAA TTA CTC ACC CCT GAA GCG AGA AAA CTC TTA GAA GAA Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys Leu Leu Glu Glu 895 900 905			2739
GCT AAA GAG AGC GTT AAA GCT TAT AAA GAC TGC GTA TCA AAA GCT AGG Ala Lys Glu Ser Val Lys Ala Tyr Lys Asp Cys Val Ser Lys Ala Arg 910 915 920			2787
AAT GAA AAA GAG AAA AAA GAA TGC GAG AAA TTA CTC ACG CCT GAA GCG Asn Glu Lys Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala 925 930 935			2835
AAA AAA CTT TTA GAG CAA CAA GTG CTA GAT TGT TTG AAA AAC GCT AAA Lys Lys Leu Leu Glu Gln Val Leu Asp Cys Leu Lys Asn Ala Lys 940 945 950			2883
ACC GAA GCT GAT AAA AAA AGG TGT GTC AAA GAT CTC CCT AAA GAC TTG Thr Glu Ala Asp Lys Lys Arg Cys Val Lys Asp Leu Pro Lys Asp Leu 955 960 965 970			2931
CAG AAA AAG GTT TTA GCT AAA GAG AGC GTT AAG GCT TAT TTG GAC TGC Gln Lys Lys Val Leu Ala Lys Glu Ser Val Lys Ala Tyr Leu Asp Cys 975 980 985			2979
GTA TCA AGA GCT AGG AAT GAA AAA GAG AAA AAA GAA TGC GAG AAA TTG Val Ser Arg Ala Arg Asn Glu Lys Glu Lys Lys Glu Cys Glu Lys Leu 990 995 1000			3027
CTC ACC CCT GAA GCG AAA AAA CTT TTA GAA GAA GCC AAA GAG AGT CTT Leu Thr Pro Glu Ala Lys Lys Leu Leu Glu Glu Ala Lys Glu Ser Leu 1005 1010 1015			3075
AAA GCT TAT AAA GAC TGC CTC TCT CAA GCT AGA AAT GAA GAA GAA AGG Lys Ala Tyr Lys Asp Cys Leu Ser Gln Ala Arg Asn Glu Glu Glu Arg 1020 1025 1030			3123
AGA GCT TGC GAG AAA CTA CTC ACG CCT GAA GCG AGA AAA CTC TTA GAG Arg Ala Cys Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys Leu Leu Glu 1035 1040 1045 1050			3171
CAA GAA GTT AAG AAA AGC ATT AAG GCT TAT TTG GAC TGC GTA TCA AGA Gln Glu Val Lys Lys Ser Ile Lys Ala Tyr Leu Asp Cys Val Ser Arg 1055 1060 1065			3219
GCT AGG AAT GAA AAA GAG AAA AAA GAA TGC GAG AAA TTA CTC ACG CCT Ala Arg Asn Glu Lys Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro 1070 1075 1080			3267

GAA GCG AGA AAA TTT TTA GCG AAG CAA GTG CTA AAT TGT TTG GAA AAA Glu Ala Arg Lys Phe Leu Ala Lys Gln Val Leu Asn Cys Leu Glu Lys 1085 1090 1095	3315
GCT GGA AAT GAA GAA GAA AGA AAA GCA TGT CTT AAA AAT CTC CCT AAA Ala Gly Asn Glu Glu Glu Arg Lys Ala Cys Leu Lys Asn Leu Pro Lys 1100 1105 1110	3363
GAC TTA CAG GAA AAT ATT TTA GCT AAA GAG AGT CTT AAA GCT TAT AAA Asp Leu Gln Glu Asn Ile Leu Ala Lys Glu Ser Leu Lys Ala Tyr Lys 1115 1120 1125 1130	3411
GAC TGC CTC TCT CAA GCT AGA AAT GAA GAA GAA AGG AGA GCT TGC GAG Asp Cys Leu Ser Gln Ala Arg Asn Glu Glu Glu Arg Arg Ala Cys Glu 1135 1140 1145	3459
AAA CTA CTC ACG CCT GAA GCG AGA AAA CTC TTA GAG CAA GAA GTT AAG Lys Leu Leu Thr Pro Glu Ala Arg Lys Leu Leu Glu Gln Glu Val Lys 1150 1155 1160	3507
AAA AGC GTT AAG GCT TAT TTG GAC TGC GTA TCA AGA GCT AGG AAT GAA Lys Ser Val Lys Ala Tyr Leu Asp Cys Val Ser Arg Ala Arg Asn Glu 1165 1170 1175	3555
AAA GAG AAA AAA GAA TGC GAG AAA TTA CTC ACG CCT GAA GCG AGA AAA Lys Glu Lys Lys Glu Cys Glu Lys Leu Leu Thr Pro Glu Ala Arg Lys 1180 1185 1190	3603
TTT TTA GCG AAA GAA CTC CAA CAA AAA GAT AAA GCG ATC AAA GAT TGC Phe Leu Ala Lys Glu Leu Gln Gln Lys Asp Lys Ala Ile Lys Asp Cys 1195 1200 1205 1210	3651
TTG AAA AAC GCC GAT CCT AAC GAC AGA GCG GCT ATC ATG AAG TGT TTG Leu Lys Asn Ala Asp Pro Asn Asp Arg Ala Ala Ile Met Lys Cys Leu 1215 1220 1225	3699
GAT GGT TTG AGC GAT GAA GAG AAG CTC AAA TAC CTG CAA GAA GCT AGA Asp Gly Leu Ser Asp Glu Glu Lys Leu Lys Tyr Leu Gln Glu Ala Arg 1230 1235 1240	3747
GAA AAG GCT GTT GCG GAT TGT TTG GCT ATG GCT AAA ACC GAT GAA GAA Glu Lys Ala Val Ala Asp Cys Leu Ala Met Ala Lys Thr Asp Glu Glu 1245 1250 1255	3795
AAA AGG AAA TGC CAA AAC CTT TAT AGC GAT TTG ATC CAA GAA ATC CAA Lys Arg Lys Cys Gln Asn Leu Tyr Ser Asp Leu Ile Gln Glu Ile Gln 1260 1265 1270	3843
AAT AAA AGG ACA CAA AAC AAA CAA AAT CAA TTG AGT AAA ACA GAA AGG Asn Lys Arg Thr Gln Asn Lys Gln Asn Gln Leu Ser Lys Thr Glu Arg 1275 1280 1285 1290	3891
TTG CAT CAA GCA AGC GAG TGC TTG GAT AAC TTA GAT GAC CCT ACT GAT Leu His Gln Ala Ser Glu Cys Leu Asp Asn Leu Asp Asp Pro Thr Asp 1295 1300 1305	3939
CAA GAG GCC ATA GAG CAA TGT TTA GAG GGC TTG AGC GAT AGT GAA AGG Gln Glu Ala Ile Glu Gln Cys Leu Glu Gly Leu Ser Asp Ser Glu Arg 1310 1315 1320 1325 1330 1335	3987

	1310						1315						1320						
GCG	CTA	ATT	CTA	GGA	ATT	AAA	CGA	CAA	GCT	GAT	GAA	GTG	GAT	CTG	ATT	4035			
Ala	Leu	Ile	Leu	Gly	Ile	Lys	Arg	Gln	Ala	Asp	Glu	Val	Asp	Leu	Ile				
	1325					1330					1335								
TAT	AGC	GAT	CTA	AGA	AAC	CGT	AAA	ACC	TTT	GAT	AAC	ATG	GCG	GCT	AAA	4083			
Tyr	Ser	Asp	Leu	Arg	Asn	Arg	Lys	Thr	Phe	Asp	Asn	Met	Ala	Ala	Lys				
	1340					1345					1350								
GGT	TAT	CCA	TTG	TTA	CCA	ATG	GAT	TTC	AAA	AAT	GGC	GGC	GAT	ATT	GCC	4131			
Gly	Tyr	Pro	Leu	Leu	Pro	Met	Asp	Phe	Lys	Asn	Gly	Gly	Asp	Ile	Ala				
1355				1360					1365					1370					
ACT	ATT	AAC	GCC	ACT	AAT	GTT	GAT	GCG	GAC	AAA	ATA	GCT	AGC	GAT	AAT	4179			
Thr	Ile	Asn	Ala	Thr	Asn	Val	Asp	Ala	Asp	Lys	Ile	Ala	Ser	Asp	Asn				
			1375					1380					1385						
CCT	ATT	TAT	GCT	TCC	ATA	GAG	CCT	GAT	ATT	GCC	AAG	CAA	TAC	GAA	ACA	4227			
Pro	Ile	Tyr	Ala	Ser	Ile	Glu	Pro	Asp	Ile	Ala	Lys	Gln	Tyr	Glu	Thr				
	1390						1395					1400							
GAA	AAA	ACC	ATT	AAG	GAT	AAG	AAT	TTA	GAA	GCT	AAA	TTA	GCT	AAG	GCT	4275			
Glu	Lys	Thr	Ile	Lys	Asp	Lys	Asn	Leu	Glu	Ala	Lys	Leu	Ala	Lys	Ala				
	1405					1410					1415								
TTA	GGT	GGC	AAT	AAA	AAA	GAT	GAC	GAT	AAA	GAA	AAA	AGT	AAA	AAA	TCC	4323			
Leu	Gly	Gly	Asn	Lys	Lys	Asp	Asp	Asp	Lys	Glu	Lys	Ser	Lys	Lys	Ser				
	1420					1425					1430								
ACA	GCA	GAA	GCT	AAA	GCA	GAA	AAC	AAT	AAG	ATA	GAC	AAA	GAT	GTC	GCA	4371			
Thr	Ala	Glu	Ala	Lys	Ala	Glu	Asn	Asn	Lys	Ile	Asp	Lys	Asp	Val	Ala				
1435				1440					1445					1450					
GAA	ACT	GCC	AAG	AAT	ATC	AGT	GAA	ATC	GCT	CTT	AAG	AAC	AAA	AAA	GAA	4419			
Glu	Thr	Ala	Lys	Asn	Ile	Ser	Glu	Ile	Ala	Leu	Lys	Asn	Lys	Lys	Glu				
			1455					1460					1465						
AAG	AGT	GGG	GAA	TTT	GTA	GAT	GAA	AAT	GGT	AAT	CCC	ATT	GAT	GAC	AAA	4467			
Lys	Ser	Gly	Glu	Phe	Val	Asp	Glu	Asn	Gly	Asn	Pro	Ile	Asp	Asp	Lys				
	1470						1475					1480							
AAG	AAA	GCA	GAA	AAA	CAA	GAT	GAA	ACA	AGC	CCT	GTC	AAA	CAG	GCC	TTT	4515			
Lys	Lys	Ala	Glu	Lys	Gln	Asp	Glu	Thr	Ser	Pro	Val	Lys	Gln	Ala	Phe				
	1485					1490					1495								
ATA	GGC	AAG	AGT	GAT	CCC	ACA	TTT	GTT	TTA	GCG	CAA	TAC	ACC	CCC	ATT	4563			
Ile	Gly	Lys	Ser	Asp	Pro	Thr	Phe	Val	Leu	Ala	Gln	Tyr	Thr	Pro	Ile				
	1500					1505					1510								
GAA	ATC	ACT	CTG	ACT	TCT	AAA	GTA	GAT	GCC	ACT	CTC	ACA	GGT	ATA	GTG	4611			
Glu	Ile	Thr	Leu	Thr	Ser	Lys	Val	Asp	Ala	Thr	Leu	Thr	Gly	Ile	Val				
1515				1520					1525					1530					
AGT	GGG	GTT	GTA	GCC	AAA	GAT	GTA	TGG	AAC	ATG	AAC	GGC	ACT	ATG	ATC	4659			
Ser	Gly	Val																	

TTA TTA GAC AAA GGC ACT AAG GTG TAT GGG AAT TAT CAA AGC GTG AAA	4707
Leu Leu Asp Lys Gly Thr Lys Val Tyr Gly Asn Tyr Gln Ser Val Lys	
1550 1555 1560	
GGT GGC ACA CCC ATT ATG ACA CGC TTA ATG ATA GTC TTT ACT AAA GCC	4755
Gly Gly Thr Pro Ile Met Thr Arg Leu Met Ile Val Phe Thr Lys Ala	
1565 1570 1575	
ATT ACG CCT GAT GGT GTG ATA ATA CCT CTA GCA AAC GCT CAA GCA GCA	4803
Ile Thr Pro Asp Gly Val Ile Ile Pro Leu Ala Asn Ala Gln Ala Ala	
1580 1585 1590	
GGC ATG TTG GGT GAA GCA GGG GTA GAT GGC TAT GTG AAT AAT CAC TTT	4851
Gly Met Leu Gly Glu Ala Gly Val Asp Gly Tyr Val Asn Asn His Phe	
1595 1600 1605 1610	
ATG AAG CGC ATA GGC TTT GCT GTG ATA GCA AGC GTG GTT AAT AGC TTC	4899
Met Lys Arg Ile Gly Phe Ala Val Ile Ala Ser Val Val Asn Ser Phe	
1615 1620 1625	
TTG CAA ACT GCG CCT ATC ATA GCT CTA GAT AAA CTC ATA GGC CTT GGC	4947
Leu Gln Thr Ala Pro Ile Ile Ala Leu Asp Lys Leu Ile Gly Leu Gly	
1630 1635 1640	
AAA GGT AGA AGT GAA AGG ACA CCT GAA TTT AAT TAC GCT TTG GGT CAA	4995
Lys Gly Arg Ser Glu Arg Thr Pro Glu Phe Asn Tyr Ala Leu Gly Gln	
1645 1650 1655	
GCT ATC AAT GGT AGC ATG CAA AGT TCA GCT CAG ATG TCT AAT CAA ATT	5043
Ala Ile Asn Gly Ser Met Gln Ser Ser Ala Gln Met Ser Asn Gln Ile	
1660 1665 1670	
CTA GGG CAA CTG ATG AAT ATC CCC CCA AGT TTT TAC AAA AAC GAG GGC	5091
Leu Gly Gln Leu Met Asn Ile Pro Pro Ser Phe Tyr Lys Asn Glu Gly	
1675 1680 1685 1690	
GAT AGT ATT AAG ATT CTC ACA ATG GAC GAT ATT GAT TTT AGC GGT GTG	5139
Asp Ser Ile Lys Ile Leu Thr Met Asp Asp Ile Asp Phe Ser Gly Val	
1695 1700 1705	
TAT GAT GTT AAA ATT ACT AAC AAA TCT GTG GTA GAT GAA ATT ATC AAA	5187
Tyr Asp Val Lys Ile Thr Asn Lys Ser Val Val Asp Glu Ile Ile Lys	
1710 1715 1720	
CAA AGC ACC AAA ACT TTG TCT AGA GAA CAT GAA GAA ATC ACC ACA AGC	5235
Gln Ser Thr Lys Thr Leu Ser Arg Glu His Glu Glu Ile Thr Thr Ser	
1725 1730 1735	
CCC AAA GGT GGC AAT TAATTCAAGA GAAAGGATAA AATATATTCA TGTTACTAAA C	5291
Pro Lys Gly Gly Asn	
1740	
TCGGTTCTTT ACAAATAAAA AGACAAAACC AACACAGGC TCT	5334

(2) INFORMATION FOR SEQ ID NO:624:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1743 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

Met	Asn	Glu	Glu	Asn	Asp	Lys	Leu	Glu	Thr	Ser	Lys	Lys	Ala	Gln	Gln
1				5					10					15	
Asp	Ser	Pro	Gln	Asp	Leu	Ser	Asn	Glu	Glu	Ala	Thr	Glu	Ala	Asn	His
			20					25					30		
Phe	Glu	Asn	Leu	Leu	Lys	Glu	Ser	Lys	Glu	Ser	Ser	Asp	His	His	Leu
		35					40					45			
Asp	Asn	Pro	Thr	Glu	Thr	Gln	Thr	His	Phe	Asp	Gly	Asp	Lys	Ser	Glu
	50					55				60					
Glu	Thr	Gln	Thr	Gln	Met	Asp	Ser	Glu	Gly	Asn	Glu	Thr	Ser	Glu	Ser
65					70				75					80	
Ser	Asn	Gly	Ser	Leu	Ala	Asp	Lys	Leu	Phe	Lys	Lys	Ala	Arg	Lys	Leu
				85					90					95	
Val	Asp	Asn	Lys	Lys	Pro	Phe	Thr	Gln	Gln	Lys	Asn	Leu	Asp	Glu	Glu
			100					105					110		
Thr	Gln	Glu	Leu	Asn	Glu	Glu	Asp	Gln	Glu	Asn	Asn	Glu	Tyr	Gln	
		115					120					125			
Glu	Glu	Thr	Gln	Thr	Asp	Leu	Ile	Asp	Asp	Glu	Thr	Ser	Lys	Lys	Thr
		130				135					140				
Gln	Gln	His	Ser	Pro	Gln	Asp	Leu	Ser	Asn	Glu	Glu	Ala	Thr	Glu	Ala
145					150					155				160	
Asn	His	Phe	Glu	Asn	Leu	Leu	Lys	Glu	Ser	Lys	Glu	Ser	Ser	Asp	His
				165					170					175	
His	Leu	Asp	Asn	Pro	Thr	Glu	Thr	Gln	Thr	Asn	Phe	Asp	Gly	Asp	Lys
			180					185					190		
Ser	Glu	Glu	Thr	Gln	Thr	Gln	Met	Asp	Ser	Glu	Gly	Asn	Glu	Thr	Ser
		195				200						205			
Glu	Ser	Ser	Asn	Gly	Ser	Leu	Ala	Asp	Lys	Leu	Phe	Lys	Lys	Ala	Arg
		210				215					220				
Lys	Leu	Val	Asp	Asn	Lys	Lys	Pro	Phe	Thr	Gln	Gln	Lys	Asn	Leu	Asp
225					230					235				240	
Glu	Glu	Thr	Gln	Glu	Leu	Asn	Glu	Glu	Asp	Asp	Gln	Glu	Asn	Asn	Glu
				245					250					255	
Tyr	Gln	Glu	Glu	Thr	Gln	Thr	Asp	Leu	Ile	Asp	Asp	Glu	Thr	Ser	Lys
		260				265							270		
Lys	Thr	Gln	Gln	His	Ser	Pro	Gln	Asp	Leu	Ser	Asn	Glu	Glu	Ala	Thr
		275				280						285			
Glu	Ala	Asn	His	Phe	Glu	Asn	Leu	Leu	Lys	Glu	Ser	Lys	Glu	Ser	Ser
	290					295					300				
Asp	His	His	Leu	Asp	Asn	Pro	Thr	Glu	Thr	Gln	Thr	Asn	Phe	Asp	Gly
305					310					315					320
Asp	Lys	Ser	Glu	Glu	Ile	Thr	Asp	Asp	Ser	Asn	Asp	Gln	Glu	Ile	Ile
			325						330					335	
Lys	Gly	Ser	Lys	Lys	Lys	Tyr	Ile	Ile	Gly	Gly	Ile	Val	Val	Ala	Val
			340					345					350		
Leu	Ile	Val	Ile	Ile	Leu	Phe	Ser	Arg	Ser	Ile	Phe	His	Tyr	Phe	Met
		355				360						365			
Pro	Leu	Glu	Asp	Lys	Ser	Ser	Arg	Phe	Ser	Lys	Asp	Arg	Asn	Leu	Tyr
	370					375					380				
Val	Asn	Asp	Glu	Ile	Gln	Ile	Arg	Gln	Glu	Tyr	Asn	Arg	Leu	Leu	Lys
385					390					395					400

Glu	Arg	Asn	Glu	Lys	Gly	Asn	Met	Ile	Asp	Lys	Asn	Leu	Phe	Phe	Asn
				405					410					415	
Asp	Asp	Pro	Asn	Arg	Thr	Leu	Tyr	Asn	Tyr	Leu	Asn	Ile	Ala	Glu	Ile
			420					425					430		
Glu	Asp	Lys	Asn	Pro	Leu	Arg	Ala	Phe	Tyr	Glu	Cys	Ile	Ser	Asn	Gly
		435					440					445			
Gly	Asn	Tyr	Glu	Glu	Cys	Leu	Lys	Leu	Ile	Lys	Asp	Lys	Lys	Leu	Gln
	450				455						460				
Asp	Gln	Met	Lys	Lys	Thr	Leu	Glu	Ala	Tyr	Asn	Asp	Cys	Ile	Lys	Asn
465					470					475					480
Ala	Lys	Thr	Glu	Glu	Glu	Arg	Ile	Lys	Cys	Leu	Asp	Leu	Ile	Lys	Asp
				485					490					495	
Glu	Asn	Leu	Lys	Lys	Ser	Leu	Leu	Asn	Gln	Gln	Lys	Val	Gln	Val	Ala
			500					505					510		
Leu	Asp	Cys	Leu	Lys	Asn	Ala	Lys	Thr	Asp	Glu	Glu	Arg	Asn	Glu	Cys
		515					520					525			
Leu	Lys	Leu	Ile	Asn	Asp	Pro	Glu	Ile	Arg	Glu	Lys	Phe	Arg	Lys	Glu
	530				535						540				
Leu	Glu	Leu	Gln	Lys	Glu	Leu	Gln	Glu	Tyr	Lys	Asp	Cys	Ile	Lys	Asn
545				550						555					560
Ala	Lys	Thr	Glu	Ala	Glu	Lys	Asn	Lys	Cys	Leu	Lys	Gly	Leu	Ser	Lys
				565					570					575	
Glu	Ala	Ile	Glu	Arg	Leu	Lys	Gln	Gln	Ala	Leu	Asp	Cys	Leu	Lys	Asn
			580					585					590		
Ala	Lys	Thr	Asp	Glu	Glu	Arg	Asn	Glu	Cys	Leu	Lys	Asn	Ile	Pro	Gln
		595					600					605			
Asp	Leu	Gln	Lys	Glu	Leu	Leu	Ala	Asp	Met	Ser	Val	Lys	Ala	Tyr	Lys
	610					615					620				
Asp	Cys	Val	Ser	Lys	Ala	Arg	Asn	Glu	Lys	Glu	Lys	Gln	Glu	Cys	Glu
625				630						635					640
Lys	Leu	Leu	Thr	Pro	Glu	Ala	Arg	Lys	Lys	Leu	Glu	Gln	Gln	Val	Leu
				645					650					655	
Asp	Cys	Leu	Lys	Asn	Ala	Lys	Thr	Asp	Glu	Glu	Arg	Lys	Lys	Cys	Leu
			660					665					670		
Lys	Asp	Leu	Pro	Lys	Asp	Leu	Gln	Ser	Asp	Ile	Leu	Ala	Lys	Glu	Ser
		675					680					685			
Leu	Lys	Ala	Tyr	Lys	Asp	Cys	Val	Ser	Gln	Ala	Lys	Thr	Glu	Ala	Glu
	690					695					700				
Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Lys	Lys	Leu	Leu
705				710						715					720
Glu	Glu	Glu	Ala	Lys	Glu	Ser	Val	Lys	Ala	Tyr	Leu	Asp	Cys	Val	Ser
				725					730					735	
Gln	Ala	Lys	Thr	Glu	Ala	Glu	Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr
			740					745					750		

Leu 865	Leu	Glu	Glu	Ala	Lys	Lys	Ser	Val	Lys	Ala	Xaa	Leu	Asp	Cys	Val
Ser 885	Gln	Ala	Lys	Thr	Glu	Ala	Glu	Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu
Thr 900	Pro	Glu	Ala	Arg	Lys	Leu	Leu	Glu	Glu	Ala	Lys	Glu	Ser	Val	Lys
Ala 915	Tyr	Lys	Asp	Cys	Val	Ser	Lys	Ala	Arg	Asn	Glu	Lys	Glu	Lys	Lys
Glu 930	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Lys	Lys	Leu	Leu	Glu	Gln
Gln 945	Val	Leu	Asp	Cys	Leu	Lys	Asn	Ala	Lys	Thr	Glu	Ala	Asp	Lys	Lys
Arg 965	Cys	Val	Lys	Asp	Leu	Pro	Lys	Asp	Leu	Gln	Lys	Lys	Val	Leu	Ala
Lys 980	Glu	Ser	Val	Lys	Ala	Tyr	Leu	Asp	Cys	Val	Ser	Arg	Ala	Arg	Asn
Glu 995	Lys	Glu	Lys	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Lys
Lys 1010	Leu	Leu	Glu	Glu	Ala	Lys	Glu	Ser	Leu	Lys	Ala	Tyr	Lys	Asp	Cys
Leu 1025	Ser	Gln	Ala	Arg	Asn	Glu	Glu	Glu	Arg	Arg	Ala	Cys	Glu	Lys	Leu
Leu 1045	Thr	Pro	Glu	Ala	Arg	Lys	Leu	Leu	Glu	Gln	Glu	Val	Lys	Lys	Ser
Ile 1060	Lys	Ala	Tyr	Leu	Asp	Cys	Val	Ser	Arg	Ala	Arg	Asn	Glu	Lys	Glu
Lys 1075	Lys	Glu	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Arg	Lys	Phe	Leu
Ala 1090	Lys	Gln	Val	Leu	Asn	Cys	Leu	Glu	Lys	Ala	Gly	Asn	Glu	Glu	Glu
Arg 1105	Lys	Ala	Cys	Leu	Lys	Asn	Leu	Pro	Lys	Asp	Leu	Gln	Glu	Asn	Ile
Leu 1125	Ala	Lys	Glu	Ser	Leu	Lys	Ala	Tyr	Lys	Asp	Cys	Leu	Ser	Gln	Ala
Arg 1140	Asn	Glu	Glu	Glu	Arg	Arg	Ala	Cys	Glu	Lys	Leu	Leu	Thr	Pro	Glu
Ala 1155	Arg	Lys	Leu	Leu	Glu	Gln	Glu	Val	Lys	Lys	Ser	Val	Lys	Ala	Tyr
Leu 1170	Asp	Cys	Val	Ser	Arg	Ala	Arg	Asn	Glu	Lys	Glu	Lys	Lys	Glu	Cys
Glu 1185	Lys	Leu	Leu	Thr	Pro	Glu	Ala	Arg	Lys	Phe	Leu	Ala	Lys	Glu	Leu
Gln 1205	Gln	Lys	Asp	Lys	Ala	Ile	Lys	Asp	Cys	Leu	Lys	Asn	Ala	Asp	Pro
Asn 1220	Asp	Arg	Ala	Ala	Ile	Met	Lys	Cys	Leu	Asp	Gly	Leu	Ser	Asp	Glu
Glu 1235	Lys	Leu	Lys	Tyr	Leu	Gln	Glu	Ala	Arg	Glu	Lys	Ala	Val	Ala	Asp
Cys 1250	Leu	Ala	Met	Ala	Lys	Thr	Asp	Glu	Glu	Lys	Arg	Lys	Cys	Gln	Asn
Leu 1265	Tyr	Ser	Asp	Leu	Ile	Gln	Glu	Ile	Gln	Asn	Lys	Arg	Thr	Gln	Asn
Lys 1285	Gln	Asn	Gln	Leu	Ser	Lys	Thr	Glu	Arg	Leu	His	Gln	Ala	Ser	Glu
Cys 1300	Leu	Asp	Asn	Leu	Asp	Asp	Pro	Thr	Asp	Gln	Glu	Ala	Ile	Glu	Gln
Cys 1315	Leu	Glu	Gly	Leu	Ser	Asp	Ser	Glu	Arg	Ala	Leu	Ile	Leu	Gly	Ile

Lys	Arg	Gln	Ala	Asp	Glu	Val	Asp	Leu	Ile	Tyr	Ser	Asp	Leu	Arg	Asn
1330						1335				1340					
Arg	Lys	Thr	Phe	Asp	Asn	Met	Ala	Ala	Lys	Gly	Tyr	Pro	Leu	Leu	Pro
345					1350					1355					1360
Met	Asp	Phe	Lys	Asn	Gly	Gly	Asp	Ile	Ala	Thr	Ile	Asn	Ala	Thr	Asn
				1365					1370					1375	
Val	Asp	Ala	Asp	Lys	Ile	Ala	Ser	Asp	Asn	Pro	Ile	Tyr	Ala	Ser	Ile
			1380					1385				1390			
Glu	Pro	Asp	Ile	Ala	Lys	Gln	Tyr	Glu	Thr	Glu	Lys	Thr	Ile	Lys	Asp
		1395				1400						1405			
Lys	Asn	Leu	Glu	Ala	Lys	Leu	Ala	Lys	Ala	Leu	Gly	Gly	Asn	Lys	Lys
1410						1415				1420					
Asp	Asp	Asp	Lys	Glu	Lys	Ser	Lys	Lys	Ser	Thr	Ala	Glu	Ala	Lys	Ala
425					1430					1435					1440
Glu	Asn	Asn	Lys	Ile	Asp	Lys	Asp	Val	Ala	Glu	Thr	Ala	Lys	Asn	Ile
				1445					1450					1455	
Ser	Glu	Ile	Ala	Leu	Lys	Asn	Lys	Lys	Glu	Lys	Ser	Gly	Glu	Phe	Val
		1460					1465						1470		
Asp	Glu	Asn	Gly	Asn	Pro	Ile	Asp	Asp	Lys	Lys	Lys	Ala	Glu	Lys	Gln
		1475				1480						1485			
Asp	Glu	Thr	Ser	Pro	Val	Lys	Gln	Ala	Phe	Ile	Gly	Lys	Ser	Asp	Pro
1490					1495					1500					
Thr	Phe	Val	Leu	Ala	Gln	Tyr	Thr	Pro	Ile	Glu	Ile	Thr	Leu	Thr	Ser
505					1510					1515					1520
Lys	Val	Asp	Ala	Thr	Leu	Thr	Gly	Ile	Val	Ser	Gly	Val	Val	Ala	Lys
				1525					1530					1535	
Asp	Val	Trp	Asn	Met	Asn	Gly	Thr	Met	Ile	Leu	Leu	Asp	Lys	Gly	Thr
		1540						1545					1550		
Lys	Val	Tyr	Gly	Asn	Tyr	Gln	Ser	Val	Lys	Gly	Gly	Thr	Pro	Ile	Met
		1555				1560						1565			
Thr	Arg	Leu	Met	Ile	Val	Phe	Thr	Lys	Ala	Ile	Thr	Pro	Asp	Gly	Val
1570					1575					1580					
Ile	Ile	Pro	Leu	Ala	Asn	Ala	Gln	Ala	Ala	Gly	Met	Leu	Gly	Glu	Ala
585					1590					1595					1600
Gly	Val	Asp	Gly	Tyr	Val	Asn	Asn	His	Phe	Met	Lys	Arg	Ile	Gly	Phe
			1605						1610					1615	
Ala	Val	Ile	Ala	Ser	Val	Val	Asn	Ser	Phe	Leu	Gln	Thr	Ala	Pro	Ile
			1620					1625					1630		
Ile	Ala	Leu	Asp	Lys	Leu	Ile	Gly	Leu	Gly	Lys	Gly	Arg	Ser	Glu	Arg
		1635				1640						1645			
Thr	Pro	Glu	Phe	Asn	Tyr	Ala	Leu	Gly	Gln	Ala	Ile	Asn	Gly	Ser	Met
1650					1655					1660					
Gln	Ser	Ser	Ala	Gln	Met	Ser	Asn	Gln	Ile	Leu	Gly	Gln	Leu	Met	Asn
665															

(2) INFORMATION FOR SEQ ID NO:625:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 877 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 22...825
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

AACAAATAAA GGAGTATTAA A ATG AAA CAA AGT TTG CGC GAA CAA AAA TTA	51
Met Lys Gln Ser Leu Arg Glu Gln Lys Leu	
1 5 10	
TTG AAA ATT TTA GAA AAT GAT GTC TTG ACG ATT TTG GAT AGT TTT TCT	99
Leu Lys Ile Leu Glu Asn Asp Val Leu Thr Ile Leu Asp Ser Phe Ser	
15 20 25	
AAT TAT CTT TTT GAA CTG AGA GAA GAG TTG GAC TTC ATA GAA GAA GAA	147
Asn Tyr Leu Phe Glu Leu Arg Glu Glu Leu Asp Phe Ile Glu Glu Glu	
30 35 40	
ATG GAA GGT GAA ATC ACC GAA CAA AAC CTT ACC GCT CTT TAT GAT TTT	195
Met Glu Gly Glu Ile Thr Glu Gln Asn Leu Thr Ala Leu Tyr Asp Phe	
45 50 55	
TCT AAT TTC TTA GAA GAC CAT GTC AAT GTA TTT TAT GAG AAT GTT TTG	243
Ser Asn Phe Leu Glu Asp His Val Asn Val Phe Tyr Glu Asn Val Leu	
60 65 70	
AAT ATA GAT GAT GTC AAA ACA GAA CAC CTT TAT TCA GGT CTC ATA GAT	291
Asn Ile Asp Asp Val Lys Thr Glu His Leu Tyr Ser Gly Leu Ile Asp	
75 80 85 90	
AGT CTT AAC GCT AAT CTT CAC TTT GTC AAG TCA TTT CTC AGT AAT CAG	339
Ser Leu Asn Ala Asn Leu His Phe Val Lys Ser Phe Leu Ser Asn Gln	
95 100 105	
GAT TTA GAC TTC CGC TTT TTT AAG GAA ATA AAC GAT GGG CAA GAT CCC	387
Asp Leu Asp Phe Arg Phe Phe Lys Glu Ile Asn Asp Gly Gln Asp Pro	
110 115 120	
CAA AAA ACA TTA TCA AGA TTA ATT CCT CTT CAA AGT GGG AAA AAT GAT	435
Gln Lys Thr Leu Ser Arg Leu Ile Pro Leu Gln Ser Gly Lys Asn Asp	
125 130 135	
GCA AGC TCG TTT AAA GCC AAT AAT TCT TTT GTT TCA TTA GTT TAT GTT	483
Ala Ser Ser Phe Lys Ala Asn Asn Ser Phe Val Ser Leu Val Tyr Val	
140 145 150	
TAT GTT TAC TTC ATG CTA GAA ACT ATC ATG CAG TCG TAT AGG ATT CTC	531
Tyr Val Tyr Phe Met Leu Glu Thr Ile Met Gln Ser Tyr Arg Ile Leu	
155 160 165 170	
AGA TTG CTA GAA AAA CCT ATC AAT AAC AAC ATA AGC GAG GAC ATG CAG	579

Arg	Leu	Leu	Glu	Lys	Pro	Ile	Asn	Asn	Asn	Ile	Ser	Glu	Asp	Met	Gln		
				175					180					185			
AAC	GAT	ATA	GAG	AAT	TTT	TTT	GTT	CAA	GCG	AAT	TTT	TTA	GAA	TAC	TAT	627	
Asn	Asp	Ile	Glu	Asn	Phe	Phe	Val	Gln	Ala	Asn	Phe	Leu	Glu	Tyr	Tyr		
			190					195					200				
GTT	CAG	AAC	AAA	ATA	TAC	CCA	ACC	AAT	CAT	GCC	TAT	GAC	TTC	ACG	CAT	675	
Val	Gln	Asn	Lys	Ile	Tyr	Pro	Thr	Asn	His	Ala	Tyr	Asp	Phe	Thr	His		
			205				210					215					
TTG	ATC	ATG	GAC	TCC	ATT	ATT	CCT	AAT	TGG	ATT	CAA	ACT	GAT	ATG	AGC	723	
Leu	Ile	Met	Asp	Ser	Ile	Ile	Pro	Asn	Trp	Ile	Gln	Thr	Asp	Met	Ser		
	220					225					230						
GTT	GAA	GCT	AAA	AAG	AAA	GAG	CTT	TTT	GAA	AAA	TAT	TTT	CAA	AAC	ATT	771	
Val	Glu	Ala	Lys	Lys	Lys	Glu	Leu	Phe	Glu	Lys	Tyr	Phe	Gln	Asn	Ile		
	235				240					245					250		
GAT	GAA	GTA	ACA	AAC	AAA	ATG	CTC	GAT	CAA	AAA	ANT	CAA	AAC	AAA	AGT	819	
Asp	Glu	Val	Thr	Asn	Lys	Met	Leu	Asp	Gln	Lys	Xaa	Gln	Asn	Lys	Ser		
				255					260					265			
AAC	GAT	TGAGTGGCGT	TAATGCGCTA	GAATAGTGCT	AAAAATAAGA	ATAAAGGAGT	CA	877									
Asn	Asp																

877

(2) INFORMATION FOR SEQ ID NO:626:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 268 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

Met	Lys	Gln	Ser	Leu	Arg	Glu	Gln	Lys	Leu	Leu	Lys	Ile	Leu	Glu	Asn		
1				5					10					15			
Asp	Val	Leu	Thr	Ile	Leu	Asp	Ser	Phe	Ser	Asn	Tyr	Leu	Phe	Glu	Leu		
		20						25					30				
Arg	Glu	Glu	Leu	Asp	Phe	Ile	Glu	Glu	Met	Glu	Gly	Glu	Ile	Thr			
		35					40				45						
Glu	Gln	Asn	Leu	Thr	Ala	Leu	Tyr	Asp	Phe	Ser	Asn	Phe	Leu	Glu	Asp		
		50				55					60						
His	Val	Asn	Val	Phe	Tyr	Glu	Asn	Val	Leu	Asn	Ile	Asp	Asp	Val	Lys		
				70						75				80			
Thr	Glu	His	Leu	Tyr	Ser	Gly	Leu	Ile	Asp	Ser	Leu	Asn	Ala	Asn	Leu		
			85						90					95			
His	Phe	Val	Lys	Ser	Phe	Leu	Ser	Asn	Gln	Asp	Leu	Asp	Phe	Arg	Phe		
			100					105					110				
Phe	Lys	Glu	Ile	Asn	Asp	Gly	Gln	Asp	Pro	Gln	Lys	Thr	Leu	Ser	Arg		
		115				120					125						
Leu	Ile	Pro	Leu	Gln	Ser	Gly	Lys	Asn	Asp	Ala	Ser	Ser	Phe	Lys	Ala		

130	135	140
Asn Asn Ser Phe Val	Ser Leu Val Tyr Val	Tyr Val Tyr Phe Met Leu
145	150	155
Glu Thr Ile Met Gln	Ser Tyr Arg Ile Leu Arg	Leu Leu Glu Lys Pro
165	170	175
Ile Asn Asn Asn Ile	Ser Glu Asp Met Gln Asn Asp	Ile Glu Asn Phe
180	185	190
Phe Val Gln Ala Asn	Phe Leu Glu Tyr Tyr Val	Gln Asn Lys Ile Tyr
195	200	205
Pro Thr Asn His Ala	Tyr Asp Phe Thr His Leu	Ile Met Asp Ser Ile
210	215	220
Ile Pro Asn Trp Ile	Gln Thr Asp Met Ser Val	Glu Ala Lys Lys Lys
225	230	235
Glu Leu Phe Glu Lys	Tyr Phe Gln Asn Ile Asp	Glu Val Thr Asn Lys
245	250	255
Met Leu Asp Gln Lys	Xaa Gln Asn Lys Ser	Asn Asp
260	265	

(2) INFORMATION FOR SEQ ID NO:627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 736 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 26...706
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

AAAAAATCAA TAAAGGGGT TTAGC ATG CAA GCA GTA ATT TAT GGC AAG CAA	52
Met Gln Ala Val Ile Tyr Gly Lys Gln	
1 5	
GTG ATT ATG CAC CTT CTA AAC TCT CAT CAA GAA AAA TTG CAA GAA ATC	100
Val Ile Met His Leu Leu Asn Ser His Gln Glu Lys Leu Gln Glu Ile	
10 15 20 25	
TAT CTT TCT AAA GAA ATA GAC AAG AAA CTT TTT TTC GCG CTC AAA AAA	148
Tyr Leu Ser Lys Glu Ile Asp Lys Lys Leu Phe Phe Ala Leu Lys Lys	
30 35 40	
GCA TGC CCT AAT ATC ATC AAA GTG GAT AAT AAA AAA GCG CAA AGC TTG	196
Ala Cys Pro Asn Ile Ile Lys Val Asp Asn Lys Lys Ala Gln Ser Leu	
45 50 55	
GCT AAG GGG GGG AAT CAT CAA GGG GTT TTG GCT AAG GTG GAA CTG CCC	244
Ala Lys Gly Gly Asn His Gln Gly Val Leu Ala Lys Val Glu Leu Pro	
60 65 70	
TTA GCG GTT TCT TTA AAA GAG GTT AAA AAA GCT CAA AAA CTT TTG GTG	292
Leu Ala Val Ser Leu Lys Glu Val Lys Lys Ala Gln Lys Leu Leu Val	

75	80	85	
CTT TGC GGG ATT ACG GAT GTG GGG AAT ATT GGA GGT ATT TTT AGG AGC			340
Leu Cys Gly Ile Thr Asp Val Gly Asn Ile Gly Gly Ile Phe Arg Ser			
90	95	100	105
GCG TAT TGC TTA GGA ATG GGT GGC GTT ATT TTA GAT TTT GCT AAA GAA			388
Ala Tyr Cys Leu Gly Met Gly Gly Val Ile Leu Asp Phe Ala Lys Glu			
	110	115	120
TTG GCT TAT GAG GGG ATT GTG CGA TCC AGC TTG GGG CTT ATG TAT GAT			436
Leu Ala Tyr Glu Gly Ile Val Arg Ser Ser Leu Gly Leu Met Tyr Asp			
	125	130	135
TTG CCT TTT AGC GTT ATG CCT AAC ACG CTG GAT TTA ATC AAT GAA TTG			484
Leu Pro Phe Ser Val Met Pro Asn Thr Leu Asp Leu Ile Asn Glu Leu			
	140	145	150
AAA ACG AGC GGG TTT TTA TGT TTG GGC GCG AGC ATG CAA GGC TCT AGT			532
Lys Thr Ser Gly Phe Leu Cys Leu Gly Ala Ser Met Gln Gly Ser Ser			
	155	160	165
CAA ATA GAA AAT CTA TCC TTA AAA AAA TGC GCT CTT TTT TTG GGG AGC			580
Gln Ile Glu Asn Leu Ser Leu Lys Lys Cys Ala Leu Phe Leu Gly Ser			
	170	175	185
GAG CAT GAG GGG TTG TCT AAA AAA ATC CTT GCT AAA ATG GAT ACT ATA			628
Glu His Glu Gly Leu Ser Lys Lys Ile Leu Ala Lys Met Asp Thr Ile			
	190	195	200
TTG AGC GTA AAA ATG CGA AGA GAT TTT GAT TCG CTC AAT GTG AGC GTG			676
Leu Ser Val Lys Met Arg Arg Asp Phe Asp Ser Leu Asn Val Ser Val			
	205	210	215
GCA GCA GGG ATC TTA ATG GAT AAA ATC AAC TAGGTGGTCA ATTGAATGGA ACA			729
Ala Ala Gly Ile Leu Met Asp Lys Ile Asn			
	220	225	
GAATAAA			736

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

Met	Gln	Ala	Val	Ile	Tyr	Gly	Lys	Gln	Val	Ile	Met	His	Leu	Leu	Asn
1				5					10					15	
Ser	His	Gln	Glu	Lys	Leu	Gln	Glu	Ile	Tyr	Leu	Ser	Lys	Glu	Ile	Asp
		20						25					30		
Lys	Lys	Leu	Phe	Phe	Ala	Leu	Lys	Lys	Ala	Cys	Pro	Asn	Ile	Ile	Lys
		35					40					45			

Val	Asp	Asn	Lys	Lys	Ala	Gln	Ser	Leu	Ala	Lys	Gly	Gly	Asn	His	Gln
50						55					60				
Gly	Val	Leu	Ala	Lys	Val	Glu	Leu	Pro	Leu	Ala	Val	Ser	Leu	Lys	Glu
65					70					75					80
Val	Lys	Lys	Ala	Gln	Lys	Leu	Leu	Val	Leu	Cys	Gly	Ile	Thr	Asp	Val
				85					90					95	
Gly	Asn	Ile	Gly	Gly	Ile	Phe	Arg	Ser	Ala	Tyr	Cys	Leu	Gly	Met	Gly
			100					105					110		
Gly	Val	Ile	Leu	Asp	Phe	Ala	Lys	Glu	Leu	Ala	Tyr	Glu	Gly	Ile	Val
			115					120				125			
Arg	Ser	Ser	Leu	Gly	Leu	Met	Tyr	Asp	Leu	Pro	Phe	Ser	Val	Met	Pro
130						135					140				
Asn	Thr	Leu	Asp	Leu	Ile	Asn	Glu	Leu	Lys	Thr	Ser	Gly	Phe	Leu	Cys
145					150					155					160
Leu	Gly	Ala	Ser	Met	Gln	Gly	Ser	Ser	Gln	Ile	Glu	Asn	Leu	Ser	Leu
				165					170					175	
Lys	Lys	Cys	Ala	Leu	Phe	Leu	Gly	Ser	Glu	His	Glu	Gly	Leu	Ser	Lys
			180					185					190		
Lys	Ile	Leu	Ala	Lys	Met	Asp	Thr	Ile	Leu	Ser	Val	Lys	Met	Arg	Arg
			195				200					205			
Asp	Phe	Asp	Ser	Leu	Asn	Val	Ser	Val	Ala	Ala	Gly	Ile	Leu	Met	Asp
210						215					220				
Lys	Ile	Asn													
225															

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 30...290
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

AACCATGCCT	TTTCATCGTC	TCTATCAAAA	ATG	TTA	GGG	TCT	AAA	ACA	TAT	TCC	53					
			Met	Leu	Gly	Ser	Lys	Thr	Tyr	Ser						
			1				5									
GTT	TTA	AGA	TCG	TAT	GAA	AAA	ACA	TTC	TCG	CCT	GAA	GAG	CTT	TGC	ATT	101
Val	Leu	Arg	Ser	Tyr	Glu	Lys	Thr	Phe	Ser	Pro	Glu	Glu	Leu	Cys	Ile	
	10					15					20					
TTA	ATG	GGC	AAA	ACA	TAC	GAA	TAC	CCC	ATC	ATG	CTT	AAA	GAA	TTA	TTG	149
Leu	Met	Gly	Lys	Thr	Tyr	Glu	Tyr	Pro	Ile	Met	Leu	Lys	Glu	Leu	Leu	
	25				30				35					40		
ATG	CTT	TTG	GCA	AAC	GCT	AGG	GGA	TTG	CTT	GAA	GCC	TTG	AAA	GTG	ATT	197
Met	Leu	Leu	Ala	Asn	Ala	Arg	Gly	Leu	Leu	Glu	Ala	Leu	Lys	Val	Ile	
			45					50						55		

TTC AAC ATG CTT GGC TTG TCA AAA TTA AAA GAC AAA AGC CCG TTT TCT 245
Phe Asn Met Leu Gly Leu Ser Lys Leu Lys Asp Lys Ser Pro Phe Ser
60 65 70

TTG AGA GTG TTG AGC AGT TTC AAG GAA TCC AAA CGC CCC ATT ACA TAGAA 295
Leu Arg Val Leu Ser Ser Phe Lys Glu Ser Lys Arg Pro Ile Thr
75 80 85

AGCCTTACGA TTTTAAACA AACGCTCTAA AAAAAGCTTG TTCGTATGA 344

(2) INFORMATION FOR SEQ ID NO:630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

Met Leu Gly Ser Lys Thr Tyr Ser Val Leu Arg Ser Tyr Glu Lys Thr
1 5 10 15
Phe Ser Pro Glu Glu Leu Cys Ile Leu Met Gly Lys Thr Tyr Glu Tyr
20 25 30
Pro Ile Met Leu Lys Glu Leu Leu Met Leu Leu Ala Asn Ala Arg Gly
35 40 45
Leu Leu Glu Ala Leu Lys Val Ile Phe Asn Met Leu Gly Leu Ser Lys
50 55 60
Leu Lys Asp Lys Ser Pro Phe Ser Leu Arg Val Leu Ser Ser Phe Lys
65 70 75 80
Glu Ser Lys Arg Pro Ile Thr
85

(2) INFORMATION FOR SEQ ID NO:631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

CTGAATTCGA ATGAAAAGAA TTTTAGTCTC T 31

(2) INFORMATION FOR SEQ ID NO:632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

CCGCTCGAGT TAAAACTCAT AATTCAAAT

29

(2) INFORMATION FOR SEQ ID NO:633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

CGCGGATCCG AAGACATGTG CAACCGATG

29

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

CCGCTCGAGC TAAAAGTTTT GCAAAATCAC

30

(2) INFORMATION FOR SEQ ID NO:635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

CGCGGATCCG ATTTTACTTG AAAAATTTAA AC

32

(2) INFORMATION FOR SEQ ID NO:636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

CCGCTCGAGT TAGAAAGTGT AGTTCAAATA C

31

(2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

GCGGATCCTT TTCTTCAATG TTTG

24

(2) INFORMATION FOR SEQ ID NO:638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

CCGCTCGAGT CAAAGTTTTA AACAAATTC

29